STIC Search Report
Biotech-Chem Library

USPTO

TO: Patricia Duffy
Location: REM-3B05&3C18
Art Unit: 1645
Friday, April 08, 2005

Case Serial Number: 10/063563

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

paul.schulwitz@uspto.gov

Search Notes

AA

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149934

In re: 10/063,563

Please search SEQ ID NO:56 and oligomers thereof.
Please include a commercial and interference search.
Standard SPDI printout.

CRFG

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

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OM protein - protein search, using sw model
                    GenCore version 5.1.6
Run on:      April 7, 2005, 04:43:49 ; Search time 172 Seconds
                              (without alignments)
                              173.143 Million cell updates/sec

Title:          US-10-063-563-56
Perfect score:  77
Sequence:       1 MGPVKQLKRMFEPTRLIATI.........LSFIPFARDAVKKCFAVCLA 77
Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0
Searched:       2105692 seqs, 38760381 residues
Total number of hits satisfying chosen parameters:       2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Database :      A_Geneseq_16Dec04.*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
                              SUMMARIES

No.     Score  Match Length DB  ID                       Description
RESULT 1
ID   AAY66715 standard; protein; 77 AA.
DE   Membrane-bound protein PRO1027.
PN   WO963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 77;  DB 3;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 2
ID   AAU29130 standard; protein; 77 AA.
DE   Human PRO polypeptide sequence #107.
PN   WO20016848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 77;  DB 4;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 3
ID   AAB87553 standard; protein; 77 AA.
DE   Human PRO1027.
PN   WO20011618-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 77;  DB 4;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 4
ID   AAB65238 standard; protein; 77 AA.
DE   Human PRO1027 (UNQ512) protein sequence SEQ ID NO:283.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 77;  DB 4;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 5
ID   ABG95878 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 77;  DB 5;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 6
ID   ABU58506 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003027272-A1.
PD   06-FEB-2003.

Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 7
ID   ABU88054 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032127-A1.
PD   13-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 8
ID   ABU84369 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032112-A1.
PD   13-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 9
ID   ABR66243 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027278-A1.
PD   06-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 10
ID   ABR65633 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036159-A1.
PD   20-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 11
ID   ABU99573 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040070-A1.
PD   27-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 12
ID   ABU58053 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003027163-A1.
PD   06-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 13
ID   ABU59131 standard; protein; 77 AA.
DE   Novel human secreted or transmembrane protein PRO1027.
PN   US2003013252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 14
ID   ABU82643 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003032023-A1.
PD   13-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 15
ID   ABU82812 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032113-A1.
PD   13-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 16
ID   ABU89933 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036147-A1.
PD   20-FEB-2003.
Query Match        100.0%;   Score 77;  DB 6;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
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RESULT 17
ID   ABR68182 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027264-A1.
PD   06-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 18
ID   ABU60562 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein, #115.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 19
ID   ABU96235 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036144-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 20
ID   ABU92666 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036149-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 21
ID   ABO08743 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044923-A1.
PD   06-MAR-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 22
ID   ABO02795 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040062-A1.
PD   27-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 23
ID   ABR74949 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044056-A1.
PD   06-MAR-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 24
ID   ABR94711 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2002103125-A1.
PD   01-AUG-2002.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 25
ID   ABU13944 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003018173-A1.
PD   (GETH) GENENTECH LTD.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 26
ID   ABU85684 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 27
ID   ABU98844 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003013153-A1.
PD   16-JAN-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 28
ID   ABU98059 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003017544-A1.
PD   23-JAN-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 29
ID   ABU91765 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003027277-A1.
PD   06-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 30
ID   ABU89458 standard; protein; 77 AA.
DE   Human PRO polypeptide #107
PN   US2003036141-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 31
ID   ABU86299 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 32
ID   ABU67512 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 33
ID   ABU80540 standard; protein; 77 AA.
DE   Human PRO protein #107.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 34
ID   ABU72529 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003003531-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 35
ID   ABU90903 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 6;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 36
ID   ABO33962 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003009013-A1.
PD   09-JAN-2003.

PA   (GETH) GENENTECH INC.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 37
ID   ABR99458 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040063-A1.
PD   27-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 38
ID   ABR98848 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040064-A1.
PD   27-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 39
ID   ABO16371 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003027267-A1.
PD   06-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 40
ID   ABR92271 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036160-A1.
PD   20-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 41
ID   ABO18912 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044925-A1.
PD   06-MAR-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 42
ID   ABR78333 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054474-A1.
PD   20-MAR-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
PA   (GETH) GENENTECH INC.
RESULT 43
ID   ABU71979 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003018183-A1.
PD   23-JAN-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
PA   (GETH) GENENTECH INC.
RESULT 44
ID   ABU85069 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032114-A1.
PD   13-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 45
ID   ABO00208 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032101-A1.
PD   13-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 46
ID   ABO11540 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036124-A1.
PD   20-FEB-2003.

      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 47
ID   ABO02185 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040054-A1.
PD   27-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 48
ID   ABU88759 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036133-A1.
PD   20-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 49
ID   ABU83454 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036134-A1.
PD   20-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 50
ID   ABO06255 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003022294-A1.
PD   30-JAN-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 51
ID   ABR59291 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027275-A1.
PD   06-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 52
ID   ABO09953 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003027324-A1.
PD   06-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 53
ID   ABO19217 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036118-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 54
ID   ABO11235 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036123-A1.
PD   20-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 55
ID   ABR66853 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036148-A1.
PD   20-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 56
ID   ABO16066 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040060-A1.
PD   27-FEB-2003.
      Query Match   100.0%; Score 77; DB 6; Length 77;
      Best Local Similarity   100.0%; Pred. No. 4.4e-75;

RESULT 57
ID AB013772 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003044916-Al.
PD 06-MAR-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 58
ID ABU71533 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027.
PN US2003013855-Al.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 59
ID ABU65675 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, SEQ ID 214.
PN US2003036156-Al.
PD 20-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 60
ID AB007523 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032117-Al.
PD 13-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 61
ID AB003710 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036128-Al.
PD 20-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 62
ID ABR67158 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027266-Al.
PD 06-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 63
ID AB015761 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003054483-Al.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 64
ID ABU56042 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, PRO1027.
PN US2003022298-Al.
PD 30-JAN-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 65
ID ABU72314 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2002182638-Al.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 66
ID ABU65370 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003033102-Al.
PD 13-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 67
ID ABU95315 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036117-Al.
PD 20-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 68
ID ABU71218 standard; protein; 77 AA.
DE Human PRO1027 protein.
PN US2003036143-Al.
PD 20-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 69
ID AB007828 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032130-Al.
PD 13-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 70
ID ABR70069 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032138-Al.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 71
ID ABR69402 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003036132-Al.
PD 20-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 72
ID AB001543 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003008853-Al.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 73
ID ABU81345 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003017542-Al.
PD 23-JAN-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 74
ID ABR60142 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032137-Al.
PD 13-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 75
ID ABU90987 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003018168-Al.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 76
ID ABR67877 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027269-Al.
PD 06-FEB-2003.
Query Match 100.0%; Score 77; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 77
ID   ABR65265 standard; protein; 77 AA.
DB   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027268-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 78
ID   ABR68487 standard; protein; 77 AA.
DB   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027274-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 79
ID   ABR71899 standard; protein; 77 AA.
DB   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 80
ID   ABU59278 standard; protein; 77 AA.
DB   Human secreted/transmembrane protein, #115.
PN   US2003027162-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 81
ID   ABU85379 standard; protein; 77 AA.
DB   Human PRO polypeptide #107.
PN   US2003022295-A1.
PD   30-JAN-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 82
ID   ABU89069 standard; protein; 77 AA.
DB   Human secreted/transmembrane protein (PRO) #107.
PN   US2003022297-A1.
PD   30-JAN-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 83
ID   ABU83149 standard; protein; 77 AA.
DB   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032105-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 84
ID   ABU95005 standard; protein; 77 AA.
DB   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032123-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 85
ID   ABU90553 standard; protein; 77 AA.
DB   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032108-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 86
ID   ABU84064 standard; protein; 77 AA.
DB   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032111-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 87
ID   ABU93715 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 88
ID   ABO25975 standard; protein; 77 AA.
DB   Human PRO1027 polypeptide.
PN   US2002127576-A1.
PD   12-SEP-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 89
ID   ABR64960 standard; protein; 77 AA.
DB   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027263-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 90
ID   ABO27308 standard; protein; 77 AA.
DB   Human secreted/transmembrane polypeptide PRO1027.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 91
ID   ABR68792 standard; protein; 77 AA.
DB   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027271-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 92
ID   ABO06608 standard; protein; 77 AA.
DB   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036125-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 93
ID   ABR99153 standard; protein; 77 AA.
DB   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040068-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 94
ID   ABU57037 standard; protein; 77 AA.
DB   Human PRO polypeptide #107.
PN   US2003027280-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 95
ID   ABU85989 standard; protein; 77 AA.
DB   Novel human secreted and transmembrane protein PRO1027.
PN   US2003022300-A1.
PD   30-JAN-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 96
ID   ABU82276 standard; protein; 77 AA.
DB   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036136-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;
RESULT 97
ID   ABU87287 standard; protein; 77 AA.

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DE   Human PRO polypeptide #107.
PN   US2003036138-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 98
ID   ABU83759 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032109-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 99
ID   ABO08133 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003040066-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 100
ID   ABU81844 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003032104-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 101
ID   ABU66008 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036157-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 102
PA   (GETH ) GENENTECH INC.
ID   ABU81173 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027.
PN   US2003027212-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 103
ID   ABR59837 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032120-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 104
ID   ABU94025 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036155-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 105
ID   ABU99878 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003022296-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 106
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 107
ID   ABR66548 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.


PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 108
ID   ABR90966 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040058-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 109
ID   ABO53288 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003027986-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 110
ID   ABU58984 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein, #115.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 111
ID   ABU94393 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003017540-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 112
ID   ABU79275 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032116-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 113
ID   ABU86604 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032129-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 114
ID   ABU86909 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032131-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 115
ID   ABU94698 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032103-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 116
ID   ABO04625 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032107-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 117
ID   ABR70374 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
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PN   US2003032139-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 118
ID   ABU92362 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003022187-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 119
ID   ABU98539 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003022301-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 120
ID   ABR65938 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 121
ID   ABR64655 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027262-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 122
ID   ABU59427 standard; protein; 77 AA.
DE   Novel human secreted or transmembrane protein PRO107.
PN   US2003027985-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 123
ID   ABU79580 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032110-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 124
ID   ABU92971 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036142-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 125
ID   ABU95930 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003036145-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 126
ID   ABU91150 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036154-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 127
ID   ABU90243 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036153-A1.
PD   20-FEB-2003.

     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 128
ID   ABO09658 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044931-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 129
ID   ABO10930 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036150-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 130
ID   ABR70984 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040069-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 131
ID   ABU98290 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 132
ID   ABU87592 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003022293-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 133
ID   ABU91460 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032128-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 134
ID   ABU89295 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 135
ID   ABU84674 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032116-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 136
ID   ABR69764 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032122-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 137
ID   ABU80141 standard; protein; 77 AA.
DE   Human PRO protein #107.
PN   US2003036139-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
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      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 138
ID    ABU82502 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2002183494-A1.
PD    05-DEC-2002.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 139
ID    ABU92193 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003017476-A1.
PD    23-JAN-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 140
ID    ABU93410 standard; protein; 77 AA.
DE    Human PRO polypeptide #107.
PN    US2003017541-A1.
PD    23-JAN-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 141
ID    ABO09963 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003017543-A1.
PD    23-JAN-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 142
ID    ABO09048 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003036152-A1.
PD    20-FEB-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 143
ID    ABU96466 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003027993-A1.
PD    06-FEB-2003.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 144
ID    ABU10899 standard; protein; 77 AA.
DE    Human PRO polypeptide #85.
PN    US2002123463-A1.
PD    05-SEP-2002.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 145
ID    ABU10616 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2002127584-A1.
PD    12-SEP-2002.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 146
ID    ABU81651 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2002177164-A1.
PD    28-NOV-2002.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 147
ID    ABU72136 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003023042-A1.

PD    30-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 148
ID    ABU95625 standard; protein; 77 AA.
DE    Human PRO polypeptide #107.
PN    US2003032115-A1.
PD    13-FEB-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 149
ID    ABU96834 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003032140-A1.
PD    13-FEB-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 150
ID    ABR70679 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003040076-A1.
PD    27-FEB-2003.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 151
ID    ABO05030 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003008352-A1.
PD    09-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 152
ID    ABO08438 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003044922-A1.
PD    06-MAR-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 153
ID    ABU88590 standard; protein; 77 AA.
DE    Human secreted and transmembrane polypeptide PRO1027.
PN    US2002197615-A1.
PD    26-DEC-2002.
PA    (GETH ) GENENTECH INC.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 154
ID    ABO34104 standard; protein; 77 AA.
DE    Human PRO1027 polypeptide.
PN    US2003017981-A1.
PD    23-JAN-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 155
ID    ABO05645 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003032118-A1.
PD    13-FEB-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 156
ID    ABR74034 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003036135-A1.
PD    20-FEB-2003.
      Query Match        100.0%;  Score 77;  DB 6;  Length 77;
      Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 157
ID    ABR95626 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
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PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 158
ID ABR80923 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 159
ID ABR81228 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 160
ID ABM00924 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 161
ID ABR88526 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 162
ID ABM77347 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 163
ID ABO28831 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 164
ID ABO31576 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 165
ID ABM07993 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 166
ID ABO40473 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068682-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 167
ID ABO35898 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 168
ID ABO44037 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 169
ID ADA77966 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 170
ID ABM24832 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 171
ID ABO03100 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 172
ID ABR90356 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 173
ID ABM17270 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 174
ID ABR95016 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 175
ID ABR95321 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 77; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 176

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ID   ADB17113 standard; protein; 77 AA.
DE   Human transmembrane PRO polypeptide (SeqID 56).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
ID   ABO21559 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 178
ID   ABR97823 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 179
ID   ABR87611 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 180
ID   ABM77652 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 181
ID   ABM27882 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064440-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 182
ID   ABM06163 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 183
ID   ABM03669 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 184
ID   ABM35120 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 185
ID   ABM26357 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
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PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 186
ID   ABO48139 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049949-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 187
ID   ABR92881 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 188
ID   ABO24642 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 189
ID   ADA37794 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 190
ID   ABM11653 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 191
ID   ABM02754 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 192
ID   ABM16050 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 193
ID   ABO27611 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 194
ID   ABM29102 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068721-A1.
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PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 195
ID   ABM07078 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 196
ID   ABM21172 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 197
ID   ABM09518 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 198
ID   AB041388 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 199
ID   AB036203 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 200
ID   AB043732 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 201
ID   ABM76432 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003082717-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 202
ID   ABM76128 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 203
ID   ABM25747 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104542-A1.
PD   05-JUN-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;


     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 204
ID   ABM26052 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104543-A1.
PD   05-JUN-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 205
ID   ADA21480 standard; protein; 77 AA.
DE   Human secreted/transmembrane polypeptide PRO1027.
PN   US2003054404-A1.
PD   20-MAR-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 206
ID   AB003405 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036127-A1.
PD   20-FEB-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 207
ID   AB002490 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040061-A1.
PD   27-FEB-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 208
ID   AB044266 standard; protein; 77 AA.
DE   Human secreted/transmembrane polypeptide PRO 1027.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 209
ID   ABR90661 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036130-A1.
PD   20-FEB-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 210
ID   ABR73729 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 211
ID   AB016981 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 212
ID   ABR94406 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044917-A1.
PD   06-MAR-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
     Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 213
ID   ABR75913 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044929-A1.
PD   06-MAR-2003.
     Query Match           100.0%;  Score  77;  DB  6;  Length 77;
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     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 214
ID   ABR71289 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 215
ID   ABR93186 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 216
ID   ABR93491 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 217
ID   ADA10267 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein, PRO1027.
PN   US2003059831-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 218
ID   ABR87916 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 219
ID   ABO27916 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 220
ID   ABO30051 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 221
ID   ABO33260 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 222
ID   ABM04948 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 223

ID   ABM08908 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 224
ID   ABO36508 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 225
ID   ABO35593 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 226
ID   ABO39558 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 227
ID   ABM10433 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 228
ID   ABM11958 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 229
ID   ABO52104 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 230
ID   ABO52409 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 231
ID   ADA19918 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 232
ID   ABO23727 standard; protein; 77 AA.
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DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032134-A1.
PD   13-FEB-2003.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 233
ID   ADB17301 standard; protein; 77 AA.
DE   Human transmembrane PRO polypeptide (SeqID 56).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 234
ID   ADA17811 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 235
ID   ABR97213 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 236
ID   ABR87001 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 237
ID   ABM11043 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 238
ID   ABM28187 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 239
ID   ABO32186 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 240
ID   ABM15313 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 241
ID   ABM06468 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068709-A1.
PD   10-APR-2003.

PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 242
ID   ABM04279 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 243
ID   ABM22392 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 244
ID   ABM07688 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 245
ID   ABO40778 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 246
ID   ABM35425 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 247
ID   ABM33188 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 248
ID   ABO52714 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 249
ID   ABO50274 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 250
ID   ABU99268 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040055-A1.
PD   27-FEB-2003.
       Query Match   100.0%;   Score 77;   DB 6;   Length 77;
       Best Local Similarity 100.0%;   Pred. No. 4.4e-75;

RESULT 251
ID   AB004320 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036164-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 252
ID   AB005950 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040074-A1.
PD   27-FEB-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 253
ID   ABM18490 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 254
ID   ADA27919 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003054359-A1.
PD   20-MAR-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 255
ID   ABR97518 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 256
ID   ABR80618 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 257
ID   ABM01229 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 258
ID   ABR88831 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073169-A1.
PD   17-APR-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 259
ID   ABM13483 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064457-A1.
PD   03-APR-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 260
ID   ABM20867 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068711-A1.
PD   10-APR-2003.

PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 261
ID   AB041998 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 262
ID   AB042608 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 263
ID   ABM10128 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 264
ID   AB038643 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 265
ID   ABM32883 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 266
ID   ABM22697 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003087373-A1.
PD   08-MAY-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 267
ID   ABM74908 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096353-A1.
PD   22-MAY-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 268
ID   ADA79758 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003073173-A1.
PD   17-APR-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 269
ID   ABR96298 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054458-A1.
PD   20-MAR-2003.
     Query Match   100.0%;   Score 77;   DB 6;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 270
ID   ABM02449 standard; protein; 77 AA.

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DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 271
ID   ABR86391 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 272
ID   ABR86696 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 273
ID   ABM16660 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 274
ID   ABM29712 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 275
ID   ABO29136 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 276
ID   ABM23917 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 277
ID   ABM23307 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 278
ID   ABM22087 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 279
ID   ABO37728 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.

PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 280
ID   ABM28492 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003082715-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 281
ID   ABM28797 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003082716-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 282
ID   ABM65441 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 283
ID   ABM75823 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 284
ID   ABM34103 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096359-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 285
ID   ABM34408 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003100061-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 286
ID   ABO20339 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003031125-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 287
ID   ABO21254 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054454-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 288
ID   ABO22169 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054477-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
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RESULT 289
ID ADA20090 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 290
ID ABO34194 standard; protein; 77 AA.
DE Human secreted/transmembrane polypeptide PRO 1027.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 291
ID ABR96603 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 292
ID ADA94499 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 293
ID ABR85781 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 294
ID ABR99763 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 295
ID ABM00314 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 296
ID ABM00619 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 297
ID ABO29746 standard; protein; 77 AA.
DE Human secreted/transmembrane polypeptide (PRO) #107.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 298
ID ABM23612 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 299
ID ABM29407 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 300
ID ABO38338 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 301
ID ABO45638 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 302
ID ABM20562 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 303
ID ADA81485 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 304
ID ABO16676 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 305
ID ABO18302 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 306
ID ABO22729 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 307
ID ABO23034 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   100.0%; Score 77; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 308
ID   ABR92576 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 309
ID   ABR81533 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 310
ID   ABM77957 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 311
ID   ABR89746 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073171-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 312
ID   ABM26662 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032121-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 313
ID   ABM13788 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 314
ID   ABO28526 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064460-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 315
ID   ABO30356 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 316
ID   ABM07383 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 317
ID   ABM03974 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.

PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 318
ID   ABO37118 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 319
ID   ABO41693 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 320
ID   ABO35288 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 321
ID   ABM25137 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104540-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 322
ID   ABO47529 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 323
ID   ABO47834 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 324
ID   ABO48444 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 325
ID   ABO51494 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 326
ID   ABO51799 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049767-A1.
PD   13-MAR-2003.

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PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 327
ID  ABO50579 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049779-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 328
ID  ABR79703 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003040059-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 329
ID  ABM16965 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003040078-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 330
ID  ABO17997 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003032132-A1.
PD  13-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 331
ID  ABO20949 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003032132-A1.
PD  13-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 332
ID  ABR96908 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003054462-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 333
ID  ADA38724 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein PRO1027.
PN  US2003059780-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 334
ID  ABM12263 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064445-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 335
ID  ABM16355 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064449-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 336
ID  ABM24222 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064441-A1.
PD  03-APR-2003.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 337
ID  ABM14703 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068696-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 338
ID  ABM04584 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068712-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 339
ID  ABM06773 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068730-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 340
ID  ABM09213 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003071174-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 341
ID  AB039253 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003068775-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 342
ID  ABM75518 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003104545-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 343
ID  ABM25442 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003104541-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 344
ID  ABM19952 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003104554-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 77;   DB 6;   Length 77;
    Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 345
ID  ABO46858 standard; protein; 77 AA.
DE  Human PRO polypeptide #107.
PN  US2003049762-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
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          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 346
ID   ABO47163 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 347
ID   ADA83283 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 348
ID   ABR71594 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032133-A1.
PD   13-FEB-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 349
ID   ABR72204 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032136-A1.
PD   13-FEB-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 350
ID   ABR98543 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036129-A1.
PD   20-FEB-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 351
ID   ABO06913 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040053-A1.
PD   27-FEB-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 352
ID   ABR84866 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040057-A1.
PD   27-FEB-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 353
ID   ABR73424 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054467-A1.
PD   20-MAR-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 354
ID   ABR76518 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044932-A1.
PD   06-MAR-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 355
ID   ABR73119 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027270-A1.
PD   06-FEB-2003.

          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 356
ID   ABM18185 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 357
ID   ABO20644 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032126-A1.
PD   13-FEB-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 358
ID   ABO25387 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003054463-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 359
ID   ABO25692 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003054466-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 360
ID   ABR94101 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059879-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 361
ID   ADA92845 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003060407-A1.
PD   27-MAR-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 362
ID   ABR80008 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049738-A1.
PD   13-MAR-2003.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 363
ID   ABM11348 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064469-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 364
ID   ABO32955 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003064453-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 77;   DB 6;   Length 77;
          Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 365
ID   ABO30661 standard; protein; 77 AA.
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DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003064466-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 366
ID    ABO30966 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003064468-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 367
ID    ABM27272 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068760-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 368
ID    ABM30017 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068769-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 369
ID    ABM05553 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003045700-A1.
PD    06-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 370
ID    ABM15618 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068698-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 371
ID    ABM08603 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068759-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 372
ID    ABO42303 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003049748-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 373
ID    ABO38033 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003068765-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 374
ID    ABO45943 standard; protein; 77 AA.
DE    Human PRO polypeptide #107.


PN    US2003049754-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 375
ID    ABM66746 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068688-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 376
ID    ADB20326 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003082767-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 377
ID    ABM19647 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003104552-A1.
PD    05-JUN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 378
ID    ABO49359 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003049774-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 379
ID    ABO49664 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003049775-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 380
ID    ADA78578 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein (PRO) #107.
PN    US2003073181-A1.
PD    17-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 381
ID    ABR88221 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068720-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 382
ID    ADA00387 standard; protein; 77 AA.
DE    Human secreted/transmembrane polypeptide PRO 1027.
PN    US2003027992-A1.
PD    06-FEB-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            100.0%;    Score 77;   DB 6;  Length 77;
      Best Local Similarity  100.0%;    Pred. No. 4.4e-75;
RESULT 383
ID    ABM26967 standard; protein; 77 AA.
DE    Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN    US2003068739-A1.
PD    10-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 384
ID ABM03364 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 385
ID ABO39863 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US20030066689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 386
ID ABO49969 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US20030049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 387
ID ABO50884 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US20030049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 388
ID ABO05340 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US20030036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 389
ID ABR74644 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 390
ID ABR77123 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 391
ID ABM17880 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030044072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 392
ID ABR95931 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 393
ID ABO21864 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.

PN US20030054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 394
ID ABO20034 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US20030032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 395
ID ABO24337 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US20030064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 396
ID ABR86086 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 397
ID ABM10738 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 398
ID ABM76737 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 399
ID ABR89441 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 400
ID ABM12568 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 401
ID ABM05858 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US20030068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;   Score 77;   DB 7; Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 402
ID ABO34983 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US20030068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 403
ID   ABM03059 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 404
ID   ABM19037 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 405
ID   ABM19342 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 406
ID   ABO46553 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 407
ID   ABO49054 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 408
ID   ABR69097 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027273-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 409
ID   ABR89116 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036119-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 410
ID   ABR72509 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036120-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 411
ID   ABR74339 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 412
ID   ABO18607 standard; protein; 77 AA.

DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044921-A1.
PD   06-MAR-2003.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 413
ID   ABR80313 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 414
ID   ABM01534 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 415
ID   ABM02144 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 416
ID   ABR87306 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 417
ID   ABM12873 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 418
ID   ABM30627 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 419
ID   ABM24527 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 420
ID   ABO29441 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 7;   Length 77;
Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 421
ID   ABO31271 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068710-A1.

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PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 422
ID  ABM14398 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068686-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 423
ID  ABM09823 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003073178-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 424
ID  ABO38948 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003068774-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 425
ID  ABM34713 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003104538-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 426
ID  ABO51189 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049781-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 427
ID  ABO04015 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003036158-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 428
ID  ABO10485 standard; protein; 77 AA.
DE  Human PRO polypeptide #107.
PN  US2003036151-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 429
ID  ABO53190 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein PRO1027.
PN  US2003044806-A1.
PD  06-MAR-2003.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 430
ID  ABR77728 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003040067-A1.
PD  27-FEB-2003.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 431
ID  ABR78938 standard; protein; 77 AA.

DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003054456-A1.
PD  20-MAR-2003.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 432
ID  ABO24032 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003054482-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 433
ID  ABR93796 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003054457-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 434
ID  ABM01839 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003059883-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 435
ID  ABM78262 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003049764-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 436
ID  ABR90051 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003073177-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 437
ID  ADA22406 standard; protein; 77 AA.
DE  Human secreted/transmembrane polypeptide PRO1027.
PN  US2003040473-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 438
ID  ABM27577 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064442-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 439
ID  ABM13178 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064450-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 77;  DB 7;  Length 77;
    Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 440
ID  ABO31881 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003068731-A1.
PD  10-APR-2003.
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PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 441
ID   ABM14093 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068683-A1.
PD   10-APR-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 442
ID   ABM08298 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 443
ID   ABO40168 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068681-A1.
PD   10-APR-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 444
ID   ABM74603 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 445
ID   ABM33798 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096358-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 446
ID   ABM20257 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 447
ID   ABO48749 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 448
ID   ABO22560 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003017982-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 449
ID   ABR72814 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036122-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 450
ID   ABO15456 standard; protein; 77 AA.

DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 451
ID   ABR85171 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040065-A1.
PD   27-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 452
ID   ABO15151 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044919-A1.
PD   06-MAR-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 453
ID   ABO17286 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040077-A1.
PD   27-FEB-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 454
ID   ABM17575 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044928-A1.
PD   06-MAR-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 455
ID   ADA06572 standard; protein; 77 AA.
DE   Human secreted/transmembrane PRO polypeptide #85.
PN   US2003049638-A1.
PD   13-MAR-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 456
ID   ADA39265 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003059782-A1.
PD   27-MAR-2003.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 457
ID   ABR85476 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049746-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 458
ID   ABM77042 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054464-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 459
ID   ABO28221 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064459-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 77;   DB 7;   Length 77;
      Best Local Similarity 100.0%;   Pred. No. 4.4e-75;
RESULT 460

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ID   ABM23002 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068757-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 461
ID   ABM30322 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068723-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 462
ID   ABM21782 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068741-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 463
ID   ABM21477 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068744-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 464
ID   ABM15008 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068766-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 465
ID   ABO41083 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068694-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 466
ID   ABO36813 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068715-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 467
ID   ABO37423 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068726-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 468
ID   ABM75213 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104544-Al.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 469
ID   ABM33493 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003099357-Al.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 470
ID   ABO46248 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049760-Al.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 471
ID   ADA82649 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049755-Al.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 472
ID   ADB85629 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003049735-Al.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 473
ID   ADB96291 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003054403-Al.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 474
ID   ABM31847 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068680-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 475
ID   ABM31237 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068762-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 476
ID   ADB85957 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054472-Al.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 477
ID   ABM32152 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068708-Al.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 478
ID   ABM32457 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068713-Al.
PD   10-APR-2003.
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PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 479
ID   ADB68308 standard; protein; 77 AA.
DE   Human PRO1027 protein.
PN   US2003065161-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 480
ID   ADB68115 standard; protein; 77 AA.
DE   Human PRO1027 protein.
PN   US2003060600-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 481
ID   ABM31542 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068761-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 482
ID   ABM30932 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068771-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 483
ID   ADB90932 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003083473-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 484
ID   ADC57763 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003027754-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 485
ID   ADC55127 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003045463-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 486
ID   ADC11994 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003049681-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 487
ID   ADC07012 standard; protein; 77 AA.
DE   Human PRO1027 protein.
PN   US2003060602-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 488

ID   ADC56416 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003064375-A1.
PD   03-APR-2003.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 489
ID   ADC17191 standard; protein; 77 AA.
DE   Mammalian PRO polypeptide (SeqID 56).
PN   US2003065143-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 490
ID   ADC07471 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003068647-A1.
PD   10-APR-2003.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 491
ID   ADC11461 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003069403-A1.
PD   10-APR-2003.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 492
ID   ADC14889 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003073208-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 493
ID   ADC52384 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003138882-A1.
PD   24-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 494
ID   ADC14583 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003082546-A1.
PD   01-MAY-2003.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 495
ID   ADD08115 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003068623-A1.
PD   10-APR-2003.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 496
ID   ADC81940 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003083461-A1.
PD   01-MAY-2003.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 497
ID   ADD07582 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity   100.0%;   Pred. No. 4.4e-75;

RESULT 498
ID   ADC82473 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003059833-A1.
PD   27-MAR-2003.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 499
ID   ADD05687 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 500
ID   ADD08653 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 501
ID   ADD06902 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003059783-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 502
ID   ADC83149 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003077593-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 503
ID   ADD55256 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003077594-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 504
ID   ADD36060 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 505
ID   ADD56214 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 506
ID   ADD54652 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003077594-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 507
ID   ADE26806 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003087304-A1.
PD   08-MAY-2003.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 508
ID   ADE26273 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003087305-A1.
PD   08-MAY-2003.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 509
ID   ADF67210 standard; protein; 77 AA.
DE   Human PRO1027 amino acid sequence SEQ ID NO:283.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 510
ID   ADG01061 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 511
ID   ADG08614 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 512
ID   ADG02682 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 513
ID   ADG01389 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 514
ID   ADF95564 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 515
ID   ADF95235 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 516
ID   ADG12379 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207392-A1.
PD   06-NOV-2003.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 517
ID   ADH24088 standard; protein; 77 AA.

DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180918-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 518
ID   ADH34114 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180858-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 519
ID   ADH29947 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180859-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 520
ID   ADH23918 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180919-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 521
ID   ADH09039 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 522
ID   ADG85322 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180904-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 523
ID   ADH24598 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180907-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 524
ID   ADH37454 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 525
ID   ADH02043 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180837-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 526
ID   ADH37624 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.

PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 527
ID   ADG85662 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180905-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 528
ID   ADH24258 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180914-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 529
ID   ADH38552 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181643-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 530
ID   ADG83673 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180794-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 531
ID   ADH29481 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180860-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 532
ID   ADH27597 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180906-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 533
ID   ADH37794 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181647-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 534
ID   ADH37971 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181649-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 77; DB 7; Length 77;
     Best Local Similarity   100.0%; Pred. No. 4.4e-75;
RESULT 535
ID   ADH57391 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180920-A1.

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                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 545
                 ID   ADI03596 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003181656-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 546
                 ID   ADI11953 standard; protein; 77 AA.
                 DE   Human PRO polypeptide #28.
                 PN   US2003181686-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 547
                 ID   ADH90027 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003181697-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 548
                 ID   ADH99956 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003049682-A1.
                 PD   13-MAR-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 549
                 ID   ADH98428 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003181707-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 550
                 ID   ADI11103 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003181682-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 551
                 ID   ADI11613 standard; protein; 77 AA.
                 DE   Human PRO polypeptide #28.
                 PN   US2003181684-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 552
                 ID   ADH98258 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003181709-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
                 RESULT 553
                 ID   ADH98598 standard; protein; 77 AA.
                 DE   Novel human secreted and transmembrane protein PRO1027.
                 PN   US2003181708-A1.
                 PD   25-SEP-2003.
                 PA   (GETH ) GENENTECH INC.
                      Query Match               100.0%;    Score 77;    DB 7; Length 77;
                      Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
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PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 536
ID   ADH53533 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181636-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 537
ID   ADH53703 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181641-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 538
ID   ADH52039 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181638-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 539
ID   ADH49894 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181639-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 540
ID   ADI25404 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181696-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 541
ID   ADH90197 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181698-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 542
ID   ADI25574 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181669-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 543
ID   ADH97748 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181672-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;    Score 77;    DB 7; Length 77;
     Best Local Similarity     100.0%;    Pred. No. 4.4e-75;
RESULT 544
ID   ADI35464 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003050457-A1.
PD   13-MAR-2003.
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RESULT 554
ID   ADH98088 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein protein PRO1027.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 555
ID   ADI05076 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 556
ID   ADI03426 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 557
ID   ADI04821 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 558
ID   ADH78275 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 559
ID   ADI19619 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 560
ID   ADH90367 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 561
ID   ADI03086 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 562
ID   ADH77935 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 563
ID   ADH97918 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 564
ID   ADI01303 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003190669-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 565
ID   ADI01998 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181652-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 566
ID   ADI03256 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181655-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 567
ID   ADI11443 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181681-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 568
ID   ADI02345 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181650-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 569
ID   ADI11783 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181685-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 570
ID   ADI05420 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003190716-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 571
ID   ADH79492 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003191290-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 77;   DB 7;   Length 77;
     Best Local Similarity  100.0%;              Pred. No. 4.4e-75;
RESULT 572
ID   ADI19449 standard; protein; 77 AA.
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DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181675-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 573
ID  ADI05250 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181677-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 574
ID  ADH79662 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003191288-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 575
ID  ADI01488 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181678-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 576
ID  ADI01658 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181679-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 577
ID  ADI01828 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181680-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 578
ID  ADH79832 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003191289-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 579
ID  ADI04650 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003171550-A1.
PD  11-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 580
ID  ADI02786 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181651-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 581
ID  ADH78105 standard; protein; 77 AA.
DE  Human PRO polypeptide #28.
PN  US2003181667-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 582
ID  ADI25744 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181670-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 583
ID  ADI25914 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003181671-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 584
ID  ADK65426 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003073821-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 585
ID  ADH98768 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003191284-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 586
ID  ADH80009 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003191287-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 587
ID  ADL32820 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003207396-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 588
ID  ADM30354 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003073813-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 589
ID  ADL93740 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003040013-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;    Score 77;    DB 7;  Length 77;
    Best Local Similarity 100.0%;  Pred. No. 4.4e-75;
RESULT 590
ID  ADC52194 standard; protein; 77 AA.
DE  Novel human secreted and transmembrane protein PRO1027.
PN  US2003130483-A1.
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PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 591
ID   ADE74351 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003211572-A1.
PD   13-NOV-2003.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 592
ID   ADE74963 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003211574-A1.
PD   13-NOV-2003.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 593
ID   ADF35409 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003194760-A1.
PD   16-OCT-2003.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 594
ID   ADG11659 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 595
ID   ADF96176 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003215909-A1.
PD   20-NOV-2003.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 596
ID   ADG04447 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003215912-A1.
PD   20-NOV-2003.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 597
ID   ADG00607 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180852-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 598
ID   ADH06626 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 599
ID   ADH06456 standard; protein; 77 AA.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 600


ID   ADG68877 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 601
ID   ADH27767 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 602
ID   ADH25108 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 603
ID   ADH33740 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181645-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 604
ID   ADG82863 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003215910-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 605
ID   ADH02383 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180839-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 606
ID   ADH07990 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180845-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 607
ID   ADG69387 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 608
ID   ADH39208 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180917-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 77;  DB 8;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 4.4e-75;
RESULT 609
ID   ADH26144 standard; protein; 77 AA.
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DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003068770-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 610
ID    ADG83948 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003180842-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 611
ID    ADH19529 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein PRO1027.
PN    US2003228656-A1.
PD    11-DEC-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 612
ID    ADG5492 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003166848-A1.
PD    04-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 613
ID    ADH06286 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180854-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 614
ID    ADH30116 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180856-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 615
ID    ADH24428 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180910-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 616
ID    ADH33113 standard; protein; 77 AA.
DE    Human PRO polypeptide #107.
PN    US2003068768-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 617
ID    ADG69557 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180844-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 618
ID    ADH07820 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.

PN    US2003180851-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 619
ID    ADG85832 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180861-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 620
ID    ADH39378 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180916-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 621
ID    ADH33570 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003181637-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 622
ID    ADH33910 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003181644-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 623
ID    ADH01120 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003180838-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 624
ID    ADG69727 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180843-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 625
ID    ADH21022 standard; protein; 77 AA.
DE    Human secreted/transmembrane protein PRO1027.
PN    US2003224358-A1.
PD    04-DEC-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 626
ID    ADH02213 standard; protein; 77 AA.
DE    Human PRO polypeptide #28.
PN    US2003180841-A1.
PD    25-SEP-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         100.0%;  Score 77;  DB 8;  Length 77;
      Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 627
ID    ADG69217 standard; protein; 77 AA.
DE    Novel human secreted and transmembrane protein PRO1027.
PN    US2003180847-A1.
PD    25-SEP-2003.
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PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 628
ID ADG86002 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180862-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 629
ID ADH24938 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180909-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 630
ID ADH39555 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180915-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 631
ID ADH20062 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003219856-Al.
PD 27-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 632
ID ADH02553 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180840-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 633
ID ADG69047 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180849-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 634
ID ADH07650 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180850-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 635
ID ADG86172 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180863-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 636
ID ADH24768 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180908-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 637
ID ADH25816 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180911-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 638
ID ADH38382 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180922-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 639
ID ADH57221 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181642-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 640
ID ADH52208 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180921-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 641
ID ADH49575 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180857-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 642
ID ADH90537 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181700-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 643
ID ADI11273 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181683-Al.
PD 25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 644
ID ADH98938 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003190698-Al.
PD 09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;
Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 645
ID ADI02168 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003190699-Al.
PD 09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 77;   DB 8; Length 77;

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                  Best Local Similarity  100.0%;  Pred. No. 4.4e-75;
RESULT 646
ID   ADH90707 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 647
ID   ADJ54852 standard; protein; 77 AA.
DE   Human PRO Polypeptide #107.
PN   US2004023321-A1.
PD   05-FEB-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 648
ID   ADJ98582 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187197-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 649
ID   ADJ98752 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 650
ID   ADH78911 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 651
ID   ADJ99145 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 652
ID   ADJ99315 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 653
ID   ADJ98933 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 654
ID   ADH79081 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181702-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
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RESULT 655
ID   ADK00941 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003186407-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 656
ID   ADK14462 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187229-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 657
ID   ADJ64623 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2004038337-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 658
ID   ADM31519 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004048334-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 659
ID   ADM36566 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004053358-A1.
PD   18-MAR-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 660
ID   ADM40371 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004048335-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 661
ID   ADM80911 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2004058411-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 662
ID   ADN37979 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004091959-A1.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
       Query Match             100.0%;   Score 77;   DB 8;  Length 77;
       Best Local Similarity   100.0%;   Pred. No. 4.4e-75;
RESULT 663
ID   AAB12126 standard; protein; 160 AA.
DE   Hydrophobic domain protein isolated from HT-1080 cells.
PN   WO200029448-A2.
PD   25-MAY-2000.
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
       Query Match             100.0%;   Score 77;   DB 3;  Length 160;
       Best Local Similarity   100.0%;   Pred. No. 8.8e-75;
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RESULT 664
ID ABB11987 standard; peptide; 170 AA.
DE Human secreted protein homologue, SEQ ID NO:2357.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   100.0%; Score 77; DB 4; Length 170;
    Best Local Similarity   100.0%; Pred. No. 9.3e-75;

RESULT 665
ID AAY35997 standard; protein; 160 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 382.
PN WO931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
    Query Match   89.6%; Score 69; DB 2; Length 160;
    Best Local Similarity   100.0%; Pred. No. 3.8e-66;

RESULT 666
ID ADP19305 standard; protein; 160 AA.
DE Human secreted polypeptide #156.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
    Query Match   89.6%; Score 69; DB 8; Length 160;
    Best Local Similarity   100.0%; Pred. No. 3.8e-66;

RESULT 667
ID ABP75976 standard; protein; 77 AA.
DE Human GENSET protein SEQ ID 183.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
    Query Match   49.4%; Score 38; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 5.8e-33;

RESULT 668
ID ABP76142 standard; protein; 77 AA.
DE Human GENSET protein SEQ ID 468.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
    Query Match   49.4%; Score 38; DB 6; Length 77;
    Best Local Similarity   100.0%; Pred. No. 5.8e-33;

RESULT 669
ID ABB89647 standard; protein; 124 AA.
DE Human polypeptide SEQ ID NO 2023.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   10.4%; Score 8; DB 5; Length 124;
    Best Local Similarity   100.0%; Pred. No. 2.3;

RESULT 670
ID AAM39275 standard; protein; 159 AA.
DE Human polypeptide SEQ ID NO 2420.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (GEST) GENSET.
    Query Match   10.4%; Score 8; DB 4; Length 159;
    Best Local Similarity   100.0%; Pred. No. 2.9;

RESULT 671
ID AAG89299 standard; protein; 159 AA.
DE Human secreted protein, SEQ ID NO: 419.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST) GENSET.
    Query Match   10.4%; Score 8; DB 4; Length 159;
    Best Local Similarity   100.0%; Pred. No. 2.9;

RESULT 672
ID ADP55700 standard; protein; 159 AA.
DE Human PRO protein sequence SEQ ID NO:1676.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
    Query Match   10.4%; Score 8; DB 8; Length 159;
    Best Local Similarity   100.0%; Pred. No. 2.9;

RESULT 673
ID ADF76452 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein SeqID 126.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.4%; Score 8; DB 7; Length 178;
    Best Local Similarity   100.0%; Pred. No. 3.2;

RESULT 674
ID ADR14033 standard; protein; 178 AA.
DE Human NF-kappaB pathway-associated protein SeqID34.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
    Query Match   10.4%; Score 8; DB 8; Length 178;
    Best Local Similarity   100.0%; Pred. No. 3.2;

RESULT 675
ID AAY31835 standard; protein; 179 AA.
DE Human foetal kidney secreted protein pk266_4.
PN WO9947555-A1.
PD 23-SEP-1999.
PA (GEMY) GENETICS INST INC.
    Query Match   10.4%; Score 8; DB 2; Length 179;
    Best Local Similarity   100.0%; Pred. No. 3.2;

RESULT 676
ID AAM41061 standard; protein; 203 AA.
DE Human polypeptide SEQ ID NO 5992.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   10.4%; Score 8; DB 4; Length 203;
    Best Local Similarity   100.0%; Pred. No. 3.6;

RESULT 677
ID ABU45593 standard; protein; 412 AA.
DE Protein encoded by Prokaryotic essential gene #31120.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   10.4%; Score 8; DB 6; Length 412;
    Best Local Similarity   100.0%; Pred. No. 7.1;

RESULT 678
ID ABU32397 standard; protein; 436 AA.
DE Protein encoded by Prokaryotic essential gene #17924.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   10.4%; Score 8; DB 6; Length 436;
    Best Local Similarity   100.0%; Pred. No. 7.4;

RESULT 679
ID ABU48248 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #33775.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   10.4%; Score 8; DB 6; Length 438;
    Best Local Similarity   100.0%; Pred. No. 7.5;

RESULT 680
ID ABU15404 standard; protein; 438 AA.
DE Klebsiella pneumoniae polypeptide seqid 10091.
PN US661083-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   10.4%; Score 8; DB 6; Length 438;
    Best Local Similarity   100.0%; Pred. No. 7.5;

RESULT 681
ID ABG63574 standard; protein; 441 AA.
DE Klebsiella pneumoniae polypeptide seqid 10091.
PN US661083-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   10.4%; Score 8; DB 7; Length 441;
    Best Local Similarity   100.0%; Pred. No. 7.5;

RESULT 682
ID ABG29718 standard; protein; 72 AA.

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DE   Novel human diagnostic protein #29709.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
   Query Match       9.1%;   Score 7;   DB 4;   Length 72;
   Best Local Similarity   100.0%;   Pred. No. 16;
RESULT 683
ID   AAU44109 standard; protein; 96 AA.
DE   Propionibacterium acnes immunogenic protein #5005.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
   Query Match       9.1%;   Score 7;   DB 4;   Length 96;
   Best Local Similarity   100.0%;   Pred. No. 22;
RESULT 684
ID   ABM40628 standard; protein; 96 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #5304.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
   Query Match       9.1%;   Score 7;   DB 4;   Length 96;
   Best Local Similarity   100.0%;   Pred. No. 22;
RESULT 685
ID   ABG24335 standard; protein; 146 AA.
DE   Novel human diagnostic protein #24326.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
   Query Match       9.1%;   Score 7;   DB 4;   Length 146;
   Best Local Similarity   100.0%;   Pred. No. 32;
RESULT 686
ID   ABB71351 standard; protein; 163 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40845.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
   Query Match       9.1%;   Score 7;   DB 4;   Length 163;
   Best Local Similarity   100.0%;   Pred. No. 35;
RESULT 687
ID   ABB53448 standard; protein; 183 AA.
DE   Lactococcus lactis protein ybeH.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
   Query Match       9.1%;   Score 7;   DB 5;   Length 183;
   Best Local Similarity   100.0%;   Pred. No. 40;
RESULT 688
ID   ABB55201 standard; protein; 197 AA.
DE   Lactococcus lactis protein ytcA.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
   Query Match       9.1%;   Score 7;   DB 5;   Length 197;
   Best Local Similarity   100.0%;   Pred. No. 42;
RESULT 689
ID   ABQ64144 standard; protein; 199 AA.
DE   Klebsiella pneumoniae polypeptide seqid 10661.
PN   US5610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
   Query Match       9.1%;   Score 7;   DB 7;   Length 199;
   Best Local Similarity   100.0%;   Pred. No. 43;
RESULT 690
ID   ABB90704 standard; protein; 212 AA.
DE   Chlamydia pneumoniae cp6723 protein, SEQ ID NO:357.
PN   WO200202606-A2.
PD   10-JAN-2002.
PA   (CHIR-) CHIRON SPA.
   Query Match       9.1%;   Score 7;   DB 5;   Length 212;
   Best Local Similarity   100.0%;   Pred. No. 45;
RESULT 691
ID   AAY35043 standard; protein; 220 AA.
DE   Chlamydia pneumoniae transmembrane protein sequence.


PN   WO9927105-A2.
PD   03-JUN-1999.
PA   (GEST ) GENSET.
   Query Match       9.1%;   Score 7;   DB 2;   Length 220;
   Best Local Similarity   100.0%;   Pred. No. 47;
RESULT 692
ID   ABP28531 standard; protein; 247 AA.
DE   Streptococcus polypeptide SEQ ID NO 6238.
PN   WO200034771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
   Query Match       9.1%;   Score 7;   DB 5;   Length 247;
   Best Local Similarity   100.0%;   Pred. No. 52;
RESULT 693
ID   ABU43092 standard; protein; 304 AA.
DE   Protein encoded by Prokaryotic essential gene #28619.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELITR-) ELITRA PHARM INC.
   Query Match       9.1%;   Score 7;   DB 6;   Length 304;
   Best Local Similarity   100.0%;   Pred. No. 64;
RESULT 694
ID   AAG71882 standard; protein; 314 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1563.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
   Query Match       9.1%;   Score 7;   DB 4;   Length 314;
   Best Local Similarity   100.0%;   Pred. No. 66;
RESULT 695
ID   AAU24647 standard; protein; 314 AA.
DE   Human olfactory receptor AOLFR143.
PN   WO200168805-A2.
PD   20-SEP-2001.
PA   (SENO-) SENOMYX INC.
   Query Match       9.1%;   Score 7;   DB 4;   Length 314;
   Best Local Similarity   100.0%;   Pred. No. 66;
RESULT 696
ID   ABJ03989 standard; protein; 314 AA.
DE   Human G-protein coupled receptor SEQ ID NO: 44.
PN   WO200255558-A2.
PD   18-JUL-2002.
PA   (CURA-) CURAGEN CORP.
   Query Match       9.1%;   Score 7;   DB 5;   Length 314;
   Best Local Similarity   100.0%;   Pred. No. 66;
RESULT 697
ID   ABP95687 standard; protein; 314 AA.
DE   Human GPCR polypeptide SEQ ID NO 184.
PN   WO200216548-A2.
PD   28-FEB-2002.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
   Query Match       9.1%;   Score 7;   DB 5;   Length 314;
   Best Local Similarity   100.0%;   Pred. No. 66;
RESULT 698
ID   AAU95721 standard; protein; 314 AA.
DE   Human olfactory and pheromone G protein-coupled receptor #208.
PN   WO200224726-A2.
PD   28-MAR-2002.
PA   (CHEM-) CHEMCOM SA.
   Query Match       9.1%;   Score 7;   DB 5;   Length 314;
   Best Local Similarity   100.0%;   Pred. No. 66;
RESULT 699
ID   AAU85267 standard; protein; 314 AA.
DE   G-coupled olfactory receptor #128.
PN   WO200198526-A2.
PD   27-DEC-2001.
PA   (SENO-) SENOMYX INC.
   Query Match       9.1%;   Score 7;   DB 5;   Length 314;
   Best Local Similarity   100.0%;   Pred. No. 66;
RESULT 700
ID   ADH30852 standard; protein; 314 AA.
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DE   Human G-protein coupled receptor (GPCR) polypeptide #22.
PN   US2003232332-A1.
PD   18-DEC-2003.
PA   (PADI/) PADIGARU M.
PA   (KEKU/) KEKUDA R.
PA   (LILL/) LI L.
PA   (BALL/) BALLINGER R A.
PA   (CASM/) CASMAN S J.
PA   (SPYT/) SPYTEK K A.
PA   (COLM/) COLMAN S D.
PA   (VERN/) VERNET C A M.
PA   (SHEN/) SHENOY S G.
PA   (GUSE/) GUSEV V Y.
PA   (MALY/) MALYANKAR U M.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (SMIT/) SMITHSON G.
PA   (STON/) STONE D J.
PA   (SCIO/) SCIORE P.
PA   (MACD/) MACDOUGALL J R.
PA   (GUNT/) GUNTHER E.
PA   (PEYM/) PEYMAN J A.
PA   (ELLE/) ELLERMAN K.
PA   (MILL/) MILLET I.
PA   (TCHE/) TCHERNEV V T.
PA   (ANDE/) ANDERSON D W.
PA   (WOLE/) WOLENC A R.
     Query Match   9.1%;   Score 7;   DB 8;   Length 314;
     Best Local Similarity   100.0%;   Pred. No. 66;

RESULT 701
ID   ABG26995 standard; protein; 347 AA.
DE   Novel human diagnostic protein #26986.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   9.1%;   Score 7;   DB 4;   Length 347;
     Best Local Similarity   100.0%;   Pred. No. 72;

RESULT 702
ID   ABG24341 standard; protein; 359 AA.
DE   Novel human diagnostic protein #24332.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   9.1%;   Score 7;   DB 4;   Length 359;
     Best Local Similarity   100.0%;   Pred. No. 75;

RESULT 703
ID   ABG29719 standard; protein; 368 AA.
DE   Novel human diagnostic protein #29710.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   9.1%;   Score 7;   DB 4;   Length 368;
     Best Local Similarity   100.0%;   Pred. No. 76;

RESULT 704
ID   ADG86524 standard; protein; 373 AA.
DE   Human endogenous orphan GPCR hARE-2 mutant G285K.
PN   US2003229216-A1.
PD   11-DEC-2003.
PA   (CHEN/) CHEN R.
PA   (LIAW/) LIAW C W.
PA   (LOWI/) LOWITZ K.
PA   (CHAL/) CHALMERS D T.
PA   (BEHA/) BEHAN D P.
     Query Match   9.1%;   Score 7;   DB 4;   Length 373;
     Best Local Similarity   100.0%;   Pred. No. 77;

RESULT 705
ID   ADQ75135 standard; protein; 373 AA.
DE   Human G protein-coupled receptor ARE-2, Gly285Lys mutant.
PN   US2004137509-A1.
PD   15-JUL-2004.
PA   (LIAW/) LIAW C W.
PA   (LINI/) LIN I.
     Query Match   9.1%;   Score 7;   DB 8;   Length 373;

     Best Local Similarity   100.0%;   Pred. No. 77;

RESULT 706
ID   ABB58557 standard; protein; 441 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2463.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   9.1%;   Score 7;   DB 4;   Length 441;
     Best Local Similarity   100.0%;   Pred. No. 90;

RESULT 707
ID   ADN17847 standard; protein; 448 AA.
DE   Bacterial polypeptide #500.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   9.1%;   Score 7;   DB 8;   Length 448;
     Best Local Similarity   100.0%;   Pred. No. 92;

RESULT 708
ID   ADS42790 standard; protein; 449 AA.
DE   Bacterial polypeptide #21220.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   9.1%;   Score 7;   DB 8;   Length 449;
     Best Local Similarity   100.0%;   Pred. No. 92;

RESULT 709
ID   ABM70211 standard; protein; 459 AA.
DE   Photorhabdus luminescens protein sequence #3308.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   9.1%;   Score 7;   DB 6;   Length 459;
     Best Local Similarity   100.0%;   Pred. No. 94;

RESULT 710
ID   ABP74127 standard; protein; 552 AA.
DE   Human TRICH SEQ ID NO 32.
PN   WO200246415-A2.
PD   13-JUN-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   9.1%;   Score 7;   DB 5;   Length 552;
     Best Local Similarity   100.0%;   Pred. No. 1.1e+02;

RESULT 711
ID   ABB47595 standard; protein; 672 AA.
DE   Listeria monocytogenes protein #299.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   9.1%;   Score 7;   DB 5;   Length 672;
     Best Local Similarity   100.0%;   Pred. No. 1.3e+02;

RESULT 712
ID   ADS20997 standard; protein; 891 AA.
DE   Bacterial polypeptide #10030.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   9.1%;   Score 7;   DB 8;   Length 891;
     Best Local Similarity   100.0%;   Pred. No. 1.8e+02;

RESULT 713
ID   ADS23514 standard; protein; 1053 AA.
DE   Bacterial polypeptide #12547.

PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match   9.1%; Score 7; DB 8; Length 1053;
Best Local Similarity   100.0%;   Pred. No. 2.1e+02;
RESULT 714
ID   ABU41551 standard; protein; 1215 AA.
DE   Protein encoded by Prokaryotic essential gene #27078.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   9.1%; Score 7; DB 6; Length 1215;
Best Local Similarity   100.0%;   Pred. No. 2.3e+02;
RESULT 715
ID   ADM33093 standard; peptide; 6 AA.
DE   Human immunodeficiency virus 1 cell entry inhibitor peptide #121.
PN   WO2004024173-A2.
PD   25-MAR-2004.
PA   (CREA-) CREABILIS THERAPEUTICS SRL.
Query Match   7.8%; Score 6; DB 8; Length 6;
Best Local Similarity   100.0%;   Pred. No. 1.8e+06;
RESULT 716
ID   AAB90019 standard; peptide; 15 AA.
DE   HIV gp120 protein binding peptide #1112.
PN   WO200116182-A2.
PD   08-MAR-2001.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match   7.8%; Score 6; DB 4; Length 15;
Best Local Similarity   100.0%;   Pred. No. 45;
RESULT 717
ID   AAB90036 standard; peptide; 15 AA.
DE   HIV gp120 protein binding peptide #1129.
PN   WO200116182-A2.
PD   08-MAR-2001.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match   7.8%; Score 6; DB 4; Length 15;
Best Local Similarity   100.0%;   Pred. No. 45;
RESULT 718
ID   ABR44049 standard; peptide; 16 AA.
DE   Mutant LhAtOG4-17 fragment.
PN   WO2003035882-A2.
PD   01-MAY-2003.
PA   (SYGN) SYNGENTA LTD.
Query Match   7.8%; Score 6; DB 6; Length 16;
Best Local Similarity   100.0%;   Pred. No. 48;
RESULT 719
ID   ADS33743 standard; peptide; 22 AA.
DE   cMET-HGF binding peptide #396.
PN   WO2004078778-A2.
PD   16-SEP-2004.
PA   (DYAX-) DYAX CORP.
PA   (BRAC) BRACCO INT BV.
Query Match   7.8%; Score 6; DB 3; Length 22;
Best Local Similarity   100.0%;   Pred. No. 65;
RESULT 720
ID   AAB51941 standard; protein; 26 AA.
DE   Human secreted protein sequence encoded by gene 13 SEQ ID NO:73.
PN   WO200058334-A1.
PD   05-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%; Score 6; DB 3; Length 26;
Best Local Similarity   100.0%;   Pred. No. 76;
RESULT 721
ID   AAM89067 standard; protein; 38 AA.
DE   Human immune/haematopoietic antigen SEQ ID NO:16660.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%; Score 6; DB 4; Length 38;

Best Local Similarity   100.0%;   Pred. No. 1.1e+02;
RESULT 722
ID   AAU22331 standard; protein; 56 AA.
DE   Human cardiovascular system antigen polypeptide SEQ ID No 1105.
PN   WO200155321-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%; Score 6; DB 4; Length 56;
Best Local Similarity   100.0%;   Pred. No. 1.6e+02;
RESULT 723
ID   ADE46299 standard; protein; 56 AA.
DE   Human cardiovascular system related polypeptide #480.
PN   US2003059908-A1.
PD   27-MAR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%; Score 6; DB 7; Length 56;
Best Local Similarity   100.0%;   Pred. No. 1.6e+02;
RESULT 724
ID   ADJ07717 standard; protein; 56 AA.
DE   Human cardiovascular system associated polypeptide SeqID1105.
PN   US2004005575-A1.
PD   08-JAN-2004.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%; Score 6; DB 8; Length 56;
Best Local Similarity   100.0%;   Pred. No. 1.6e+02;
RESULT 725
ID   AAO09696 standard; protein; 58 AA.
DE   Human polypeptide SEQ ID NO 23588.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSB-) HYSEQ INC.
Query Match   7.8%; Score 6; DB 4; Length 58;
Best Local Similarity   100.0%;   Pred. No. 1.6e+02;
RESULT 726
ID   AAB38599 standard; protein; 62 AA.
DE   Human secreted protein sequence encoded by gene 17 SEQ ID NO:136.
PN   WO200056882-A1.
PD   28-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%; Score 6; DB 3; Length 62;
Best Local Similarity   100.0%;   Pred. No. 1.7e+02;
RESULT 727
ID   AAM20362 standard; protein; 62 AA.
DE   Peptide #6796 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match   7.8%; Score 6; DB 4; Length 62;
Best Local Similarity   100.0%;   Pred. No. 1.7e+02;
RESULT 728
ID   ABB40953 standard; peptide; 62 AA.
DE   Peptide #8459 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match   7.8%; Score 6; DB 4; Length 62;
Best Local Similarity   100.0%;   Pred. No. 1.7e+02;
RESULT 729
ID   AAM34727 standard; protein; 62 AA.
DE   Peptide #8764 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match   7.8%; Score 6; DB 4; Length 62;
Best Local Similarity   100.0%;   Pred. No. 1.7e+02;
RESULT 730
ID   ABB25065 standard; protein; 62 AA.
DE   Protein #7064 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match   7.8%; Score 6; DB 4; Length 62;
Best Local Similarity   100.0%;   Pred. No. 1.7e+02;

RESULT 731
ID   AAM74616 standard; protein; 62 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 34922.
PN   WO200157276-A2.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
PD   09-AUG-2001.
     Query Match   7.8%; Score 6; DB 4; Length 62;
     Best Local Similarity   100.0%; Pred. No. 1.7e+02;

RESULT 732
ID   AAU41414 standard; protein; 62 AA.
DE   Propionibacterium acnes immunogenic protein #2310.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
     Query Match   7.8%; Score 6; DB 4; Length 62;
     Best Local Similarity   100.0%; Pred. No. 1.7e+02;

RESULT 733
ID   AAM61815 standard; protein; 62 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 33920.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   7.8%; Score 6; DB 4; Length 62;
     Best Local Similarity   100.0%; Pred. No. 1.7e+02;

RESULT 734
ID   ABG56400 standard; peptide; 62 AA.
DE   Human liver peptide, SEQ ID No 35048.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   7.8%; Score 6; DB 4; Length 62;
     Best Local Similarity   100.0%; Pred. No. 1.7e+02;

RESULT 735
ID   ABG44443 standard; peptide; 62 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 34108.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   7.8%; Score 6; DB 5; Length 62;
     Best Local Similarity   100.0%; Pred. No. 1.7e+02;

RESULT 736
ID   ABM37933 standard; protein; 62 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #2609.
PN   WO200303515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
     Query Match   7.8%; Score 6; DB 6; Length 62;
     Best Local Similarity   100.0%; Pred. No. 1.7e+02;

RESULT 737
ID   AAB85512 standard; protein; 66 AA.
DE   Human protein kinase SGK162.
PN   WO200155356-A2.
PD   02-AUG-2001.
PA   (SUGE-) SUGEN INC.
     Query Match   7.8%; Score 6; DB 6; Length 66;
     Best Local Similarity   100.0%; Pred. No. 1.8e+02;

RESULT 738
ID   AAQ10410 standard; protein; 69 AA.
DE   Human polypeptide SEQ ID NO 24302.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 69;
     Best Local Similarity   100.0%; Pred. No. 1.9e+02;

RESULT 739
ID   AAG58965 standard; protein; 71 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO 76221.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 71;
     Best Local Similarity   100.0%; Pred. No. 2e+02;

RESULT 740
ID   AAU31963 standard; protein; 76 AA.

DE   Novel human secreted protein #2454.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 76;
     Best Local Similarity   100.0%; Pred. No. 2.1e+02;

RESULT 741
ID   AAG58964 standard; protein; 77 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 76220.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.1e+02;

RESULT 742
ID   ADQ91844 standard; protein; 77 AA.
DE   Amino acid sequence of the IDA protein.
PN   WO200405704-A2.
PD   08-JUL-2004.
PA   (BUTE/) BUTENKO M.
PA   (AALE/) AALEN R.
     Query Match   7.8%; Score 6; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.1e+02;

RESULT 743
ID   ABR38910 standard; protein; 78 AA.
DE   pBAL ORF 41 # SEQ ID 6.
PN   WO200316536-A2.
PD   27-FEB-2003.
PA   (UYDE-) UNIV DENMARK TECH DTU.
     Query Match   7.8%; Score 6; DB 6; Length 78;
     Best Local Similarity   100.0%; Pred. No. 2.1e+02;

RESULT 744
ID   ABU55738 standard; protein; 82 AA.
DE   Tomato growth regulating protein, LeGREP4.
PN   WO200283901-A2.
PD   24-OCT-2002.
PA   (CROP-) CROPDESIGN NV.
PA   (SAUT/) SAUTER M.
     Query Match   7.8%; Score 6; DB 6; Length 82;
     Best Local Similarity   100.0%; Pred. No. 2.2e+02;

RESULT 745
ID   ABI12217 standard; peptide; 83 AA.
DE   Human adapter protein homologue, SEQ ID NO:2587.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 83;
     Best Local Similarity   100.0%; Pred. No. 2.3e+02;

RESULT 746
ID   ABU55718 standard; protein; 83 AA.
DE   Rape partial growth regulating protein, BnGREP1.
PN   WO200283901-A2.
PD   24-OCT-2002.
PA   (CROP-) CROPDESIGN NV.
PA   (SAUT/) SAUTER M.
     Query Match   7.8%; Score 6; DB 6; Length 83;
     Best Local Similarity   100.0%; Pred. No. 2.3e+02;

RESULT 747
ID   ABI7001 standard; protein; 86 AA.
DE   Human nervous system related polypeptide SEQ ID NO 5658.
PN   WO200159063-A2.
PD   16-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   7.8%; Score 6; DB 4; Length 86;
     Best Local Similarity   100.0%; Pred. No. 2.3e+02;

RESULT 748
ID   ABI17956 standard; protein; 86 AA.
DE   Human nervous system related polypeptide SEQ ID NO 6613.
PN   WO200159063-A2.
PD   16-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   7.8%; Score 6; DB 4; Length 86;
     Best Local Similarity   100.0%; Pred. No. 2.3e+02;

RESULT 749

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ID   AAM16451 standard; protein; 89 AA.
DE   Peptide #2885 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 89;
Best Local Similarity 100.0%;  Pred. No. 2.4e+02;
RESULT 750
ID   ABP06561 standard; protein; 90 AA.
DE   Human ORFX protein sequence SEQ ID NO:13104.
PN   WO200192523-A2.
PD   06-DEC-2001.
PA   (CURA-) CURAGEN CORP.
Query Match           7.8%;  Score 6;  DB 5;  Length 90;
Best Local Similarity 100.0%;  Pred. No. 2.4e+02;
RESULT 751
ID   AAM84021 standard; protein; 92 AA.
DE   Human immune/haematopoietic antigen SEQ ID NO:11614.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 92;
Best Local Similarity 100.0%;  Pred. No. 2.5e+02;
RESULT 752
ID   ADM19869 standard; protein; 94 AA.
DE   Protein encoded by novel human channel/transporter gene #187.
PN   WO200154472-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 94;
Best Local Similarity 100.0%;  Pred. No. 2.5e+02;
RESULT 753
ID   ABB11577 standard; peptide; 95 AA.
DE   Human secreted protein homologue, SEQ ID NO:1947.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 95;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 754
ID   AAU21547 standard; protein; 95 AA.
DE   Human novel foetal antigen, SEQ ID NO 1791.
PN   WO200155312-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 95;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 755
ID   AAM96161 standard; protein; 96 AA.
DE   Human reproductive system related antigen SEQ ID NO: 4819.
PN   WO200155320-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 96;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 756
ID   AAU22855 standard; protein; 96 AA.
DE   Human prostate cancer antigen, Seq ID No 374.
PN   WO200155316-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           7.8%;  Score 6;  DB 4;  Length 96;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 757
ID   ADJ09428 standard; protein; 96 AA.
DE   Human prostate cancer associated polypeptide SeqID374.
PN   US2003054373-A1.
PD   20-MAR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           7.8%;  Score 6;  DB 7;  Length 96;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 758
ID   ADR95657 standard; protein; 96 AA.

DE   Novel S. pneumoniae protein sequence, SEQ ID 4292.
PN   US6800744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match           7.8%;  Score 6;  DB 8;  Length 96;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 759
ID   ABB79227 standard; protein; 98 AA.
DE   Human prostate specific protein sequence SEQ ID NO:176.
PN   WO200236808-A2.
PD   10-MAY-2002.
PA   (DIAD-) DIADEXUS INC.
Query Match           7.8%;  Score 6;  DB 5;  Length 98;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
RESULT 760
ID   AAU60442 standard; protein; 100 AA.
DE   Propionibacterium acnes immunogenic protein #21338.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
Query Match           7.8%;  Score 6;  DB 4;  Length 100;
Best Local Similarity 100.0%;  Pred. No. 2.7e+02;
RESULT 761
ID   ABM56961 standard; protein; 100 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #21637.
PN   WO200303515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
Query Match           7.8%;  Score 6;  DB 6;  Length 100;
Best Local Similarity 100.0%;  Pred. No. 2.7e+02;
RESULT 762
ID   ABP11255 standard; protein; 106 AA.
DE   Human ORFX protein sequence SEQ ID NO:22492.
PN   WO200192523-A2.
PD   06-DEC-2001.
PA   (CURA-) CURAGEN CORP.
Query Match           7.8%;  Score 6;  DB 5;  Length 106;
Best Local Similarity 100.0%;  Pred. No. 2.8e+02;
RESULT 763
ID   AAO27176 standard; protein; 107 AA.
DE   S7 protein -11_17.
PN   CN1381478-A.
PD   27-NOV-2002.
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match           7.8%;  Score 6;  DB 6;  Length 107;
Best Local Similarity 100.0%;  Pred. No. 2.9e+02;
RESULT 764
ID   AAG58963 standard; protein; 109 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 76219.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (CURA-) CURAGEN CORP.
Query Match           7.8%;  Score 6;  DB 3;  Length 109;
Best Local Similarity 100.0%;  Pred. No. 2.9e+02;
RESULT 765
ID   ADC95743 standard; protein; 112 AA.
DE   B. faecium protein sequence SEQ ID 5370.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match           7.8%;  Score 6;  DB 7;  Length 112;
Best Local Similarity 100.0%;  Pred. No. 3e+02;
RESULT 766
ID   AAM25544 standard; protein; 118 AA.
DE   Human NF-E2-associated factor 13.
PN   WO200175024-A2.
PD   11-OCT-2001.
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match           7.8%;  Score 6;  DB 5;  Length 118;
Best Local Similarity 100.0%;  Pred. No. 3.1e+02;
RESULT 767
ID   AAY95028 standard; protein; 120 AA.
DE   Human clone vp7_1 ORF2, SEQ ID NO:128.
PN   WO200011015-A1.
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PD   02-MAR-2000.
PA   (ALPH-) ALPHAGENE INC.
     Query Match   7.8%; Score 6; DB 3; Length 120;
     Best Local Similarity 100.0%; Pred. No. 3.2e+02;
RESULT 768
ID   ABO61313 standard; protein; 120 AA.
DE   Klebsiella pneumoniae polypeptide seqid 7830.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 120;
     Best Local Similarity 100.0%; Pred. No. 3.2e+02;
RESULT 769
ID   ABO65064 standard; protein; 123 AA.
DE   Klebsiella pneumoniae polypeptide seqid 11581.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 123;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 770
ID   AAY42642 standard; protein; 124 AA.
DE   B. subtilis response regulator protein SpoOF.
PN   WO9949046-A1.
PD   30-SEP-1999.
PA   (BIOG-) BIOGEMMA UK LTD.
     Query Match   7.8%; Score 6; DB 2; Length 124;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 771
ID   AAO29554 standard; protein; 124 AA.
DE   Human Pco370 protein.
PN   WO2003040331-A2.
PD   15-MAY-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   7.8%; Score 6; DB 6; Length 124;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 772
ID   ABR58286 standard; protein; 124 AA.
DE   BCU0149 protein #SEQ ID 18.
PN   WO2003029421-A2.
PD   10-APR-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   7.8%; Score 6; DB 6; Length 124;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 773
ID   ABB11372 standard; peptide; 126 AA.
DE   Human breast cancer related protein BCRB2 homologue, SEQ ID NO:1742.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 126;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 774
ID   ADS12020 standard; protein; 126 AA.
DE   Human therapeutic contig protein - SEQ ID 2257.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
     Query Match   7.8%; Score 6; DB 8; Length 126;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 775
ID   ADS11864 standard; protein; 126 AA.
DE   Human therapeutic contig protein - SEQ ID 2101.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
     Query Match   7.8%; Score 6; DB 8; Length 126;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 776
ID   ADS11863 standard; protein; 126 AA.
DE   Human therapeutic contig protein - SEQ ID 2100.
PN   WO2004080148-A2.
PD   23-SEP-2004.

PA   (NUVE-) NUVELO INC.
     Query Match   7.8%; Score 6; DB 8; Length 126;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
RESULT 777
ID   ADC97370 standard; protein; 128 AA.
DE   E. faecium protein sequence SEQ ID 6997.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 128;
     Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 778
ID   ADF04401 standard; protein; 128 AA.
DE   Bacterial polypeptide #514.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 128;
     Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 779
ID   AAB85730 standard; protein; 130 AA.
DE   Enzyme involved in carotenoid biosynthetic pathway.
PN   JP200114077-A.
PD   05-JUN-2001.
PA   (MITU) MITSUBISHI CHEM CORP.
     Query Match   7.8%; Score 6; DB 4; Length 130;
     Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 780
ID   AAG90438 standard; protein; 130 AA.
DE   C glutamicum protein fragment SEQ ID NO: 4192.
PN   EP1108790-A2.
PD   20-JUN-2001.
PA   (KYOW) KYOWA HAKKO KOGYO KK.
     Query Match   7.8%; Score 6; DB 4; Length 130;
     Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 781
ID   AAR45156 standard; protein; 133 AA.
DE   Botrocetin alpha subunit.
PN   EP574621-A1.
PD   22-DEC-1993.
PA   (UYFU-) UNIV FUJITA HEALTH.
PA   (GENZ) GENZYME CORP.
     Query Match   7.8%; Score 6; DB 2; Length 133;
     Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 782
ID   AAM41921 standard; protein; 135 AA.
DE   Human polypeptide SEQ ID NO 6852.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 135;
     Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 783
ID   ADE10004 standard; protein; 135 AA.
DE   Novel protein-related contig polypeptide sequence #592.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 7; Length 135;
     Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 784
ID   ADA55086 standard; protein; 136 AA.
DE   Human protein, SEQ ID 2654.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   7.8%; Score 6; DB 6; Length 136;
     Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 785
ID   ABU26249 standard; protein; 142 AA.
DE   Protein encoded by Prokaryotic essential gene #11776.
PN   WO200277183-A2.

PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match 7.8%; Score 6; DB 6; Length 142;
    Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 786
ID ADE08443 standard; protein; 146 AA.
DE Novel protein (useful for identifying genetic disorders) #598.
PN WO200305154152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
    Query Match 7.8%; Score 6; DB 7; Length 146;
    Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 787
ID AAM93730 standard; protein; 147 AA.
DE Human polypeptide, SEQ ID NO:3691.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
    Query Match 7.8%; Score 6; DB 4; Length 147;
    Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 788
ID ADL31658 standard; protein; 147 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3691.
PN EP1396541-A2.
PD 10-MAR-2004.
PA (REAS-) RBS ASSOC BIOTECHNOLOGY.
    Query Match 7.8%; Score 6; DB 8; Length 147;
    Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 789
ID ABP39482 standard; protein; 160 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4327.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match 7.8%; Score 6; DB 5; Length 160;
    Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 790
ID ADC86547 standard; protein; 160 AA.
DE Human GPCR protein SEQ ID NO:1000.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match 7.8%; Score 6; DB 7; Length 160;
    Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 791
ID ADS05359 standard; protein; 160 AA.
DE Staphylococcus epidermis polypeptide seqid 4654.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
    Query Match 7.8%; Score 6; DB 8; Length 160;
    Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 792
ID AAU32072 standard; protein; 164 AA.
DE Novel human secreted protein #2563.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
    Query Match 7.8%; Score 6; DB 4; Length 164;
    Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 793
ID ABP08409 standard; protein; 164 AA.
DE Human ORFX protein sequence SEQ ID NO:16800.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
    Query Match 7.8%; Score 6; DB 5; Length 164;
    Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 794
ID ABB50914 standard; protein; 167 AA.
DE Human secreted protein encoded by gene 96 SEQ ID NO:867.

PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match 7.8%; Score 6; DB 4; Length 167;
    Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 795
ID AAG65162 standard; protein; 167 AA.
DE Human 5-phosphatase 18.
PN WO200164730-A1.
PD 07-SEP-2001.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
    Query Match 7.8%; Score 6; DB 4; Length 167;
    Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 796
ID ABO45171 standard; protein; 167 AA.
DE Novel human secreted protein #96 fragment #2.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match 7.8%; Score 6; DB 6; Length 167;
    Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 797
ID ABO26651 standard; protein; 167 AA.
DE Protein associated with novel secreted protein gene 96 #2.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match 7.8%; Score 6; DB 7; Length 167;
    Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 798
ID ADC32791 standard; protein; 171 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2873.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
    Query Match 7.8%; Score 6; DB 7; Length 171;
    Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 799
ID ADF60188 standard; protein; 171 AA.
DE Human contig polypeptide sequence SEQ ID NO:2555.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
    Query Match 7.8%; Score 6; DB 7; Length 171;
    Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 800
ID ADF28442 standard; protein; 171 AA.
DE Human neurological therapy-related protein - SED ID 352.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
    Query Match 7.8%; Score 6; DB 7; Length 171;
    Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 801
ID ABO72027 standard; protein; 171 AA.
DE Pseudomonas aeruginosa polypeptide #4202.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match 7.8%; Score 6; DB 7; Length 171;
    Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 802
ID ADJ49069 standard; protein; 173 AA.
DE Oil-associated gene related protein #569.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
    Query Match 7.8%; Score 6; DB 8; Length 173;
    Best Local Similarity 100.0%; Pred. No. 4.5e+02;

RESULT 803
ID AAB60280 standard; protein; 174 AA.
DE Neurospora crassa Cdc68 protein fragment.
PN WO0007215-A1.
PD 21-DEC-2000.
PA (ANAD-) ANADYS PHARM INC.
    Query Match   7.8%; Score 6; DB 4; Length 174;
    Best Local Similarity 100.0%; Pred. No. 4.5e+02;

RESULT 804
ID ABM73677 standard; protein; 179 AA.
DE DNA clone originating in barley containing SNP sequence #87.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
    Query Match   7.8%; Score 6; DB 7; Length 179;
    Best Local Similarity 100.0%; Pred. No. 4.7e+02;

RESULT 805
ID ABU45301 standard; protein; 181 AA.
DE Protein encoded by Prokaryotic essential gene #30828.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   7.8%; Score 6; DB 6; Length 181;
    Best Local Similarity 100.0%; Pred. No. 4.7e+02;

RESULT 806
ID AAU38465 standard; protein; 182 AA.
DE Salmonella typhi cellular proliferation protein #356.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   7.8%; Score 6; DB 4; Length 182;
    Best Local Similarity 100.0%; Pred. No. 4.7e+02;

RESULT 807
ID ABU54893 standard; protein; 182 AA.
DE Metabolic pathway (MP) protein #23.
PN US2002142422-A1.
PD 03-OCT-2002.
PA (LERC/) LERCHL J.
PA (RENZ/) RENZ A.
PA (EHRH/) EHRHARDT T.
PA (REIN/) REINDL A.
PA (CIRP/) CIRPUS P.
PA (BISC/) BISCHOFF F.
PA (FRAN/) FRANK M.
PA (FREU/) FREUND A.
PA (DUWE/) DUWENIG E.
PA (SCHM/) SCHMIDT R.
PA (RESK/) RESKI R.
    Query Match   7.8%; Score 6; DB 6; Length 182;
    Best Local Similarity 100.0%; Pred. No. 4.7e+02;

RESULT 808
ID ABU48016 standard; protein; 182 AA.
DE Protein encoded by Prokaryotic essential gene #33543.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   7.8%; Score 6; DB 6; Length 182;
    Best Local Similarity 100.0%; Pred. No. 4.7e+02;

RESULT 809
ID ADA34686 standard; protein; 185 AA.
DE Acinetobacter baumannii protein #1847.
PN US656958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   7.8%; Score 6; DB 6; Length 185;
    Best Local Similarity 100.0%; Pred. No. 4.8e+02;

RESULT 810
ID ABB67680 standard; protein; 195 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29832.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   7.8%; Score 6; DB 4; Length 195;

RESULT 811
ID ADR08929 standard; protein; 201 AA.
DE Human protein useful for treating neurological disease Seq 2435.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
    Query Match   7.8%; Score 6; DB 8; Length 201;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 812
ID ABM67845 standard; protein; 202 AA.
DE Photorhabdus luminescens protein sequence #942.
PN WO20029486-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
    Query Match   7.8%; Score 6; DB 6; Length 202;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 813
ID AAB93444 standard; protein; 203 AA.
DE Human protein sequence SEQ ID NO:12686.
PN EP1074617-A1.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
    Query Match   7.8%; Score 6; DB 4; Length 203;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 814
ID ABB89562 standard; protein; 203 AA.
DE Human polypeptide SEQ ID NO 1938.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   7.8%; Score 6; DB 5; Length 203;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 815
ID ABU56465 standard; protein; 203 AA.
DE Lung cancer-associated polypeptide #58.
PN WO20028443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
    Query Match   7.8%; Score 6; DB 6; Length 203;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 816
ID ADN05076 standard; protein; 203 AA.
DE Antipsoriatic protein sequence #717.
PN WO200402879-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
    Query Match   7.8%; Score 6; DB 8; Length 203;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 817
ID AAU50621 standard; protein; 207 AA.
DE Propionibacterium acnes immunogenic protein #11517.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
    Query Match   7.8%; Score 6; DB 4; Length 207;
    Best Local Similarity 100.0%; Pred. No. 5.3e+02;

RESULT 818
ID ABM47140 standard; protein; 207 AA.
DE Propionibacterium acnes secreted polypeptide #11816.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
    Query Match   7.8%; Score 6; DB 6; Length 207;
    Best Local Similarity 100.0%; Pred. No. 5.3e+02;

RESULT 819
ID AAB18245 standard; protein; 209 AA.
DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:102.
PN WO20025728-A2.
PD 11-MAY-2000.
PA (HOPF/) HOFFMAN S.
PA (CARU/) CARUCCI D.

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PA  (GARD/) GARDNER M.
PA  (VENT/) VENTER J C.
    Query Match      7.8%;    Score 6;  DB 3;  Length 209;
    Best Local Similarity  100.0%;  Pred. No. 5.4e+02;
RESULT 820
ID  AAM27724 standard; protein; 210 AA.
DE  Amino acid sequence of the specification.
PN  WO9737019-A1.
PD  09-OCT-1997.
PA  (NINA-) JAPAN NAT INST HEALTH SCI.
PA  (NICA-) JAPANESE FOUND CANCER RES.
    Query Match      7.8%;    Score 6;  DB 2;  Length 210;
    Best Local Similarity  100.0%;  Pred. No. 5.4e+02;
RESULT 821
ID  AAM40135 standard; protein; 210 AA.
DE  Human polypeptide SEQ ID NO 3280.
PN  WO200153312-A1.
PD  26-JUL-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match      7.8%;    Score 6;  DB 4;  Length 210;
    Best Local Similarity  100.0%;  Pred. No. 5.4e+02;
RESULT 822
ID  ABO01414 standard; protein; 210 AA.
DE  Human protein NOV40b.
PN  WO2003023008-A2.
PD  20-MAR-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match      7.8%;    Score 6;  DB 6;  Length 210;
    Best Local Similarity  100.0%;  Pred. No. 5.4e+02;
RESULT 823
ID  ADN96200 standard; protein; 210 AA.
DE  Human NOVX polypeptide #127.
PN  US2004067490-A1.
PD  08-APR-2004.
PA  (ZHON/) ZHONG M.
PA  (LILL/) LI L.
PA  (GORM/) GORMAN L.
PA  (SPYT/) SPYTEK K A.
PA  (KEKU/) KEKUDA R.
PA  (TAUP/) TAUPIER R J.
PA  (ANDE/) ANDERSON D W.
PA  (VERN/) VERNET C A M.
PA  (CATT/) CATTERTON E.
PA  (MILL/) MILLER C E.
PA  (SHEN/) SHENOY S G.
PA  (PATT/) PATTURAJAN M.
PA  (PENA/) PENA C E A.
PA  (TCHE/) TCHERNEV V T.
PA  (PADI/) PADIGARU M.
PA  (GUSE/) GUSEV V Y.
PA  (MALY/) MALYANKAR U M.
PA  (BURG/) BURGESS C E.
PA  (GERL/) GERLACH V.
PA  (CASM/) CASMAN S J.
PA  (RIEG/) RIEGER D K.
PA  (GROS/) GROSSE W M.
PA  (SMIT/) SMITHSON G.
PA  (PEYM/) PEYMAN J A.
PA  (STAR/) STARLING G.
PA  (ROTH/) ROTHENBERG M E.
PA  (LARO/) LAROCHELLE W J.
PA  (SHIM/) SHIMKETS R A.
PA  (CRAB/) CRABTREE J.
PA  (RAST/) RASTELLI L.
PA  (VOSS/) VOSS E Z.
PA  (BOLD/) BOLDOG F L.
PA  (EDIN/) EDINGER S R.
PA  (MILL/) MILLET I.
PA  (MACD/) MACDOUGALL J R.
PA  (ELLE/) ELLERMAN K.
PA  (CHAP/) CHAPOVAL A.
    Query Match      7.8%;    Score 6;  DB 8;  Length 210;
    Best Local Similarity  100.0%;  Pred. No. 5.4e+02;

RESULT 824
ID  ADF07175 standard; protein; 212 AA.
DE  Bacterial polypeptide #3288.
PN  US605709-B1.
PD  12-AUG-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match      7.8%;    Score 6;  DB 7;  Length 212;
    Best Local Similarity  100.0%;  Pred. No. 5.5e+02;
RESULT 825
ID  ABB61788 standard; protein; 213 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 12156.
PN  WO20017042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match      7.8%;    Score 6;  DB 4;  Length 213;
    Best Local Similarity  100.0%;  Pred. No. 5.5e+02;
RESULT 826
ID  AAR45007 standard; protein; 215 AA.
DE  Sequence encoded by a human CD30-L cDNA clone.
PN  WO9324135-A1.
PD  09-DEC-1993.
PA  (IMMV ) IMMUNEX CORP.
    Query Match      7.8%;    Score 6;  DB 2;  Length 215;
    Best Local Similarity  100.0%;  Pred. No. 5.5e+02;
RESULT 827
ID  ADL24285 standard; protein; 215 AA.
DE  Human CD30-L #1.
PN  WO2004019866-A2.
PD  11-MAR-2004.
PA  (IMMV ) IMMUNEX CORP.
    Query Match      7.8%;    Score 6;  DB 8;  Length 215;
    Best Local Similarity  100.0%;  Pred. No. 5.5e+02;
RESULT 828
ID  ABR53784 standard; protein; 220 AA.
DE  Protein sequence #SEQ ID 2433.
PN  EP1258494-A1.
PD  20-NOV-2002.
PA  (CELI-) CELLZOME AG.
    Query Match      7.8%;    Score 6;  DB 6;  Length 220;
    Best Local Similarity  100.0%;  Pred. No. 5.7e+02;
RESULT 829
ID  ADK63828 standard; protein; 220 AA.
DE  Disease treating protein complex-derived protein #1461.
PN  EP1338608-A2.
PD  27-AUG-2003.
PA  (CELL-) CELLZOME AG.
    Query Match      7.8%;    Score 6;  DB 7;  Length 220;
    Best Local Similarity  100.0%;  Pred. No. 5.7e+02;
RESULT 830
ID  ADL05021 standard; protein; 224 AA.
DE  M. catarrhalis protein #787.
PN  US6673910-B1.
PD  06-JAN-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match      7.8%;    Score 6;  DB 8;  Length 224;
    Best Local Similarity  100.0%;  Pred. No. 5.8e+02;
RESULT 831
ID  ADA33598 standard; protein; 231 AA.
DE  Acinetobacter baumannii protein #759.
PN  US6562958-B1.
PD  13-MAY-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match      7.8%;    Score 6;  DB 6;  Length 231;
    Best Local Similarity  100.0%;  Pred. No. 5.9e+02;
RESULT 832
ID  ABG30262 standard; protein; 233 AA.
DE  Novel human diagnostic protein #30253.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match      7.8%;    Score 6;  DB 4;  Length 233;
    Best Local Similarity  100.0%;  Pred. No. 6e+02;
RESULT 833
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ID   ADB64902 standard; protein; 233 AA.
DE   Human protein encoded by clone PLACE6010701O.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             7.8%;  Score 6;  DB 7;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 834
ID   ADI21122 standard; protein; 233 AA.
DE   Novel human protein #97.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             7.8%;  Score 6;  DB 7;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 835
ID   ADS22095 standard; protein; 233 AA.
DE   Bacterial polypeptide #11128.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match             7.8%;  Score 6;  DB 8;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 836
ID   AAR45009 standard; protein; 234 AA.
DE   Sequence encoded by a human CD30-L cDNA clone encoding additional N-
DE   terminal amino acids.
PN   WO9324135-A1.
PD   09-DEC-1993.
PA   (IMMV ) IMMUNEX CORP.
  Query Match             7.8%;  Score 6;  DB 2;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 837
ID   AAU33818 standard; protein; 234 AA.
DE   Staphylococcus aureus cellular proliferation protein #94.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match             7.8%;  Score 6;  DB 4;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 838
ID   AAU78086 standard; protein; 234 AA.
DE   Human CD30-ligand (CD30L) protein sequence.
PN   WO200211767-A2.
PD   14-FEB-2002.
PA   (IMMV ) IMMUNEX CORP.
  Query Match             7.8%;  Score 6;  DB 5;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 839
ID   ABP97382 standard; protein; 234 AA.
DE   Human CD153 protein.
PN   WO2003000286-A1.
PD   03-JAN-2003.
PA   (SUNR ) SUNTORY LTD.
PA   (SUNT ) SUNTORY BIOMEDICAL RES LTD.
  Query Match             7.8%;  Score 6;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 840
ID   ABR42311 standard; protein; 234 AA.
DE   Human CD30LG protein.
PN   WO2003040307-A2.
PD   15-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             7.8%;  Score 6;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 841
ID   ABO01413 standard; protein; 234 AA.
DE   Human protein NOV40a.

PN   WO2003023008-A2.
PD   20-MAR-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             7.8%;  Score 6;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 842
ID   ADC35198 standard; protein; 234 AA.
DE   Human TNF ligand family member #8.
PN   US2003100074-A1.
PD   29-MAY-2003.
PA   (YUGG/) YU G.
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (NARD/) NARDELLI B.
  Query Match             7.8%;  Score 6;  DB 7;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 843
ID   ADD25574 standard; protein; 234 AA.
DE   Binding domain-immunoglobulin fusion protein-associated protein #64.
PN   US2003118592-A1.
PD   26-JUN-2003.
PA   (GENE-) GENECRAFT INC.
  Query Match             7.8%;  Score 6;  DB 7;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 844
ID   ABW02274 standard; protein; 234 AA.
DE   Human CD30LG protein.
PN   US2003198640-A1.
PD   23-OCT-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             7.8%;  Score 6;  DB 7;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 845
ID   ADH77718 standard; protein; 234 AA.
DE   Enterococcus faecalis polypeptide #2198.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
  Query Match             7.8%;  Score 6;  DB 7;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 846
ID   ADL24287 standard; protein; 234 AA.
DE   Human CD30-L #2.
PN   WO2004019866-A2.
PD   11-MAR-2004.
PA   (IMMV ) IMMUNEX CORP.
  Query Match             7.8%;  Score 6;  DB 8;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;

RESULT 847
ID   ADN96198 standard; protein; 234 AA.
DE   Human NOVX polypeptide #126.
PN   US2004067490-A1.
PD   08-APR-2004.
PA   (ZHON/) ZHONG M.
PA   (LILL/) LI L.
PA   (GORM/) GORMAN L.
PA   (SPYT/) SPYTEK K A.
PA   (KEKU/) KEKUDA R.
PA   (TAUP/) TAUPIER R J.
PA   (ANDE/) ANDERSON D W.
PA   (VERN/) VERNET C A M.
PA   (CATT/) CATTERTON E.
PA   (MILL/) MILLER C E.
PA   (SHEN/) SHENOY S G.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (TCHE/) TCHERNEV V T.
PA   (PADI/) PADIGARU M.
PA   (GUSE/) GUSEV V Y.
PA   (MALY/) MALYANKAR U M.
PA   (BURG/) BURGESS C E.
PA   (GERL/) GERLACH V.
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PA   (CASM/) CASMAN S J.
PA   (RIEG//) RIEGER D K.
PA   (GROS//) GROSSE W M.
PA   (SMIT/) SMITHSON G.
PA   (PEYM/) PEYMAN J A.
PA   (STAR/) STARLING G.
PA   (ROTH/) ROTHENBERG M E.
PA   (LARO/) LAROCHELLE W J.
PA   (SHIM/) SHIMKETS R A.
PA   (CRAB/) CRABTREE J.
PA   (RAST/) RASTELLI L.
PA   (VOSS/) VOSS E Z.
PA   (BOLD/) BOLDOG F L.
PA   (EDIN/) EDINGER S R.
PA   (MILL/) MILLET I.
PA   (MACD/) MACDOUGALL J R.
PA   (ELLE/) ELLERMAN K.
PA   (CHAP/) CHAPOVAL A.
      Query Match   7.8%;   Score 6; DB 8; Length 234;
      Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 848
ID   ADQ59514 standard; protein; 234 AA.
DE   Human cancer-associated (CA) protein sequence SEQ ID NO:150.
PN   WO200405288-A1.
PD   15-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
      Query Match   7.8%;   Score 6; DB 8; Length 234;
      Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 849
ID   AAU37009 standard; protein; 241 AA.
DE   Staphylococcus aureus cellular proliferation protein #1179.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   7.8%;   Score 6; DB 4; Length 241;
      Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 850
ID   ABU16028 standard; protein; 241 AA.
DE   Protein encoded by Prokaryotic essential gene #1555.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   7.8%;   Score 6; DB 6; Length 241;
      Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 851
ID   ABM73572 standard; protein; 241 AA.
DE   Staphylococcus aureus protein #2812.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
      Query Match   7.8%;   Score 6; DB 5; Length 243;
      Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 852
ID   ABB47788 standard; protein; 243 AA.
DE   Listeria monocytogenes protein #492.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
      Query Match   7.8%;   Score 6; DB 4; Length 244;
      Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 853
ID   AAU35290 standard; protein; 244 AA.
DE   Enterococcus faecalis cellular proliferation protein #577.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   7.8%;   Score 6; DB 4; Length 244;
      Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 854
ID   ABU29336 standard; protein; 244 AA.
DE   Protein encoded by Prokaryotic essential gene #14863.
PN   WO200277183-A2.
PD   03-OCT-2002.

PA   (ELIT-) ELITRA PHARM INC.
      Query Match   7.8%;   Score 6; DB 6; Length 244;
      Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 855
ID   AAW64220 standard; protein; 245 AA.
DE   Human secreted protein from clone CG300_3.
PN   WO9827205-A2.
PD   25-JUN-1998.
PA   (GEMY) GENETICS INST INC.
      Query Match   7.8%;   Score 6; DB 2; Length 245;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 856
ID   AAM93721 standard; protein; 245 AA.
DE   Human polypeptide, SEQ ID NO: 3671.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
      Query Match   7.8%;   Score 6; DB 4; Length 245;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 857
ID   AAB90730 standard; protein; 245 AA.
DE   Human CG300_3 protein sequence SEQ ID 159.
PN   WO200119988-A1.
PD   22-MAR-2001.
PA   (GEMY) GENETICS INST INC.
      Query Match   7.8%;   Score 6; DB 4; Length 245;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 858
ID   ADL31638 standard; protein; 245 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3671.
PN   EP139543-A2.
PD   10-MAR-2004.
PA   (REAS) RES ASSOC BIOTECHNOLOGY.
      Query Match   7.8%;   Score 6; DB 8; Length 245;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 859
ID   AAB11054 standard; protein; 246 AA.
DE   S. mutans sortase transamidase srtA protein.
PN   WO200062804-A2.
PD   26-OCT-2000.
PA   (REGC) UNIV CALIFORNIA.
      Query Match   7.8%;   Score 6; DB 3; Length 246;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 860
ID   AAE36578 standard; protein; 246 AA.
DE   Streptococcus mutans SrtA enzyme.
PN   WO200302085-A2.
PD   13-MAR-2003.
PA   (REGC) UNIV CALIFORNIA.
      Query Match   7.8%;   Score 6; DB 6; Length 246;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 861
ID   ABU61757 standard; protein; 246 AA.
DE   Sortase-transamidase homologue from Streptococcus mutans.
PN   US2003022178-A1.
PD   30-JAN-2003.
PA   (SCHN/) SCHNEEWIND O.
PA   (MAZM/) MAZMANIAN S.
PA   (LIUG/) LIU G.
PA   (TONT/) TON-THAT H.
      Query Match   7.8%;   Score 6; DB 6; Length 246;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 862
ID   ABU44402 standard; protein; 246 AA.
DE   Protein encoded by Prokaryotic essential gene #29929.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   7.8%;   Score 6; DB 6; Length 246;
      Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 863
ID   AAR92054 standard; protein; 248 AA.
DE   Xylanase precursor.

PN AU9525086-A.
PD 08-FEB-1996.
PA (SOLV) SOLVAY SA.
Query Match 7.8%; Score 6; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 864
ID AAW44262 standard; protein; 248 AA.
DE Glycosyl hydrolase family 11 xylanase derived from Bacillus sp.
PN WO9743409-A2.
PD 20-NOV-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.8%; Score 6; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 865
ID AAW44265 standard; protein; 248 AA.
DE Xylanase activity positive clone protein SEQ ID NO:12.
PN WO9743409-A2.
PD 20-NOV-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.8%; Score 6; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 866
ID AAB42838 standard; protein; 249 AA.
DE Human ORFX ORF2602 polypeptide sequence SEQ ID NO:5204.
PN WO200101079-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 6; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 867
ID AAE35948 standard; protein; 250 AA.
DE Zea mays (Zm) Bax inhibitor (BI)-1.
PN WO200201079-A2.
PD 19-DEC-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.8%; Score 6; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 868
ID AAY00252 standard; protein; 251 AA.
DE Enterococcus faecalis protein EF130.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 6; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 869
ID ABP43471 standard; protein; 251 AA.
DE E faecalis EF130 protein.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 6; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 870
ID ABU13750 standard; protein; 251 AA.
DE E. faecalis novel protein #243.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 6; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 871
ID ABU88499 standard; protein; 251 AA.
DE Enterococcus faecalis EF040 polypeptide #243.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 6; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 872
ID ADH88100 standard; protein; 251 AA.
DE Enterococcus faecalis polypeptide #2580.
PN US6617156-B1.

PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 7.8%; Score 6; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 873
ID ABO6470 standard; protein; 254 AA.
DE Klebsiella pneumoniae polypeptide seqid 12987.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.8%; Score 6; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 874
ID ABU15858 standard; protein; 257 AA.
DE Protein encoded by Prokaryotic essential gene #1385.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 875
ID ABU39498 standard; protein; 257 AA.
DE Protein encoded by Prokaryotic essential gene #25025.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 876
ID AAU35177 standard; protein; 259 AA.
DE Enterococcus faecalis cellular proliferation protein #464.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 877
ID ABU29157 standard; protein; 259 AA.
DE Protein encoded by Prokaryotic essential gene #14684.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 878
ID AAG90297 standard; protein; 260 AA.
DE C glutamicum protein fragment SEQ ID NO: 4051.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 7.8%; Score 6; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 879
ID ADB64936 standard; protein; 262 AA.
DE Human protein encoded by clone PROST20015210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.8%; Score 6; DB 7; Length 262;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 880
ID AAU34360 standard; protein; 267 AA.
DE Staphylococcus aureus cellular proliferation protein #636.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 881
ID AAB18237 standard; protein; 269 AA.
DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:94.

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PN   WO200025728-A2.
PD   11-MAY-2000.
PA   (HOFF/) HOFFMAN S.
PA   (CARU/) CARUCCI D.
PA   (GARD/) GARDNER M.
PA   (VENT/) VENTER J C.
     Query Match         7.8%;   Score 6;  DB 3;  Length 269;
     Best Local Similarity 100.0%;  Pred. No. 6.8e+02;
RESULT 882
ID   AAU37278 standard; protein; 269 AA.
DE   Staphylococcus aureus cellular proliferation protein #1448.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match         7.8%;   Score 6;  DB 4;  Length 269;
     Best Local Similarity 100.0%;  Pred. No. 6.8e+02;
RESULT 883
ID   ABM72048 standard; protein; 269 AA.
DE   Staphylococcus aureus protein #1288.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match         7.8%;   Score 6;  DB 6;  Length 269;
     Best Local Similarity 100.0%;  Pred. No. 6.8e+02;
RESULT 884
ID   AAG27984 standard; protein; 273 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 33032.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match         7.8%;   Score 6;  DB 3;  Length 273;
     Best Local Similarity 100.0%;  Pred. No. 6.9e+02;
RESULT 885
ID   ABM67790 standard; protein; 273 AA.
DE   Photorhabdus luminescens protein sequence #887.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match         7.8%;   Score 6;  DB 6;  Length 273;
     Best Local Similarity 100.0%;  Pred. No. 6.9e+02;
RESULT 886
ID   ADF04485 standard; protein; 275 AA.
DE   Bacterial polypeptide #598.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match         7.8%;   Score 6;  DB 7;  Length 275;
     Best Local Similarity 100.0%;  Pred. No. 7e+02;
RESULT 887
ID   ADF06864 standard; protein; 275 AA.
DE   Bacterial polypeptide #2977.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match         7.8%;   Score 6;  DB 7;  Length 275;
     Best Local Similarity 100.0%;  Pred. No. 7e+02;
RESULT 888
ID   ADQ65898 standard; protein; 275 AA.
DE   Novel human protein sequence #871.
PN   EP1440981-A2.
PD   28-JUL-2004.
PA   (RRAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match         7.8%;   Score 6;  DB 8;  Length 275;
     Best Local Similarity 100.0%;  Pred. No. 7e+02;
RESULT 889
ID   ADI28917 standard; protein; 276 AA.
DE   Sarcocystis neurona antigenic protein SnSAG1.
PN   WO2004005489-A2.
PD   15-JAN-2004.
PA   (KENT ) UNIV KENTUCKY RES FOUND.
     Query Match         7.8%;   Score 6;  DB 8;  Length 276;
     Best Local Similarity 100.0%;  Pred. No. 7e+02;
RESULT 890

ID   ADR44985 standard; protein; 276 AA.
DE   Sarcocystis neurona (Sn) SAG1 antigenic protein.
PN   US200162418-A1.
PD   19-AUG-2004.
PA   (HOWE/) HOWE D K.
     Query Match         7.8%;   Score 6;  DB 8;  Length 276;
     Best Local Similarity 100.0%;  Pred. No. 7e+02;
RESULT 891
ID   AAG27983 standard; protein; 277 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 33031.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match         7.8%;   Score 6;  DB 3;  Length 277;
     Best Local Similarity 100.0%;  Pred. No. 7e+02;
RESULT 892
ID   AAR22996 standard; protein; 288 AA.
DE   Yeast proteasome YC1 subunit.
PN   JP04077497-A.
PD   11-MAR-1992.
PA   (SAKA ) OTSUKA PHARM CO LTD.
     Query Match         7.8%;   Score 6;  DB 2;  Length 288;
     Best Local Similarity 100.0%;  Pred. No. 7.3e+02;
RESULT 893
ID   ADS28887 standard; protein; 288 AA.
DE   Bacterial polypeptide #17920.
PN   US200233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match         7.8%;   Score 6;  DB 8;  Length 288;
     Best Local Similarity 100.0%;  Pred. No. 7.3e+02;
RESULT 894
ID   ABO61862 standard; protein; 290 AA.
DE   Klebsiella pneumoniae polypeptide seqid 8379.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match         7.8%;   Score 6;  DB 7;  Length 290;
     Best Local Similarity 100.0%;  Pred. No. 7.3e+02;
RESULT 895
ID   ABO62719 standard; protein; 291 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9236.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match         7.8%;   Score 6;  DB 7;  Length 291;
     Best Local Similarity 100.0%;  Pred. No. 7.4e+02;
RESULT 896
ID   ADR94661 standard; protein; 291 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 3296.
PN   US6800744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match         7.8%;   Score 6;  DB 8;  Length 291;
     Best Local Similarity 100.0%;  Pred. No. 7.4e+02;
RESULT 897
ID   AAG28282 standard; protein; 299 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 33441.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match         7.8%;   Score 6;  DB 3;  Length 299;
     Best Local Similarity 100.0%;  Pred. No. 7.5e+02;
RESULT 898
ID   ABO66231 standard; protein; 301 AA.
DE   Klebsiella pneumoniae polypeptide seqid 12748.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match         7.8%;   Score 6;  DB 7;  Length 301;
     Best Local Similarity 100.0%;  Pred. No. 7.6e+02;
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RESULT 899
ID   ADI21046 standard; protein; 302 AA.
DE   Novel human protein #21.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 7; Length 302;
     Best Local Similarity   100.0%; Pred. No. 7.6e+02;

RESULT 900
ID   AAW20903 standard; protein; 303 AA.
DE   H. pylori secreted or periplasmic protein, 14cp1121orf6.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR) ASTRA AB.
     Query Match   7.8%; Score 6; DB 2; Length 303;
     Best Local Similarity   100.0%; Pred. No. 7.6e+02;

RESULT 901
ID   AAG46594 standard; protein; 305 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 58635.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 305;
     Best Local Similarity   100.0%; Pred. No. 7.7e+02;

RESULT 902
ID   ABG27928 standard; protein; 305 AA.
DE   Novel human diagnostic protein #27919.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 305;
     Best Local Similarity   100.0%; Pred. No. 7.7e+02;

RESULT 903
ID   ABB53878 standard; protein; 306 AA.
DE   Lactococcus lactis protein yfgF.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   7.8%; Score 6; DB 5; Length 306;
     Best Local Similarity   100.0%; Pred. No. 7.7e+02;

RESULT 904
ID   AAE06590 standard; protein; 309 AA.
DE   Human protein having hydrophobic domain, HP10785.
PN   WO200149728-A2.
PD   12-JUL-2001.
PA   (PROT-) PROTEGENE INC.
     Query Match   7.8%; Score 6; DB 3; Length 309;
     Best Local Similarity   100.0%; Pred. No. 7.8e+02;

RESULT 905
ID   AAU29393 standard; protein; 310 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #14.
PN   WO200168858-A2.
PD   20-SEP-2001.
PA   (PHAA) PHARMACIA & UPJOHN CO.
     Query Match   7.8%; Score 6; DB 4; Length 310;
     Best Local Similarity   100.0%; Pred. No. 7.8e+02;

RESULT 906
ID   AAG28281 standard; protein; 310 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 33440.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 310;
     Best Local Similarity   100.0%; Pred. No. 7.8e+02;

RESULT 907
ID   ABB93747 standard; protein; 310 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2958.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.
     Query Match   7.8%; Score 6; DB 5; Length 310;
     Best Local Similarity   100.0%; Pred. No. 7.8e+02;

RESULT 908
ID   ABG60681 standard; protein; 310 AA.

RESULT 908
DE   Novel G protein coupled receptor (nGCPR-x) #14.
PN   US200205830306-A1.
PD   16-MAY-2002.
PA   (VOGE/) VOGELI G.
     Query Match   7.8%; Score 6; DB 5; Length 310;
     Best Local Similarity   100.0%; Pred. No. 7.8e+02;

RESULT 909
ID   ABO82227 standard; protein; 311 AA.
DE   Pseudomonas aeruginosa polypeptide #14402.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 311;
     Best Local Similarity   100.0%; Pred. No. 7.8e+02;

RESULT 910
ID   ABP73849 standard; protein; 314 AA.
DE   Candida albicans essential protein SEQ ID NO 7686.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 5; Length 314;
     Best Local Similarity   100.0%; Pred. No. 7.9e+02;

RESULT 911
ID   ADF04258 standard; protein; 319 AA.
DE   Bacterial polypeptide #371.
PN   US5605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 319;
     Best Local Similarity   100.0%; Pred. No. 8e+02;

RESULT 912
ID   ABG05691 standard; protein; 320 AA.
DE   Novel human diagnostic protein #5682.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 320;
     Best Local Similarity   100.0%; Pred. No. 8e+02;

RESULT 913
ID   AAG27982 standard; protein; 321 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 33030.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 4; Length 321;
     Best Local Similarity   100.0%; Pred. No. 8.1e+02;

RESULT 914
ID   ABB63129 standard; protein; 321 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 16179.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   7.8%; Score 6; DB 3; Length 321;
     Best Local Similarity   100.0%; Pred. No. 8.1e+02;

RESULT 915
ID   AAG28280 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 33439.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 322;
     Best Local Similarity   100.0%; Pred. No. 8.1e+02;

RESULT 916
ID   AAU46913 standard; protein; 327 AA.
DE   Propionibacterium acnes immunogenic protein #7809.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
     Query Match   7.8%; Score 6; DB 4; Length 327;
     Best Local Similarity   100.0%; Pred. No. 8.2e+02;

RESULT 917
ID   ABM43432 standard; protein; 327 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #8108.
PN   WO200303515-A1.
PD   24-APR-2003.

PA   (CORI-) CORIXA CORP.
     Query Match   7.8%;   Score 6;   DB 6; Length 327;
     Best Local Similarity 100.0%;   Pred. No. 8.2e+02;
RESULT 918
ID   ABP75866 standard; protein; 330 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 1050.
PN   WO20028876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   7.8%;   Score 6;   DB 6; Length 330;
     Best Local Similarity 100.0%;   Pred. No. 8.3e+02;
RESULT 919
ID   AAG67466 standard; protein; 331 AA.
DE   Breast amplified G protein coupled receptor (BCA-GPCR)-2.
PN   WO200168704-A2.
PD   20-SEP-2001.
PA   (TULA-) TULARIK INC.
PA   (POWE/) POWERS S.
PA   (YANG/) YANG J.
PA   (CUTL/) CUTLER G.
     Query Match   7.8%;   Score 6;   DB 4; Length 331;
     Best Local Similarity 100.0%;   Pred. No. 8.3e+02;
RESULT 920
ID   ABB49192 standard; protein; 331 AA.
DE   Listeria monocytogenes protein #1896.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   7.8%;   Score 6;   DB 5; Length 331;
     Best Local Similarity 100.0%;   Pred. No. 8.3e+02;
RESULT 921
ID   ABR63704 standard; protein; 331 AA.
DE   Human G-protein coupled receptor BCA-GPCR-2.
PN   WO200305442-A1.
PD   03-JUL-2003.
PA   (TULA-) TULARIK INC.
     Query Match   7.8%;   Score 6;   DB 6; Length 331;
     Best Local Similarity 100.0%;   Pred. No. 8.3e+02;
RESULT 922
ID   ABG02033 standard; protein; 332 AA.
DE   Novel human diagnostic protein #2024.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%;   Score 6;   DB 4; Length 332;
     Best Local Similarity 100.0%;   Pred. No. 8.3e+02;
RESULT 923
ID   AAY44245 standard; protein; 336 AA.
DE   Human cell signalling protein-8.
PN   WO9958558-A2.
PD   18-NOV-1999.
PA   (INCY-) INCYTE PHARM INC.
     Query Match   7.8%;   Score 6;   DB 3; Length 336;
     Best Local Similarity 100.0%;   Pred. No. 8.4e+02;
RESULT 924
ID   AAG30338 standard; protein; 337 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36251.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%;   Score 6;   DB 3; Length 337;
     Best Local Similarity 100.0%;   Pred. No. 8.4e+02;
RESULT 925
ID   ADC23919 standard; protein; 338 AA.
DE   Protein sequence (SeqID 186) exhibiting nitrilase activity.
PN   WO2003000840-A2.
PD   03-JAN-2003.
PA   (DIVE-) DIVERSA CORP.
PA   (MADD/) MADDEN D.
     Query Match   7.8%;   Score 6;   DB 7; Length 338;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 926
ID   ADH36020 standard; protein; 338 AA.
DE   Chemical process monitoring-related nitrilase protein sequence SeqID186.

PN   WO200309187-A2.
PD   27-NOV-2003.
PA   (DIVE-) DIVERSA CORP.
     Query Match   7.8%;   Score 6;   DB 8; Length 338;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 927
ID   ADG93721 standard; protein; 338 AA.
DE   Nitrilase enzyme amino acid sequence SeqID186.
PN   WO200097810-A2.
PD   27-NOV-2003.
PA   (DIVE-) DIVERSA CORP.
     Query Match   7.8%;   Score 6;   DB 8; Length 338;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 928
ID   ADI62318 standard; protein; 338 AA.
DE   Nitrilase polypeptide #93.
PN   WO2003106415-A2.
PD   24-DEC-2003.
PA   (DIVE-) DIVERSA CORP.
     Query Match   7.8%;   Score 6;   DB 8; Length 338;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 929
ID   ADI64439 standard; protein; 338 AA.
DE   Nitrilase seq id 94.
PN   US2004014195-A1.
PD   22-JAN-2004.
PA   (DIVE-) DIVERSA CORP.
     Query Match   7.8%;   Score 6;   DB 8; Length 338;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 930
ID   ABR53456 standard; protein; 340 AA.
DE   Protein sequence #SEQ ID 1777.
PN   EP1258494-A1.
PD   20-NOV-2002.
PA   (CELL-) CELLZOME AG.
     Query Match   7.8%;   Score 6;   DB 6; Length 340;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 931
ID   ADK64610 standard; protein; 340 AA.
DE   Disease treating protein complex-derived protein #1070.
PN   EP1338608-A2.
PD   27-AUG-2003.
PA   (CELL-) CELLZOME AG.
     Query Match   7.8%;   Score 6;   DB 7; Length 340;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 932
ID   ADN19288 standard; protein; 340 AA.
DE   Bacterial polypeptide #1941.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%;   Score 6;   DB 8; Length 340;
     Best Local Similarity 100.0%;   Pred. No. 8.5e+02;
RESULT 933
ID   ABB90323 standard; protein; 342 AA.
DE   Human polypeptide SEQ ID NO 2699.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   7.8%;   Score 6;   DB 5; Length 342;
     Best Local Similarity 100.0%;   Pred. No. 8.6e+02;
RESULT 934
ID   ADC87149 standard; protein; 344 AA.
DE   Human GPCR protein SEQ ID NO:1602.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match   7.8%;   Score 6;   DB 7; Length 344;

Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 935
ID ABB52512 standard; protein; 345 AA.
DE Escherichia coli polypeptide SEQ ID NO 378.
PN WO20016572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.8%; Score 6; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 936
ID AAG46593 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58634.
PN EP1033405-A2.
PD 06-SEP-2000.
RESULT 937
ID ABB90159 standard; protein; 346 AA.
DE Human polypeptide SEQ ID NO 2535.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 6; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 938
ID ABB65881 standard; protein; 350 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24435.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 6; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 939
ID ABU23172 standard; protein; 350 AA.
DE Protein encoded by Prokaryotic essential gene #8699.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 940
ID ADS29964 standard; protein; 351 AA.
DE Bacterial polypeptide #18997.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.8%; Score 6; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 941
ID ABG16162 standard; protein; 353 AA.
DE Novel human diagnostic protein #16153.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.8%; Score 6; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 942
ID ABU10305 standard; protein; 357 AA.
DE Chicken bves (cbves) carboxyl domain.
PN US6503540-B1.
PD 07-JAN-2003.
PA (REES/) REESE D E.
PA (BADE/) BADER D M.
Query Match 7.8%; Score 6; DB 7; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 943
ID ADK52127 standard; protein; 359 AA.
DE Human atopic dermatitis/psoriasis-associated protein #42.
PN WO2004016785-A1.

PD 26-FEB-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 7.8%; Score 6; DB 8; Length 359;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 944
ID ADO29599 standard; protein; 361 AA.
DE Mouse GPCR P2RY4, SEQ ID NO.701.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 7.8%; Score 6; DB 8; Length 361;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 945
ID ADN24861 standard; protein; 362 AA.
DE Bacterial polypeptide #7514.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.8%; Score 6; DB 8; Length 362;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 946
ID ADN47009 standard; protein; 364 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID887.
PN WO200402736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 7.8%; Score 6; DB 8; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
RESULT 947
ID ADN22102 standard; protein; 367 AA.
DE Bacterial polypeptide #4755.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.8%; Score 6; DB 8; Length 367;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 948
ID AAB94843 standard; protein; 368 AA.
DE Human protein sequence SEQ ID NO:16018.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.8%; Score 6; DB 4; Length 368;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 949
ID ADE31201 standard; protein; 370 AA.
DE Pseudomonas aeruginosa polypeptide #13843.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.8%; Score 6; DB 7; Length 370;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 950
ID ABO81668 standard; protein; 373 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID No 333.
PN WO200306237 6-A2.
PD 31-JUL-2003.
PA (HELI-) HELIX RES INST.
Query Match 7.8%; Score 6; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 951
ID ADP99028 standard; protein; 377 AA.
DE C. albicans specific gene, orf6.2502, protein sequence.
PN WO200405965-A2.

PD   08-JUL-2004.
PA   (ELIT-) ELITRA PHARM INC.
PA   (ELIT/) ELITRA CANADA LTD.
     Query Match   7.8%;   Score 6; DB 8; Length 377;
     Best Local Similarity   100.0%;   Pred. No. 9.4e+02;
RESULT 952
ID   AAU33703 standard; protein; 381 AA.
DE   Pseudomonas aeruginosa cellular proliferation protein #147.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%;   Score 6; DB 4; Length 381;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 953
ID   ABU40179 standard; protein; 381 AA.
DE   Protein encoded by Prokaryotic essential gene #25706.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%;   Score 6; DB 6; Length 381;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 954
ID   ABU15637 standard; protein; 381 AA.
DE   Protein encoded by Prokaryotic essential gene #1164.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   7.8%;   Score 6; DB 6; Length 381;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 955
ID   ABB54077 standard; protein; 382 AA.
DE   Lactococcus lactis protein nusA.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%;   Score 6; DB 5; Length 382;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 956
ID   ADM48197 standard; protein; 382 AA.
DE   Polypeptide sequence #247 useful in producing transgenic plants.
PN   US2003233670-A1.
PD   18-DEC-2003.
PA   (EDGE/) EDGERTON M D.
PA   (CHOM/) CHOMET P S.
PA   (LACC/) LACCETTI L B.
     Query Match   7.8%;   Score 6; DB 5; Length 382;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 957
ID   ABP69714 standard; protein; 383 AA.
DE   Human polypeptide SEQ ID NO 1761.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%;   Score 6; DB 5; Length 383;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 958
ID   ADN21352 standard; protein; 383 AA.
DE   Bacterial polypeptide #4005.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%;   Score 6; DB 8; Length 383;
     Best Local Similarity   100.0%;   Pred. No. 9.5e+02;
RESULT 959
ID   AAG22096 standard; protein; 393 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 24894.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%;   Score 6; DB 3; Length 393;

     Best Local Similarity   100.0%;   Pred. No. 9.8e+02;
RESULT 960
ID   AAG22095 standard; protein; 394 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 24893.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%;   Score 6; DB 3; Length 394;
     Best Local Similarity   100.0%;   Pred. No. 9.8e+02;
RESULT 961
ID   ADS24265 standard; protein; 394 AA.
DE   Bacterial polypeptide #13298.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%;   Score 6; DB 8; Length 394;
     Best Local Similarity   100.0%;   Pred. No. 9.8e+02;
RESULT 962
ID   ABU23064 standard; protein; 397 AA.
DE   Protein encoded by Prokaryotic essential gene #8591.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%;   Score 6; DB 6; Length 397;
     Best Local Similarity   100.0%;   Pred. No. 9.9e+02;
RESULT 963
ID   ADN21290 standard; protein; 397 AA.
DE   Bacterial polypeptide #3943.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%;   Score 6; DB 8; Length 397;
     Best Local Similarity   100.0%;   Pred. No. 9.9e+02;
RESULT 964
ID   ABG93164 standard; protein; 398 AA.
DE   S. cerevisiae BAX-associated protein fragment SEQ ID 286.
PN   WO200264766-A2.
PD   22-AUG-2002.
PA   (JANC) JANSSEN PHARM NV.
     Query Match   7.8%;   Score 6; DB 5; Length 398;
     Best Local Similarity   100.0%;   Pred. No. 9.9e+02;
RESULT 965
ID   ADA35124 standard; protein; 398 AA.
DE   Acinetobacter baumannii protein #2285.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%;   Score 6; DB 6; Length 398;
     Best Local Similarity   100.0%;   Pred. No. 9.9e+02;
RESULT 966
ID   ABR63122 standard; protein; 402 AA.
DE   Cattle plasminogen activator inhibitor-1.
PN   WO2003071267-A1.
PD   28-AUG-2003.
PA   (UYVA-) UNIV VANDERBILT.
PA   (DECL/) DECLERCK P J.
     Query Match   7.8%;   Score 6; DB 7; Length 402;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 967
ID   ADG47611 standard; protein; 402 AA.
DE   Bovine plasminogen activator inhibitor-1 (BovPAII).
PN   US6541452-B1.
PD   01-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   7.8%;   Score 6; DB 7; Length 402;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;

RESULT 968
ID   AAG22094 standard; protein; 404 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 24892.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 404;
     Best Local Similarity 100.0%; Pred. No. 1e+03;

RESULT 969
ID   ABU34333 standard; protein; 411 AA.
DE   Protein encoded by Prokaryotic essential gene #19860.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 6; Length 411;
     Best Local Similarity 100.0%; Pred. No. 1e+03;

RESULT 970
ID   AAR66223 standard; protein; 417 AA.
DE   Cystathionine gamma lyase.
PN   JP06292586-A.
PD   21-OCT-1994.
PA   (ASAH) ASAHI KASEI KOGYO KK.
     Query Match   7.8%; Score 6; DB 2; Length 417;
     Best Local Similarity 100.0%; Pred. No. 1e+03;

RESULT 971
ID   ADN27129 standard; protein; 420 AA.
DE   Bacterial polypeptide #9782.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%; Score 6; DB 8; Length 420;
     Best Local Similarity 100.0%; Pred. No. 1e+03;

RESULT 972
ID   ABG23823 standard; protein; 421 AA.
DE   Novel human diagnostic protein #23814.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 4; Length 421;
     Best Local Similarity 100.0%; Pred. No. 1e+03;

RESULT 973
ID   ADB70152 standard; protein; 425 AA.
DE   C. neoformans amino acid sequence SEQ ID NO:3196.
PN   WO2003052076-A2.
PD   26-JUN-2003.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 7; Length 425;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 974
ID   ABO62928 standard; protein; 425 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9445.
PN   US5610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   7.8%; Score 6; DB 7; Length 425;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 975
ID   AAG29446 standard; protein; 426 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 35039.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.8%; Score 6; DB 3; Length 426;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 976
ID   AAY59728 standard; protein; 431 AA.
DE   Human normal ovarian tissue derived protein 5.
PN   DE19816395-A1.
PD   07-OCT-1999.
PA   (META-) METAGEN GES GENOMFORSCHUNG MBH.
     Query Match   7.8%; Score 6; DB 2; Length 431;

RESULT 977
ID   AAR13493 standard; protein; 434 AA.
DE   P.denitrificans COB B.
PN   WO911518-A.
PD   08-AUG-1991.
PA   (RHON) RHONE-POULENC BIOCH.
     Query Match   7.8%; Score 6; DB 2; Length 434;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 978
ID   ADS23740 standard; protein; 446 AA.
DE   Bacterial polypeptide #12773.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%; Score 6; DB 8; Length 446;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 979
ID   AAU38019 standard; protein; 447 AA.
DE   Streptococcus pneumoniae cellular proliferation protein #448.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 4; Length 447;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 980
ID   AAU37897 standard; protein; 447 AA.
DE   Streptococcus pneumoniae cellular proliferation protein #326.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 4; Length 447;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 981
ID   ABU46174 standard; protein; 447 AA.
DE   Protein encoded by Prokaryotic essential gene #31701.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 6; Length 447;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 982
ID   AAY71551 standard; protein; 448 AA.
DE   Florida bitterbush delta-6 fatty acid desaturase.
PN   WO200032790-A2.
PD   08-JUN-2000.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
     Query Match   7.8%; Score 6; DB 3; Length 448;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 983
ID   ADB79971 standard; protein; 449 AA.
DE   Mycobacterium tuberculosis nutrient starvation-inducible protein #5.
PN   WO200304520-A2.
PD   16-JAN-2003.
PA   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
     Query Match   7.8%; Score 6; DB 7; Length 449;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 984
ID   AAR07295 standard; protein; 450 AA.
DE   Nucleoprotein N of Mokola virus.
PN   WO9011358-A.
PD   04-OCT-1990.
PA   (INSP) INST PASTEUR.
     Query Match   7.8%; Score 6; DB 2; Length 450;
     Best Local Similarity 100.0%; Pred. No. 1.1e+03;

RESULT 985
ID   ABB55123 standard; protein; 453 AA.
DE   Lactococcus lactis protein ysdA.
PN   FR2807446-A1.

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PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
        Query Match       7.8%;   Score 6;  DB 5; Length 453;
        Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
RESULT 986
ID   ABB54687 standard; protein; 454 AA.
DE   Lactococcus lactis protein yniG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
        Query Match       7.8%;   Score 6;  DB 5; Length 454;
        Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
RESULT 987
ID   ABU20916 standard; protein; 462 AA.
DE   Protein encoded by Prokaryotic essential gene #6443.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
        Query Match       7.8%;   Score 6;  DB 6; Length 462;
        Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
RESULT 988
ID   ABO63192 standard; protein; 462 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9709.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
        Query Match       7.8%;   Score 6;  DB 7; Length 462;
        Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
RESULT 989
ID   ABG27022 standard; protein; 463 AA.
DE   Novel human diagnostic protein #27013.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       7.8%;   Score 6;  DB 4; Length 463;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 990
ID   AAB41219 standard; protein; 472 AA.
DE   Human ORFX ORF983 polypeptide sequence SEQ ID NO:1966.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
        Query Match       7.8%;   Score 6;  DB 7; Length 462;
        Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
RESULT 991
ID   ABB97828 standard; protein; 472 AA.
DE   Human secretory polypeptide (SPTM) 80.
PN   WO200220756-A2.
PD   14-MAR-2002.
PA   (INCY-) INCYTE GENOMICS INC.
        Query Match       7.8%;   Score 6;  DB 5; Length 472;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 992
ID   ADE08673 standard; protein; 472 AA.
DE   Novel protein (useful for identifying genetic disorders) #828.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
        Query Match       7.8%;   Score 6;  DB 7; Length 472;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 993
ID   ABG29474 standard; protein; 474 AA.
DE   Novel human diagnostic protein #29465.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       7.8%;   Score 6;  DB 4; Length 474;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 994
ID   ADS44078 standard; protein; 486 AA.
DE   Bacterial polypeptide #22508.
PN   US2003233675-A1.
PD   18-DEC-2003.

PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
        Query Match       7.8%;   Score 6;  DB 8; Length 486;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 995
ID   ABU10301 standard; protein; 487 AA.
DE   Fragment of chicken bves (cbves).
PN   US6503540-B1.
PD   07-JAN-2003.
PA   (REES/) REESE D E.
PA   (BADE/) BADER D M.
        Query Match       7.8%;   Score 6;  DB 7; Length 487;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 996
ID   ABO66846 standard; protein; 488 AA.
DE   Klebsiella pneumoniae polypeptide seqid 13363.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
        Query Match       7.8%;   Score 6;  DB 7; Length 488;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 997
ID   ABB63372 standard; protein; 504 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 16908.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
        Query Match       7.8%;   Score 6;  DB 4; Length 504;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 998
ID   ADS44277 standard; protein; 504 AA.
DE   Bacterial polypeptide #22707.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
        Query Match       7.8%;   Score 6;  DB 8; Length 504;
        Best Local Similarity 100.0%;  Pred. No. 1.2e+03;
RESULT 999
ID   ABB59492 standard; protein; 525 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 5268.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
        Query Match       7.8%;   Score 6;  DB 4; Length 525;
        Best Local Similarity 100.0%;  Pred. No. 1.3e+03;
RESULT 1000
ID   ABM85858 standard; protein; 539 AA.
DE   Mouse protein sequence mCP13326.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
        Query Match       7.8%;   Score 6;  DB 7; Length 539;
        Best Local Similarity 100.0%;  Pred. No. 1.3e+03;
RESULT 1001
ID   ABG91046 standard; protein; 542 AA.
DE   Chlamydia trachomatis apolipoprotein N-acetyltransferase protein.
PN   WO200262380-A2.
PD   15-AUG-2002.
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
        Query Match       7.8%;   Score 6;  DB 5; Length 542;
        Best Local Similarity 100.0%;  Pred. No. 1.3e+03;
RESULT 1002
ID   ADD43852 standard; protein; 542 AA.
DE   Chlamydia trachomatis immunogenic protein, SEQ ID No 147.
PN   WO2003049762-A2.
PD   19-JUN-2003.
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PA   (CHIR-) CHIRON SPA.
   Query Match   7.8%;   Score 6;   DB 7; Length 542;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1003
ID   ABB68867 standard; protein; 545 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 33393.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
   Query Match   7.8%;   Score 6;   DB 4; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1004
ID   AAU38979 standard; protein; 545 AA.
DE   Drosophila G-protein coupled receptor, GCPR #57.
PN   WO200170980-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
   Query Match   7.8%;   Score 6;   DB 4; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1005
ID   AAB95605 standard; protein; 545 AA.
DE   Human protein sequence SEQ ID NO.18299.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
   Query Match   7.8%;   Score 6;   DB 4; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1006
ID   AAE38161 standard; protein; 545 AA.
DE   Fruit fly G protein-coupled receptor (GPCR) protein #10.
PN   WO2003052078-A2.
PD   26-JUN-2003.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
   Query Match   7.8%;   Score 6;   DB 7; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1007
ID   ADC31778 standard; protein; 545 AA.
DE   Human novel polypeptide sequence, SEQ ID NO:1860.
PN   WO2003029271-A2.
PD   10-APR-2003.
PA   (HYSE-) HYSEQ INC.
   Query Match   7.8%;   Score 6;   DB 7; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1008
ID   ADC35919 standard; protein; 545 AA.
DE   Drosophila G protein coupled receptor seq id 59.
PN   US2003092124-A1.
PD   15-MAY-2003.
PA   (APPL-) APPLERA CORP.
   Query Match   7.8%;   Score 6;   DB 7; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1009
ID   ADK52117 standard; protein; 545 AA.
DE   Human atopic dermatitis/psoriasis-associated protein #32.
PN   WO2004028479-A2.
PD   26-FEB-2004.
PA   (GENO-) GENOX RES INC.
PA   (UJU-) UNIV JUNTENDO.
   Query Match   7.8%;   Score 6;   DB 8; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1010
ID   ADN05311 standard; protein; 545 AA.
DE   Antipsoriatic protein sequence #829.
PN   WO2004016785-A1.
PD   08-APR-2004.
PA   (GETH) GENENTECH INC.
   Query Match   7.8%;   Score 6;   DB 8; Length 545;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1011
ID   ABO74401 standard; protein; 548 AA.
DE   Pseudomonas aeruginosa polypeptide #6576.
PN   US6551795-B1.
PD   22-APR-2003.

PA   (GENO-) GENOME THERAPEUTICS CORP.
   Query Match   7.8%;   Score 6;   DB 7; Length 548;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1012
ID   ABG91054 standard; protein; 549 AA.
DE   Chlamydia trachomatis serovar D cutE protein.
PN   WO200262380-A2.
PD   15-AUG-2002.
PA   (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
   Query Match   7.8%;   Score 6;   DB 5; Length 549;
   Best Local Similarity   100.0%;   Pred. No. 1.3e+03;
RESULT 1013
ID   ADJ33778 standard; protein; 559 AA.
DE   Protein of the invention SEQ ID NO:755.
PN   WO200187917-A1.
PD   22-NOV-2001.
PA   (HYSE-) HYSEQ INC.
   Query Match   7.8%;   Score 6;   DB 5; Length 559;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1014
ID   AAU31067 standard; protein; 560 AA.
DE   Novel human secreted protein #1558.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
   Query Match   7.8%;   Score 6;   DB 4; Length 560;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1015
ID   ADC38726 standard; protein; 560 AA.
DE   Human secreted protein #40.
PN   US2002193567-A1.
PD   19-DEC-2002.
PA   (GEMY) GENETICS INST INC.
   Query Match   7.8%;   Score 6;   DB 7; Length 560;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1016
ID   AAG31172 standard; protein; 561 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 37391.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (UNMI) UNIV MICHIGAN.
   Query Match   7.8%;   Score 6;   DB 3; Length 561;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1017
ID   AAR66929 standard; protein; 576 AA.
DE   AMML chromosome inv(16) product.
PN   WO9504067-A1.
PD   09-FEB-1995.
PA   (TEXA) UNIV TEXAS SYSTEM.
   Query Match   7.8%;   Score 6;   DB 2; Length 576;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1018
ID   ABR43182 standard; protein; 583 AA.
DE   Human REMAP-14 protein SEQ ID NO:14.
PN   WO2003025130-A2.
PD   27-MAR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
   Query Match   7.8%;   Score 6;   DB 6; Length 583;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1019
ID   AAR96246 standard; protein; 585 AA.
DE   Malic enzyme #1.
PN   JP08089250-A.
PD   09-APR-1996.
PA   (MITK) MITSUI TOATSU CHEM INC.
   Query Match   7.8%;   Score 6;   DB 2; Length 585;
   Best Local Similarity   100.0%;   Pred. No. 1.4e+03;
RESULT 1020
ID   AAR96247 standard; protein; 592 AA.
DE   Malic enzyme #2.
PN   JP08089250-A.
PD   09-APR-1996.
PA   (MITK) MITSUI TOATSU CHEM INC.

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Query Match          7.8%;  Score 6;  DB 2;  Length 592;
Best Local Similarity  100.0%;  Pred. No. 1.4e+03;
RESULT 1021
ID  ADL05729 standard; protein; 598 AA.
DE  M. catarrhalis protein #1495.
PN  US6673910-B1.
PD  06-JAN-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.
Query Match          7.8%;  Score 6;  DB 8;  Length 598;
Best Local Similarity  100.0%;  Pred. No. 1.4e+03;
RESULT 1022
ID  ADB64938 standard; protein; 602 AA.
DE  Human protein encoded by clone PROST20016760.
PN  EP1308459-A2.
PD  07-MAY-2003.
PA  (HELI-) HELIX RES INST.
         (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match          7.8%;  Score 6;  DB 7;  Length 602;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1023
ID  ADF30481 standard; protein; 621 AA.
DE  Rat angiogenesis modulating protein #17.
PN  US200316276-A1.
PD  28-AUG-2003.
PA  (PROC ) PROCTER & GAMBLE CO.
Query Match          7.8%;  Score 6;  DB 7;  Length 621;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1024
ID  ABP65819 standard; protein; 624 AA.
DE  Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:563.
PN  EP1227152-A1.
PD  31-JUL-2002.
PA  (NEST ) SOC PROD NESTLE SA.
Query Match          7.8%;  Score 6;  DB 5;  Length 624;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1025
ID  ADN19456 standard; protein; 624 AA.
DE  Bacterial polypeptide #2109.
PN  US200323675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
         (HINK/) HINKLE G J.
         (SLAT/) SLATER S C.
         (CHEN/) CHEN X.
         (GOLD/) GOLDMAN B S.
Query Match          7.8%;  Score 6;  DB 8;  Length 624;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1026
ID  AAG29253 standard; protein; 631 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 34774.
PN  EP103345-A2.
PD  06-SEP-2000.
Query Match          7.8%;  Score 6;  DB 3;  Length 631;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1027
ID  ADF23256 standard; protein; 631 AA.
DE  AT4g31670 protein #SEQ ID 2.
PN  CN1369502-A.
PD  18-SEP-2002.
PA  (UYBE-) UNIV BEIJING.
Query Match          7.8%;  Score 6;  DB 7;  Length 631;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1028
ID  AAY56516 standard; protein; 636 AA.
DE  Zea mays chlorophyll localised malic acid enzyme.
PN  JP11308994-A.
PD  09-NOV-1999.
PA  (MITA ) MITSUI CHEM INC.
Query Match          7.8%;  Score 6;  DB 3;  Length 636;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1029
ID  AAR70096 standard; protein; 638 AA.
DE  Malic acid enzyme isolated from a rice plant.
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PN  JP07023790-A.
PD  27-JAN-1995.
PA  (NISC ) NISSAN CHEM IND LTD.
Query Match          7.8%;  Score 6;  DB 2;  Length 638;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1030
ID  ADI82510 standard; protein; 638 AA.
DE  Human modifier of p21 (MP21) protein sequence SeqID76.
PN  WO2004005486-A2.
PD  15-JAN-2004.
PA  (EXEL-) EXELIXIS INC.
Query Match          7.8%;  Score 6;  DB 8;  Length 638;
Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
RESULT 1031
ID  AAY35056 standard; protein; 643 AA.
DE  Chlamydia pneumoniae transmembrane protein sequence.
PN  WO9927105-A2.
PD  03-JUN-1999.
PA  (GEST ) GENSET.
Query Match          7.8%;  Score 6;  DB 2;  Length 643;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1032
ID  AAG39461 standard; protein; 643 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 48826.
PN  EP103345-A2.
PD  06-SEP-2000.
Query Match          7.8%;  Score 6;  DB 3;  Length 643;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1033
ID  ABU26526 standard; protein; 643 AA.
DE  Protein encoded by Prokaryotic essential gene #12053.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
Query Match          7.8%;  Score 6;  DB 6;  Length 643;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1034
ID  ADN21267 standard; protein; 645 AA.
DE  Bacterial polypeptide #3920.
PN  US200323675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
         (HINK/) HINKLE G J.
         (SLAT/) SLATER S C.
         (CHEN/) CHEN X.
         (GOLD/) GOLDMAN B S.
Query Match          7.8%;  Score 6;  DB 8;  Length 645;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1035
ID  AAG39460 standard; protein; 653 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 48825.
PN  EP103345-A2.
PD  06-SEP-2000.
Query Match          7.8%;  Score 6;  DB 3;  Length 653;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1036
ID  AAG39459 standard; protein; 654 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 48824.
PN  EP103345-A2.
PD  06-SEP-2000.
Query Match          7.8%;  Score 6;  DB 3;  Length 654;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1037
ID  ABU27648 standard; protein; 655 AA.
DE  Protein encoded by Prokaryotic essential gene #13175.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
Query Match          7.8%;  Score 6;  DB 6;  Length 655;
Best Local Similarity  100.0%;  Pred. No. 1.6e+03;
RESULT 1038
ID  AAU34917 standard; protein; 659 AA.
DE  Enterococcus faecalis cellular proliferation protein #204.
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PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
       Query Match   7.8%;   Score 6; DB 4; Length 659;
       Best Local Similarity 100.0%;   Pred. No. 1.6e+03;
RESULT 1039
ID ABG21920 standard; protein; 667 AA.
DE Novel human diagnostic protein #21911.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
       Query Match   7.8%;   Score 6; DB 4; Length 667;
       Best Local Similarity 100.0%;   Pred. No. 1.6e+03;
RESULT 1040
ID AAB95883 standard; protein; 681 AA.
DE Human protein sequence SEQ ID NO:18994.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
       Query Match   7.8%;   Score 6; DB 4; Length 681;
       Best Local Similarity 100.0%;   Pred. No. 1.6e+03;
RESULT 1041
ID AAB10556 standard; protein; 684 AA.
DE Human aspartate protease psl 5 protein.
PN WO200043505-A2.
PD 27-JUL-2000.
PA (MEMO-) MEMOREC MEDICAL MOLECULAR RES COLOGNE ST.
PA (HOFM/) HOFMANN K.
       Query Match   7.8%;   Score 6; DB 3; Length 684;
       Best Local Similarity 100.0%;   Pred. No. 1.6e+03;
RESULT 1042
ID ADS42758 standard; protein; 684 AA.
DE Bacterial polypeptide #21188.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
       Query Match   7.8%;   Score 6; DB 8; Length 684;
       Best Local Similarity 100.0%;   Pred. No. 1.6e+03;
RESULT 1043
ID ABG69602 standard; protein; 689 AA.
DE Human NOV5 protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
       Query Match   7.8%;   Score 6; DB 5; Length 689;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1044
ID ADN19373 standard; protein; 694 AA.
DE Bacterial polypeptide #2026.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
       Query Match   7.8%;   Score 6; DB 8; Length 694;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1045
ID AAR71384 standard; protein; 712 AA.
DE Tribolium semaphorin I protein.
PN WO9507706-A1.
PD 23-MAR-1995.
PA (REGC) UNIV CALIFORNIA.
       Query Match   7.8%;   Score 6; DB 2; Length 712;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1046
ID ADS44332 standard; protein; 712 AA.
DE Bacterial polypeptide #22762.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
       Query Match   7.8%;   Score 6; DB 8; Length 712;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1047
ID ABU29206 standard; protein; 719 AA.
DE Protein encoded by Prokaryotic essential gene #14733.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
       Query Match   7.8%;   Score 6; DB 6; Length 719;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1048
ID ADH97068 standard; protein; 719 AA.
DE S. pneumoniae RDR alpha subunit protein #2.
PN WO2003102190-A2.
PD 11-DEC-2003.
PA (AFFI-) AFFINIUM PHARM INC.
       Query Match   7.8%;   Score 6; DB 8; Length 719;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1049
ID ADH97066 standard; protein; 719 AA.
DE S. pneumoniae RDR alpha subunit protein #1.
PN WO2003102190-A2.
PD 11-DEC-2003.
PA (AFFI-) AFFINIUM PHARM INC.
       Query Match   7.8%;   Score 6; DB 8; Length 719;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1050
ID ADH87842 standard; protein; 722 AA.
DE Enterococcus faecalis polypeptide #2322.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
       Query Match   7.8%;   Score 6; DB 7; Length 722;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1051
ID ABR58376 standard; protein; 724 AA.
DE Human NOV5b.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
       Query Match   7.8%;   Score 6; DB 6; Length 724;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1052
ID ADF78959 standard; protein; 731 AA.
DE Rice cell cycle gene cullin 3, protein.
PN US2003186362-A1.
PD 02-OCT-2003.
PA (MORG/) MORGANTE M.
PA (FAMO/) FAMODU O O.
PA (WENG/) WENG Z.
       Query Match   7.8%;   Score 6; DB 8; Length 731;
       Best Local Similarity 100.0%;   Pred. No. 1.7e+03;
RESULT 1053
ID ADB70247 standard; protein; 761 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3291.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
       Query Match   7.8%;   Score 6; DB 7; Length 761;
       Best Local Similarity 100.0%;   Pred. No. 1.8e+03;
RESULT 1054
ID ADJ83031 standard; protein; 761 AA.
DE Human NOVX NOV5 protein.
PN US2003170630-A1.
PD 11-SEP-2003.

PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match   7.8%;   Score 6;   DB 7;   Length 761;
Best Local Similarity 100.0%;   Pred. No. 1.8e+03;
RESULT 1055
ID ABU15226 standard; protein; 765 AA.
DE Protein encoded by Prokaryotic essential gene #753.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   7.8%;   Score 6;   DB 6;   Length 765;
Best Local Similarity 100.0%;   Pred. No. 1.8e+03;
RESULT 1056
ID ABU48326 standard; protein; 765 AA.
DE Protein encoded by Prokaryotic essential gene #33853.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   7.8%;   Score 6;   DB 6;   Length 765;
Best Local Similarity 100.0%;   Pred. No. 1.8e+03;
RESULT 1057
ID ABB61410 standard; protein; 798 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11022.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match   7.8%;   Score 6;   DB 4;   Length 798;
Best Local Similarity 100.0%;   Pred. No. 1.9e+03;
RESULT 1058
ID ABP96601 standard; protein; 805 AA.
DE HIV-pPIC2-alpha construct protein sequence.
PN WO2003016472-A2.
PD 27-FEB-2003.
PA (PBPG-) PEPGEN CORP.
Query Match   7.8%;   Score 6;   DB 6;   Length 805;
Best Local Similarity 100.0%;   Pred. No. 1.9e+03;
RESULT 1059
ID ABU19894 standard; protein; 807 AA.
DE Protein encoded by Prokaryotic essential gene #5421.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   7.8%;   Score 6;   DB 6;   Length 807;
Best Local Similarity 100.0%;   Pred. No. 1.9e+03;
RESULT 1060
ID AAR66931 standard; protein; 816 AA.
DE AML chromosome inv(16) product.
PN WO9504067-A1.
PD 09-FEB-1995.

PA (UNMI) UNIV MICHIGAN.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match   7.8%;   Score 6;   DB 2;   Length 816;
Best Local Similarity 100.0%;   Pred. No. 1.9e+03;
RESULT 1061
ID ABU48613 standard; protein; 823 AA.
DE Protein encoded by Prokaryotic essential gene #34160.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   7.8%;   Score 6;   DB 6;   Length 823;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1062
ID ADN47384 standard; protein; 828 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1262.
PN WO200402736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match   7.8%;   Score 6;   DB 8;   Length 828;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1063
ID ADJ49851 standard; protein; 841 AA.
DE Oil-associated gene related protein #1351.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match   7.8%;   Score 6;   DB 8;   Length 841;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1064
ID ADJ49518 standard; protein; 841 AA.
DE Oil-associated gene related protein #1018.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match   7.8%;   Score 6;   DB 8;   Length 841;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1065
ID ABB66422 standard; protein; 844 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26058.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match   7.8%;   Score 6;   DB 4;   Length 844;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1066
ID ADJ50264 standard; protein; 847 AA.
DE Oil-associated gene related protein #1764.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match   7.8%;   Score 6;   DB 8;   Length 847;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1067
ID AAB54359 standard; protein; 855 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:811.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.8%;   Score 6;   DB 3;   Length 855;
Best Local Similarity 100.0%;   Pred. No. 2e+03;
RESULT 1068

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ID   AAB96597 standard; protein; 872 AA.
DE   Putative P. abyssi superfamily II DNA and RNA helicase #8.
PN   FR2792651-A1.
PD   27-OCT-2000.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
PA   (IFRE-) IFREMER INST FR RECH EXPL MER.
     Query Match           7.8%;  Score 6; DB 4; Length 872;
     Best Local Similarity 100.0%;  Pred. No. 2.1e+03;

RESULT 1069
ID   AAR66930 standard; protein; 885 AA.
DE   AML chromosome inv(16) product.
PN   WO9504067-A1.
PD   09-FEB-1995.
PA   (UNMI ) UNIV MICHIGAN.
PA   (TEXA ) UNIV TEXAS SYSTEM.
     Query Match           7.8%;  Score 6; DB 2; Length 885;
     Best Local Similarity 100.0%;  Pred. No. 2.1e+03;

RESULT 1070
ID   AAY90238 standard; protein; 885 AA.
DE   Mature Chlamydia antigen CPN100635.
PN   WO200032794-A2.
PD   08-JUN-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
     Query Match           7.8%;  Score 6; DB 3; Length 885;
     Best Local Similarity 100.0%;  Pred. No. 2.1e+03;

RESULT 1071
ID   ABB57134 standard; protein; 889 AA.
DE   Mouse ischaemic condition related protein sequence SEQ ID NO:312.
PN   WO200188188-A2.
PD   22-NOV-2001.
PA   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
     Query Match           7.8%;  Score 6; DB 5; Length 889;
     Best Local Similarity 100.0%;  Pred. No. 2.1e+03;

RESULT 1072
ID   ADN04279 standard; protein; 889 AA.
DE   Antipsoriatic protein sequence #334.
PN   WO200402479-A2.
PD   08-APR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match           7.8%;  Score 6; DB 8; Length 889;
     Best Local Similarity 100.0%;  Pred. No. 2.1e+03;

RESULT 1073
ID   ADP24012 standard; protein; 889 AA.
DE   PRO polypeptide SEQ ID NO:1190.
PN   WO200404170-A2.
PD   21-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match           7.8%;  Score 6; DB 8; Length 889;
     Best Local Similarity 100.0%;  Pred. No. 2.1e+03;

RESULT 1074
ID   AAW88429 standard; protein; 914 AA.
DE   Chlamydia pneumoniae surface exposed protein Omp5.
PN   WO9858953-A2.
PD   30-DEC-1998.
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
     Query Match           7.8%;  Score 6; DB 2; Length 914;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1075
ID   AAW88418 standard; protein; 928 AA.
DE   Chlamydia antigen CPN100635.
PN   WO9858953-A2.
PD   30-DEC-1998.
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
     Query Match           7.8%;  Score 6; DB 2; Length 928;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1076
ID   AAY90237 standard; protein; 928 AA.
DE   Chlamydia antigen CPN100635.
PN   WO200032794-A2.
PD   08-JUN-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
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     Query Match           7.8%;  Score 6; DB 3; Length 928;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1077
ID   ABB90573 standard; protein; 928 AA.
DE   Chlamydia pneumoniae cp0010 protein, SEQ ID NO:95.
PN   WO200202606-A2.
PD   10-JAN-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match           7.8%;  Score 6; DB 5; Length 928;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1078
ID   AAM78649 standard; protein; 931 AA.
DE   Human protein SEQ ID NO 1311.
PN   WO20015190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match           7.8%;  Score 6; DB 4; Length 931;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1079
ID   ABM80675 standard; protein; 931 AA.
DE   Tumour-associated antigenic target (TAT) polypeptide PRO81297, SEQ ID NO:95.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match           7.8%;  Score 6; DB 8; Length 931;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1080
ID   ADJ83096 standard; protein; 933 AA.
DE   Fruit fly adenylate cyclase isoform 39E protein - SEQ ID 87.
PN   US2003170630-A1.
PD   11-SEP-2003.
PA   (ALSO/) ALSOBROOK J P.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM,) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.
PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.
     Query Match           7.8%;  Score 6; DB 7; Length 933;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1081
ID   ABB12315 standard; peptide; 949 AA.
DE   Human protocadherin homologue, SEQ ID NO:2685.
PN   WO20015188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match           7.8%;  Score 6; DB 4; Length 949;
     Best Local Similarity 100.0%;  Pred. No. 2.2e+03;

RESULT 1082
ID   AAM79633 standard; protein; 949 AA.
DE   Human protein SEQ ID NO 3279.
PN   WO20015190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
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Query Match        7.8%;  Score 6;  DB 4;  Length 949;
Best Local Similarity  100.0%;  Pred. No. 2.2e+03;
RESULT 1083
ID  ADS12208 standard; protein; 949 AA.
DE  Human therapeutic contig protein - SEQ ID 2445.
PN  WO2004080148-A2.
PD  23-SEP-2004.
PA  (NUVE-) NUVELO INC.

Query Match        7.8%;  Score 6;  DB 8;  Length 949;
Best Local Similarity  100.0%;  Pred. No. 2.2e+03;
RESULT 1084
ID  ADO42010 standard; protein; 992 AA.
DE  Human cell adhesion and extracellular matrix protein 39 SeqID39.
PN  WO2004048529-A2.
PD  10-JUN-2004.
PA  (INCY-) INCYTE CORP.

Query Match        7.8%;  Score 6;  DB 8;  Length 992;
Best Local Similarity  100.0%;  Pred. No. 2.3e+03;
RESULT 1085
ID  ABM83663 standard; protein; 992 AA.
DE  Human diagnostic and therapeutic pprotein SEQ ID NO:3912.
PN  WO2004023973-A2.
PD  25-MAR-2004.
PA  (INCY-) INCYTE CORP.

Query Match        7.8%;  Score 6;  DB 8;  Length 992;
Best Local Similarity  100.0%;  Pred. No. 2.3e+03;
RESULT 1086
ID  ADJ49445 standard; protein; 1032 AA.
DE  Oil-associated gene related protein #945.
PN  US2004025202-A1.
PD  05-FEB-2004.
PA  (LAUR/) LAURIE C C.
PA  (RAVA/) RAVANELLO M.
PA  (SAVA/) SAVAGE T.
PA  (LEDE/) LEDEAUX J R.
PA  (ROGE/) ROGERS J A.

Query Match        7.8%;  Score 6;  DB 8;  Length 1032;
Best Local Similarity  100.0%;  Pred. No. 2.4e+03;
RESULT 1087
ID  ADN96156 standard; protein; 1118 AA.
DE  Human NOVX polypeptide #105.
PN  US2004067490-A1.
PD  08-APR-2004.
PA  (ZHON/) ZHONG M.
PA  (LILL/) LI L.
PA  (GORM/) GORMAN L.
PA  (SPYT/) SPYTEK K A.
PA  (KEKU/) KEKUDA R.
PA  (TAUP/) TAUPIER R J.
PA  (ANDE/) ANDERSON D W.
PA  (VERN/) VERNET C A M.
PA  (CATT/) CATTERTON E.
PA  (MILL/) MILLER C E.
PA  (SHEN/) SHENOY S G.
PA  (PATT/) PATTURAJAN M.
PA  (PENA/) PENA C E A.
PA  (TCHE/) TCHERNEV V T.
PA  (PADI/) PADIGARU M.
PA  (GUSE/) GUSEV V Y.
PA  (MALY/) MALYANKAR U M.
PA  (BURG/) BURGESS C E.
PA  (GERL/) GERLACH V.
PA  (CASM/) CASMAN S J.
PA  (RIEG/) RIEGER D K.
PA  (GROS/) GROSSE W M.
PA  (SMIT/) SMITHSON G.
PA  (PEYM/) PEYMAN J A.
PA  (STAR/) STARLING G.
PA  (ROTH/) ROTHENBERG M E.
PA  (LARO/) LAROCHELLE W J.
PA  (SHIM/) SHIMKETS R A.
PA  (CRAB/) CRABTREE J.
PA  (RAST/) RASTELLI L.


PA  (VOSS/) VOSS E Z.
PA  (BOLD/) BOLDOG F L.
PA  (EDIN/) EDINGER S R.
PA  (MILL/) MILLET I.
PA  (MACD/) MACDOUGALL J R.
PA  (ELLE/) ELLERMAN K.
PA  (CHAP/) CHAPOVAL A.

Query Match        7.8%;  Score 6;  DB 8;  Length 1118;
Best Local Similarity  100.0%;  Pred. No. 2.6e+03;
RESULT 1088
ID  ADN20724 standard; protein; 1124 AA.
DE  Bacterial polypeptide #3377.
PN  US2003233675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.

Query Match        7.8%;  Score 6;  DB 8;  Length 1124;
Best Local Similarity  100.0%;  Pred. No. 2.6e+03;
RESULT 1089
ID  AAB02007 standard; protein; 1144 AA.
DE  Type III adenylyl cyclase.
PN  US6107076-A.
PD  22-AUG-2000.
PA  (TEXA ) UNIV TEXAS SYSTEM.

Query Match        7.8%;  Score 6;  DB 3;  Length 1144;
Best Local Similarity  100.0%;  Pred. No. 2.7e+03;
RESULT 1090
ID  ADJ83095 standard; protein; 1144 AA.
DE  Human adenylate cyclase 3 protein - SEQ ID 86.
PN  US2003170630-A1.
PD  11-SEP-2003.
PA  (ALSO/) ALSOBROOK J P.
PA  (TCHE/) TCHERNEV V T.
PA  (LIUX/) LIU X.
PA  (SPYT/) SPYTEK K A.
PA  (ZERH/) ZERHUSEN B D.
PA  (PATT/) PATTURAJAN M.
PA  (LEPL/) LEPLEY D M.
PA  (BURG/) BURGESS C E.
PA  (SHIM/) SHIMKETS R A.
PA  (GROS/) GROSSE W M.
PA  (SZEK/) SZEKERES E S.
PA  (VERN/) VERNET C A M.
PA  (LILL/) LI L.
PA  (CASM/) CASMAN S J.
PA  (BOLD/) BOLDOG F L.
PA  (GORM/) GORMAN L.
PA  (GANG/) GANGOLLI E A.
PA  (FERN/) FERNANDES E R.
PA  (RIEG/) RIEGER D K.
PA  (EDIN/) EDINGER S R.
PA  (GUNT/) GUNTHER E.
PA  (MILL/) MILLET I.
PA  (SCIO/) SCIORE P.
PA  (ELLE/) ELLERMAN K.
PA  (MACD/) MACDOUGALL J R.
PA  (SMIT/) SMITHSON G.

Query Match        7.8%;  Score 6;  DB 7;  Length 1144;
Best Local Similarity  100.0%;  Pred. No. 2.7e+03;
RESULT 1091
ID  ADJ83094 standard; protein; 1144 AA.
DE  Rat adenylate cyclase type III protein - SEQ ID 85.
PN  US2003170630-A1.
PD  11-SEP-2003.
PA  (ALSO/) ALSOBROOK J P.
PA  (TCHE/) TCHERNEV V T.
PA  (LIUX/) LIU X.
PA  (SPYT/) SPYTEK K A.
PA  (ZERH/) ZERHUSEN B D.
PA  (PATT/) PATTURAJAN M.
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PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM/) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.
PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.
Query Match   7.8%;   Score 6;   DB 7;   Length 1144;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1092
ID   ADJ82968 standard; protein; 1144 AA.
DE   Human adenylate cyclase 3 ADCY3 protein.
PN   WO2004005483-A2.
PD   15-JAN-2004.
PA   (EXEL-) EXELIXIS INC.
Query Match   7.8%;   Score 6;   DB 8;   Length 1144;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1093
ID   ADQ89906 standard; protein; 1144 AA.
DE   Antagonist of cell cycle progression polypeptide #168.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
Query Match   7.8%;   Score 6;   DB 8;   Length 1144;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1094
ID   ADR73440 standard; protein; 1144 AA.
DE   Human adenylate cyclase 3, ADCY3, protein.
PN   WO2004076682-A2.
PD   10-SEP-2004.
PA   (SURR-) SURROMED INC.
Query Match   7.8%;   Score 6;   DB 8;   Length 1144;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1095
ID   AAR74209 standard; protein; 1165 AA.
DE   Laminin B1k chain.
PN   WO9511972-A1.
PD   04-MAY-1995.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
Query Match   7.8%;   Score 6;   DB 2;   Length 1165;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1096
ID   AAB48462 standard; protein; 1170 AA.
DE   Human laminin 5 polypeptide, SEQ ID NO: 14.
PN   WO200066731-A2.
PD   09-NOV-2000.
PA   (BIOS-) BIOSTATUM INC.
Query Match   7.8%;   Score 6;   DB 3;   Length 1170;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1097
ID   AAW37870 standard; protein; 1172 AA.
DE   Human protein comprising secretory signal amino acid sequence 7.
PN   WO9811217-A2.
PD   19-MAR-1998.
PA   (SAGA) SAGAMI CHEM RES CENTRE.
PA   (PROT-) PROTGENE INC.
Query Match   7.8%;   Score 6;   DB 2;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1098

ID   ABG77169 standard; protein; 1172 AA.
DE   Prostate adenocarcinoma associated protein #4.
PN   US2002119463-A1.
PD   29-AUG-2002.
PA   (FARI/) FARIS M.
PA   (TURN/) TURNER C M.
Query Match   7.8%;   Score 6;   DB 5;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1099
ID   ABU56661 standard; protein; 1172 AA.
DE   Lung cancer-associated polypeptide #254.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match   7.8%;   Score 6;   DB 6;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1100
ID   ABU56417 standard; protein; 1172 AA.
DE   Lung cancer-associated polypeptide #10.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match   7.8%;   Score 6;   DB 6;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1101
ID   ABU57624 standard; protein; 1172 AA.
DE   Differentially expressed breast cancer associated protein #11.
PN   US2002156263-A1.
PD   24-OCT-2002.
PA   (CHEN/) CHEN H.
Query Match   7.8%;   Score 6;   DB 6;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1102
ID   ABR58375 standard; protein; 1172 AA.
DE   Human NOV5a.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
Query Match   7.8%;   Score 6;   DB 6;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1103
ID   ADC01885 standard; protein; 1172 AA.
DE   Human laminin beta 3 subunit.
PN   US2003103975-A1.
PD   05-JUN-2003.
PA   (JONE/) JONES J C R.
PA   (GONZ/) GONZALES M.
Query Match   7.8%;   Score 6;   DB 7;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1104
ID   ADN39002 standard; protein; 1172 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:320.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1105
ID   ABM80221 standard; protein; 1174 AA.
DE   Tumour-associated antigenic target (TAT) polypeptide PRO36468, SEQ:554.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 1172;
Best Local Similarity   100.0%;   Pred. No. 2.7e+03;
RESULT 1106
ID   ADJ48738 standard; protein; 1174 AA.
DE   Oil-associated gene related protein #238.
PN   US2004025202-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.

PA   (LEDE/) LEDEAUX J R.
PA   (ROGE/) ROGERS J A.
     Query Match   7.8%; Score 6; DB 8; Length 1174;
     Best Local Similarity   100.0%; Pred. No. 2.7e+03;
RESULT 1107
ID   ADA5131 standard; protein; 1196 AA.
DE   Human protein, SEQ ID 2699.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   7.8%; Score 6; DB 6; Length 1196;
     Best Local Similarity   100.0%; Pred. No. 2.8e+03;
RESULT 1108
ID   ABP69358 standard; protein; 1223 AA.
DE   Human polypeptide SEQ ID NO 1405.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSB-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 5; Length 1223;
     Best Local Similarity   100.0%; Pred. No. 2.8e+03;
RESULT 1109
ID   AAU96923 standard; protein; 1223 AA.
DE   Human alpha-2/delta-4 protein subunit 1.
PN   WO200226821-A2.
PD   04-APR-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   7.8%; Score 6; DB 5; Length 1223;
     Best Local Similarity   100.0%; Pred. No. 2.8e+03;
RESULT 1110
ID   ADI27951 standard; protein; 1223 AA.
DE   Human alpha-2delta-4 protein.
PN   US2003165891-A1.
PD   04-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   7.8%; Score 6; DB 8; Length 1223;
     Best Local Similarity   100.0%; Pred. No. 2.8e+03;
RESULT 1111
ID   ADN24522 standard; protein; 1241 AA.
DE   Bacterial polypeptide #7175.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%; Score 6; DB 8; Length 1241;
     Best Local Similarity   100.0%; Pred. No. 2.9e+03;
RESULT 1112
ID   ADN21766 standard; protein; 1261 AA.
DE   Bacterial polypeptide #4419.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   7.8%; Score 6; DB 8; Length 1261;
     Best Local Similarity   100.0%; Pred. No. 2.9e+03;
RESULT 1113
ID   AAB22909 standard; protein; 1274 AA.
DE   Human transporter and ion channel (TRICH) 8.
PN   WO200222684-A2.
PD   21-MAR-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   7.8%; Score 6; DB 5; Length 1274;
     Best Local Similarity   100.0%; Pred. No. 3e+03;
RESULT 1114
ID   ADC22810 standard; protein; 1286 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #82.
PN   US6555339-B1.

PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   7.8%; Score 6; DB 7; Length 1286;
     Best Local Similarity   100.0%; Pred. No. 3e+03;
RESULT 1115
ID   ADH14283 standard; protein; 1286 AA.
DE   Vector pCMV DNA ORF 3.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   7.8%; Score 6; DB 7; Length 1286;
     Best Local Similarity   100.0%; Pred. No. 3e+03;
RESULT 1116
ID   ABU19860 standard; protein; 1287 AA.
DE   Protein encoded by Prokaryotic essential gene #5387.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 6; Length 1287;
     Best Local Similarity   100.0%; Pred. No. 3e+03;
RESULT 1117
ID   ABB64155 standard; protein; 1297 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 19257.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE-) PE CORP NY.
     Query Match   7.8%; Score 6; DB 4; Length 1297;
     Best Local Similarity   100.0%; Pred. No. 3e+03;
RESULT 1118
ID   ABB99695 standard; protein; 1325 AA.
DE   Amino acid sequence of a mutant ABCC5 transporter polypeptide.
PN   WO200294378-A2.
PD   28-NOV-2002.
PA   (ACTI-) ACTIVE PASS PHARM INC.
     Query Match   7.8%; Score 6; DB 6; Length 1325;
     Best Local Similarity   100.0%; Pred. No. 3.1e+03;
RESULT 1119
ID   ABM82693 standard; protein; 1397 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:2942.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match   7.8%; Score 6; DB 8; Length 1397;
     Best Local Similarity   100.0%; Pred. No. 3.2e+03;
RESULT 1120
ID   ADQ15222 standard; protein; 1410 AA.
DE   Melon Vat-like protein, seq id 6.
PN   FR2849863-A1.
PD   16-JUL-2004.
PA   (GENO-) GENOPLANTE-VALOR SAS.
     Query Match   7.8%; Score 6; DB 8; Length 1410;
     Best Local Similarity   100.0%; Pred. No. 3.2e+03;
RESULT 1121
ID   ADN36630 standard; protein; 1419 AA.
DE   Antipsoriatic protein sequence #12.
PN   WO2004028479-A2.
PD   08-APR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   7.8%; Score 6; DB 8; Length 1419;
     Best Local Similarity   100.0%; Pred. No. 3.3e+03;
RESULT 1122
ID   ABP69396 standard; protein; 1426 AA.
DE   Human polypeptide SEQ ID NO 1443.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSB-) HYSEQ INC.
     Query Match   7.8%; Score 6; DB 5; Length 1426;
     Best Local Similarity   100.0%; Pred. No. 3.3e+03;
RESULT 1123
ID   ADJ76344 standard; protein; 1436 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1596.

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PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
     Query Match      7.8%;   Score 6;  DB 8;  Length 1436;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1124
ID   AAW80597 standard; protein; 1437 AA.
DE   Human multidrug resistance-associated protein.
PN   WO9846736-A1.
PD   22-OCT-1998.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match      7.8%;   Score 6;  DB 2;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1125
ID   AAY43542 standard; protein; 1437 AA.
DE   A human MPR-related ABC transporter designated MOAT-C.
PN   WO9949735-A1.
PD   07-OCT-1999.
PA   (FOXC-) FOX CHASE CANCER CENT.
     Query Match      7.8%;   Score 6;  DB 2;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1126
ID   AAB10225 standard; protein; 1437 AA.
DE   Human MRP-beta protein.
PN   US6077936-A.
PD   20-JUN-2000.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match      7.8%;   Score 6;  DB 3;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1127
ID   ABP52112 standard; protein; 1437 AA.
DE   Homo sapiens ABC transporter ABCC5 protein SEQ ID NO:64.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
     Query Match      7.8%;   Score 6;  DB 5;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1128
ID   ABU56560 standard; protein; 1437 AA.
DE   Lung cancer-associated polypeptide #153.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match      7.8%;   Score 6;  DB 6;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1129
ID   ABU56500 standard; protein; 1437 AA.
DE   Lung cancer-associated polypeptide #93.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match      7.8%;   Score 6;  DB 6;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1130
ID   ABU56693 standard; protein; 1437 AA.
DE   Lung cancer-associated polypeptide #286.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match      7.8%;   Score 6;  DB 6;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1131
ID   ABB99693 standard; protein; 1437 AA.
DE   Amino acid sequence of human ABCC5 transporter polypeptide.
PN   WO200294378-A2.
PD   28-NOV-2002.
PA   (ACTI-) ACTIVE PASS PHARM INC.
     Query Match      7.8%;   Score 6;  DB 6;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1132
ID   ADJ68757 standard; protein; 1437 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID563.
PN   WO2003087768-A2.

PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match      7.8%;   Score 6;  DB 7;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1133
ID   ADN39066 standard; protein; 1437 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:384.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match      7.8%;   Score 6;  DB 7;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1134
ID   ADN39950 standard; protein; 1437 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C320.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match      7.8%;   Score 6;  DB 7;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1135
ID   ADN39949 standard; protein; 1437 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C319.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match      7.8%;   Score 6;  DB 7;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1136
ID   ADJ75629 standard; protein; 1437 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:881.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
     Query Match      7.8%;   Score 6;  DB 8;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1137
ID   ADP44532 standard; protein; 1437 AA.
DE   Human ABCC5 polypeptide.
PN   US2004115649-A1.
PD   17-JUN-2004.
PA   (ISIS-) ISIS PHARM INC.
     Query Match      7.8%;   Score 6;  DB 8;  Length 1437;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1138
ID   AAB47021 standard; protein; 1453 AA.
DE   Multidrug-resistance associated polypeptide-beta.
PN   US6162616-A.
PD   19-DEC-2000.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match      7.8%;   Score 6;  DB 4;  Length 1453;
     Best Local Similarity  100.0%;  Pred. No. 3.3e+03;
RESULT 1139
ID   ABB60944 standard; protein; 1503 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 9624.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PKRE-) PE CORP NY.
     Query Match      7.8%;   Score 6;  DB 4;  Length 1503;
     Best Local Similarity  100.0%;  Pred. No. 3.4e+03;
RESULT 1140
ID   AAY06597 standard; protein; 1765 AA.
DE   Mouse sodium channel NaN.
PN   WO9938889-A2.
PD   05-AUG-1999.
PA   (UYYA ) UNIV YALE.
     Query Match      7.8%;   Score 6;  DB 2;  Length 1765;
     Best Local Similarity  100.0%;  Pred. No. 4e+03;
RESULT 1141
ID   AAB20124 standard; protein; 1765 AA.
DE   Mouse sodium channel NaN.
PN   WO200105831-A1.
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PD   25-JAN-2001.
PA   (UYYA ) UNIV YALE.
     Query Match             7.8%;   Score 6;  DB 4;  Length 1765;
     Best Local Similarity   100.0%; Pred. No. 4e+03;
RESULT 1142
ID   ADD32196 standard; protein; 1765 AA.
DE   Mouse Na v 1.9 sodium channel protein SEQ ID NO:6.
PN   WO2003080570-A2.
PD   02-OCT-2003.
PA   (TRAN-) TRANSMOLECULAR INC.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1765;
     Best Local Similarity   100.0%; Pred. No. 4e+03;
RESULT 1143
ID   AAW98354 standard; protein; 1797 AA.
DE   H. pylori GHPO 739 protein.
PN   WO9843478-A1.
PD   08-OCT-1998.
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             7.8%;   Score 6;  DB 2;  Length 1797;
     Best Local Similarity   100.0%; Pred. No. 4.1e+03;
RESULT 1144
ID   AAU84350 standard; protein; 1857 AA.
DE   Protein MYH11 differentially expressed in breast cancer tissue.
PN   WO200210436-A2.
PD   07-FEB-2002.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BAAK/) BAAK J.
     Query Match             7.8%;   Score 6;  DB 5;  Length 1857;
     Best Local Similarity   100.0%; Pred. No. 4.2e+03;
RESULT 1145
ID   AAM25750 standard; protein; 1879 AA.
DE   Human protein sequence SEQ ID NO:1265.
PN   WO200153455-A2.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             7.8%;   Score 6;  DB 4;  Length 1879;
     Best Local Similarity   100.0%; Pred. No. 4.3e+03;
RESULT 1146
ID   ABO44412 standard; protein; 1911 AA.
DE   Human protein kinase #32.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1911;
     Best Local Similarity   100.0%; Pred. No. 4.3e+03;
RESULT 1147
ID   AAB65656 standard; protein; 1920 AA.
DE   Novel protein.kinase, SEQ ID NO: 183.
PN   WO200073469-A2.
PD   07-DEC-2000.
PA   (SUGE-) SUGEN INC.
     Query Match             7.8%;   Score 6;  DB 4;  Length 1920;
     Best Local Similarity   100.0%; Pred. No. 4.3e+03;
RESULT 1148
ID   ABR92127 standard; protein; 1938 AA.
DE   Human cervical cancer cell marker protein SEQ ID NO:164.
PN   WO2002101075-A2.
PD   19-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1939;
     Best Local Similarity   100.0%; Pred. No. 4.4e+03;
RESULT 1149
ID   ABO44404 standard; protein; 1939 AA.
DE   Novel human protein kinase #24.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1939;
     Best Local Similarity   100.0%; Pred. No. 4.4e+03;
RESULT 1150
ID   ABU10398 standard; protein; 1945 AA.
DE   Human smooth muscle myosin heavy chain (hSMMyHC) variant #1.


PN   US200303018-A1.
PD   13-FEB-2003.
PA   (CYTO-) CYTOKINETICS INC.
     Query Match             7.8%;   Score 6;  DB 6;  Length 1945;
     Best Local Similarity   100.0%; Pred. No. 4.4e+03;
RESULT 1151
ID   ADI29263 standard; protein; 1952 AA.
DE   Human MARK3-associated protein #46.
PN   US2003232771-A1.
PD   18-DEC-2003.
PA   (ISIS-) ISIS PHARM INC.
     Query Match             7.8%;   Score 6;  DB 8;  Length 1952;
     Best Local Similarity   100.0%; .Pred. No. 4.4e+03;
RESULT 1152
ID   ABO44396 standard; protein; 1971 AA.
DE   Novel human protein kinase #16.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1971;
     Best Local Similarity   100.0%; Pred. No. 4.4e+03;
RESULT 1153
ID   AAW00024 standard; protein; 1972 AA.
DE   Smooth muscle myosin heavy chain SM1 isoform protein.
PN   WO9623069-A1.
PD   01-AUG-1996.
PA   (VESS-) VESSEL RES LAB CO LTD.
PA   (OSAP/) OSAKA PREFECTURAL GOVERNMENT.
     Query Match             7.8%;   Score 6;  DB 2;  Length 1972;
     Best Local Similarity   100.0%; Pred. No. 4.5e+03;
RESULT 1154
ID   ABR92126 standard; protein; 1972 AA.
DE   Human cervical cancer cell marker protein SEQ ID NO:162.
PN   WO2002101075-A2.
PD   19-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             7.8%;   Score 6;  DB 6;  Length 1972;
     Best Local Similarity   100.0%; Pred. No. 4.5e+03;
RESULT 1155
ID   ADE58724 standard; protein; 1972 AA.
DE   Human Protein P35749, SEQ ID NO 4602.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1972;
     Best Local Similarity   100.0%; Pred. No. 4.5e+03;
RESULT 1156
ID   ADE58721 standard; protein; 1972 AA.
DE   Human Protein P35749, SEQ ID NO 4598.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1972;
     Best Local Similarity   100.0%; Pred. No. 4.5e+03;
RESULT 1157
ID   ADE63520 standard; protein; 1972 AA.
DE   Human Protein NP_002465, SEQ ID NO 9464.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1972;
     Best Local Similarity   100.0%; Pred. No. 4.5e+03;
RESULT 1158
ID   ADE63516 standard; protein; 1972 AA.
DE   Human Protein P35749, SEQ ID NO 9460.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match             7.8%;   Score 6;  DB 7;  Length 1972;
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Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1159
ID ADK70527 standard; protein; 1972 AA.
DE Respiratory disease differentially expressed protein #93.
PN WO200310128J-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
    Query Match   7.8%; Score 6; DB 8; Length 1972;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1160
ID ADN03745 standard; protein; 1972 AA.
DE Antipsoriatic protein sequence #69.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
    Query Match   7.8%; Score 6; DB 8; Length 1972;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1161
ID ABB92318 standard; protein; 1973 AA.
DE Herbicidally active polypeptide SEQ ID NO 1529.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
    Query Match   7.8%; Score 6; DB 5; Length 1973;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1162
ID ABU10399 standard; protein; 1979 AA.
DE Human smooth muscle myosin heavy chain (hSMMyHC) variant #2.
PN WO2003032018-A1.
PD 13-FEB-2003.
PA (CYTO-) CYTOKINETICS INC.
    Query Match   7.8%; Score 6; DB 6; Length 1979;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1163
ID ADS11120 standard; protein; 1981 AA.
DE Human therapeutic protein - SEQ ID 1357.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
    Query Match   7.8%; Score 6; DB 8; Length 1981;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1164
ID ABU16052 standard; protein; 1983 AA.
DE Protein encoded by Prokaryotic essential gene #1579.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   7.8%; Score 6; DB 6; Length 1983;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1165
ID ABR62800 standard; protein; 1983 AA.
DE VISA Staphylococcus aureus FmtB-like protein SAV1758.
PN WO200306266-A2.
PD 31-JUL-2003.
PA (UYBR-) UNIV BRISTOL.
    Query Match   7.8%; Score 6; DB 7; Length 1983;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1166
ID ADQ26947 standard; protein; 1995 AA.
DE Human myosin heavy chain.
PN DE10266633-A1.
PD 24-JUN-2004.
PA (RAUT/) RAUTENSTRAUSS B.
    Query Match   7.8%; Score 6; DB 8; Length 1995;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1167
ID ABB66040 standard; protein; 1998 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24912.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   7.8%; Score 6; DB 4; Length 1998;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;

RESULT 1168
ID ABO44388 standard; protein; 1999 AA.
DE Novel human protein kinase #8.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
    Query Match   7.8%; Score 6; DB 7; Length 1999;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1169
ID ABO44409 standard; protein; 2004 AA.
DE Novel human protein kinase #29.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
    Query Match   7.8%; Score 6; DB 7; Length 2004;
    Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1170
ID ABB64300 standard; protein; 2030 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19692.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   7.8%; Score 6; DB 4; Length 2030;
    Best Local Similarity 100.0%; Pred. No. 4.6e+03;
RESULT 1171
ID ABO44401 standard; protein; 2032 AA.
DE Novel human protein kinase #21.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
    Query Match   7.8%; Score 6; DB 7; Length 2032;
    Best Local Similarity 100.0%; Pred. No. 4.6e+03;
RESULT 1172
ID AAR04032 standard; protein; 2037 AA.
DE Full length T4 encoded by plasmid pBG381.
PN WO911860-A.
PD 14-DEC-1989.
PA (BIOJ) BIOGEN NV INC.
PA (GEHO) GEN HOSPITAL CORP.
PA (BIOJ) BIOGEN INC.
PA (BIOJ) BIOGEN INC.
    Query Match   7.8%; Score 6; DB 2; Length 2037;
    Best Local Similarity 100.0%; Pred. No. 4.6e+03;
RESULT 1173
ID ABO44411 standard; protein; 2048 AA.
DE Novel human protein kinase #31.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
    Query Match   7.8%; Score 6; DB 7; Length 2048;
    Best Local Similarity 100.0%; Pred. No. 4.6e+03;
RESULT 1174
ID AAR07641 standard; protein; 2050 AA.
DE Deduced sequence of pBG381 comprising truncated T4 glycoprotein.
PN WO908198-A.
PD 26-JUL-1990.
PA (HARD) HARVARD COLLEGE.
    Query Match   7.8%; Score 6; DB 2; Length 2050;
    Best Local Similarity 100.0%; Pred. No. 4.6e+03;
RESULT 1175
ID ABO44393 standard; protein; 2064 AA.
DE Novel human protein kinase #13.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
    Query Match   7.8%; Score 6; DB 7; Length 2064;
    Best Local Similarity 100.0%; Pred. No. 4.6e+03;
RESULT 1176
ID ADH48388 standard; protein; 2070 AA.
DE Human KPP protein SEQ ID NO:46.
PN WO200401008-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.

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Query Match          7.8%;   Score 6;  DB 8; Length 2070;
Best Local Similarity 100.0%;  Pred. No. 4.7e+03;
RESULT 1177
ID   AAU34319 standard; protein; 2076 AA.
DE   Staphylococcus aureus cellular proliferation protein #595.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
Query Match          7.8%;   Score 6;  DB 4; Length 2076;
Best Local Similarity 100.0%;  Pred. No. 4.7e+03;
RESULT 1178
ID   ABO44403 standard; protein; 2076 AA.
DE   Novel human protein kinase #23.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2076;
Best Local Similarity 100.0%;  Pred. No. 4.7e+03;
RESULT 1179
ID   ABO44385 standard; protein; 2092 AA.
DE   Novel human protein kinase #5.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2092;
Best Local Similarity 100.0%;  Pred. No. 4.7e+03;
RESULT 1180
ID   ABO44395 standard; protein; 2108 AA.
DE   Novel human protein kinase #15.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2108;
Best Local Similarity 100.0%;  Pred. No. 4.7e+03;
RESULT 1181
ID   ADC99049 standard; protein; 2108 AA.
DE   Human KPP protein - SEQ ID 2.
PN   WO2003033680-A2.
PD   24-APR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2108;
Best Local Similarity 100.0%;  Pred. No. 4.7e+03;
RESULT 1182
ID   AAE21714 standard; protein; 2135 AA.
DE   Human PKIN-9 protein.
PN   WO200218557-A2.
PD   07-MAR-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match          7.8%;   Score 6;  DB 5; Length 2135;
Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1183
ID   ABO44387 standard; protein; 2136 AA.
DE   Novel human protein kinase #7.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2136;
Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1184
ID   ABO44408 standard; protein; 2141 AA.
DE   Novel human protein kinase #28.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2141;
Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1185
ID   ABP57679 standard; protein; 2149 AA.
DE   Saccharopolyspora busB butenyl-spinosyn biosynthetic gene product.
PN   WO200279477-A2.
PD   10-OCT-2002.
PA   (DOWC ) DOW AGROSCIENCES LLC.
Query Match          7.8%;   Score 6;  DB 6; Length 2149;

Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1186
ID   AAY39298 standard; protein; 2152 AA.
DE   SpnB a polyketide synthase.
PN   WO994387-A1.
PD   16-SEP-1999.
PA   (DOWC ) DOW AGROSCIENCES LLC.
Query Match          7.8%;   Score 6;  DB 2; Length 2152;
Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1187
ID   AAB70966 standard; protein; 2152 AA.
DE   S. spinosa protein fragment encoded by ORF19, SEQ ID 44.
PN   DE19957268-A1.
PD   08-MAR-2001.
PA   (FARB ) BAYER AG.
Query Match          7.8%;   Score 6;  DB 4; Length 2152;
Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1188
ID   ABO44406 standard; protein; 2157 AA.
DE   Novel human protein kinase #26.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2157;
Best Local Similarity 100.0%;  Pred. No. 4.8e+03;
RESULT 1189
ID   ABO44400 standard; protein; 2169 AA.
DE   Novel human protein kinase #20.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2169;
Best Local Similarity 100.0%;  Pred. No. 4.9e+03;
RESULT 1190
ID   ABO44398 standard; protein; 2185 AA.
DE   Novel human protein kinase #18.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match          7.8%;   Score 6;  DB 7; Length 2185;
Best Local Similarity 100.0%;  Pred. No. 4.9e+03;
RESULT 1191
ID   AAU37320 standard; protein; 2186 AA.
DE   Staphylococcus aureus cellular proliferation protein #1490.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
Query Match          7.8%;   Score 6;  DB 4; Length 2186;
Best Local Similarity 100.0%;  Pred. No. 4.9e+03;
RESULT 1192
ID   ABJ19059 standard; protein; 2186 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID No 336.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match          7.8%;   Score 6;  DB 6; Length 2186;
Best Local Similarity 100.0%;  Pred. No. 4.9e+03;
RESULT 1193
ID   ABM71190 standard; protein; 2186 AA.
DE   Staphylococcus aureus protein #430.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
Query Match          7.8%;   Score 6;  DB 6; Length 2186;
Best Local Similarity 100.0%;  Pred. No. 4.9e+03;
RESULT 1194
ID   ABR62805 standard; protein; 2186 AA.
DE   Methicillin resistant Staphylococcus aureus ORF SA1577-fmtB protein.
PN   WO200362466-A2.
PD   31-JUL-2003.
PA   (UYBR-) UNIV BRISTOL.
Query Match          7.8%;   Score 6;  DB 7; Length 2186;
Best Local Similarity 100.0%;  Pred. No. 4.9e+03;
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RESULT 1195
ID   ABP56875 standard; protein; 2189 AA.
DE   Staphylococcus epidermidis EkeS_MRSA protein SEQ ID NO:2.
PN   WO200210829-A2.
PD   27-DEC-2002.
PA   (INHI-) INHIBITEX INC.
PA   (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA   (UYPA-) UNIV PAVIA.
Query Match   7.8%;   Score 6;   DB 6;   Length 2189;
Best Local Similarity   100.0%;   Pred. No. 4.9e+03;

RESULT 1196
ID   ABR62792 standard; protein; 2196 AA.
DE   MRSA FmtB-like protein SA1577.
PN   WO200306246-A2.
PD   31-JUL-2003.
PA   (UYBR-) UNIV BRISTOL.
Query Match   7.8%;   Score 6;   DB 7;   Length 2196;
Best Local Similarity   100.0%;   Pred. No. 4.9e+03;

RESULT 1197
ID   ABO44392 standard; protein; 2201 AA.
DE   Novel human protein kinase #12.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2201;
Best Local Similarity   100.0%;   Pred. No. 4.9e+03;

RESULT 1198
ID   ABO44390 standard; protein; 2217 AA.
DE   Novel human protein kinase #10.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2217;
Best Local Similarity   100.0%;   Pred. No. 5e+03;

RESULT 1199
ID   ABO44384 standard; protein; 2229 AA.
DE   Novel human protein kinase #4.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2229;
Best Local Similarity   100.0%;   Pred. No. 5e+03;

RESULT 1200
ID   ABO44382 standard; protein; 2245 AA.
DE   Novel human protein kinase #2.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2245;
Best Local Similarity   100.0%;   Pred. No. 5e+03;

RESULT 1201
ID   ABO44405 standard; protein; 2294 AA.
DE   Novel human protein kinase #25.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2294;
Best Local Similarity   100.0%;   Pred. No. 5.1e+03;

RESULT 1202
ID   ABO44397 standard; protein; 2322 AA.
DE   Novel human protein kinase #17.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2322;
Best Local Similarity   100.0%;   Pred. No. 5.2e+03;

RESULT 1203
ID   ABO44389 standard; protein; 2354 AA.
DE   Novel human protein kinase #9.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2354;

RESULT 1204
ID   ABP71619 standard; protein; 2382 AA.
DE   Human WNK1 protein.
PN   WO2003007793-A2.
PD   30-JAN-2003.
PA   (UYYA) UNIV YALE.
PA   (LIFT/) LIFTON R P.
PA   (WILS/) WILSON F H.
PA   (CHOA/) CHOATE K.
PA   (NELS/) NELSON-WILLIAMS C.
PA   (ISHI/) ISHIKAWA K.
Query Match   7.8%;   Score 6;   DB 6;   Length 2382;
Best Local Similarity   100.0%;   Pred. No. 5.3e+03;

RESULT 1205
ID   ABO44381 standard; protein; 2382 AA.
DE   Novel human protein kinase #1.
PN   US6541252-B1.
PD   01-APR-2003.
PA   (LEXI-) LEXICON GENETICS INC.
Query Match   7.8%;   Score 6;   DB 7;   Length 2382;
Best Local Similarity   100.0%;   Pred. No. 5.3e+03;

RESULT 1206
ID   ADJ69598 standard; protein; 2382 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1404.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
Query Match   7.8%;   Score 6;   DB 7;   Length 2382;
Best Local Similarity   100.0%;   Pred. No. 5.3e+03;

RESULT 1207
ID   ADS11119 standard; protein; 2388 AA.
DE   Human therapeutic protein - SEQ ID 1356.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Query Match   7.8%;   Score 6;   DB 8;   Length 2388;
Best Local Similarity   100.0%;   Pred. No. 5.3e+03;

RESULT 1208
ID   ADE52217 standard; protein; 2606 AA.
DE   pG1EN-EH3.His vector and E3Bi sequence, SEQ ID 5.
PN   WO2003090513-A2.
PD   06-NOV-2003.
PA   (WILL-) WILLIAMS HOSPITAL ROGER.
Query Match   7.8%;   Score 6;   DB 7;   Length 2606;
Best Local Similarity   100.0%;   Pred. No. 5.8e+03;

RESULT 1209
ID   ADE52214 standard; protein; 2606 AA.
DE   pG1EN-EH3.His vector and E3Bi sequence, SEQ ID 2.
PN   WO2003090513-A2.
PD   06-NOV-2003.
PA   (WILL-) WILLIAMS HOSPITAL ROGER.
Query Match   7.8%;   Score 6;   DB 7;   Length 2606;
Best Local Similarity   100.0%;   Pred. No. 5.8e+03;

RESULT 1210
ID   AAU35978 standard; protein; 2890 AA.
DE   Helicobacter pylori cellular proliferation protein #291.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   7.8%;   Score 6;   DB 4;   Length 2890;
Best Local Similarity   100.0%;   Pred. No. 6.4e+03;

RESULT 1211
ID   AAU35817 standard; protein; 2890 AA.
DE   Helicobacter pylori cellular proliferation protein #130.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   7.8%;   Score 6;   DB 4;   Length 2890;
Best Local Similarity   100.0%;   Pred. No. 6.4e+03;

RESULT 1212
ID   ABU30983 standard; protein; 2890 AA.

DE   Protein encoded by Prokaryotic essential gene #16510.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.8%; Score 6; DB 6; Length 2890;
     Best Local Similarity   100.0%; Pred. No. 6.4e+03;
RESULT 1213
ID   ADH11258 standard; protein; 3614 AA.
DE   Vertebrate UNC-53 protein homologue related amino acid sequence.
PN   WO9824810-A2.
PD   11-JUN-1998.
PA   (JANC) JANSSEN PHARM NV.
     Query Match   7.8%; Score 6; DB 2; Length 3614;
     Best Local Similarity   100.0%; Pred. No. 7.9e+03;
RESULT 1214
ID   ABP76679 standard; protein; 19938 AA.
DE   Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN   WO20026436-A1.
PD   06-SEP-2002.
PA   (COMB-) COMBINATURE BIOPHARM AG.
     Query Match   7.8%; Score 6; DB 6; Length 19938;
     Best Local Similarity   100.0%; Pred. No. 3.9e+04;
RESULT 1215
ID   ADM33096 standard; peptide; 6 AA.
DE   Human immunodeficiency virus 1 cell entry inhibitor peptide #124.
PN   WO2004024173-A2.
PD   25-MAR-2004.
PA   (CREA-) CREABILIS THERAPEUTICS SRL.
     Query Match   6.5%; Score 5; DB 8; Length 6;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1216
ID   ADE78187 standard; peptide; 7 AA.
DE   Synthetic peptide (SeqID 438) that binds atherosclerotic lesions.
PN   WO200301445-A2.
PD   20-FEB-2003.
PA   (NOVS) NOVARTIS AG.
PA   (NOVS) NOVARTIS PHARMA GMBH.
PA   (SCRI) SCRIPPS RES INST.
     Query Match   6.5%; Score 5; DB 7; Length 7;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1217
ID   ADE77755 standard; peptide; 7 AA.
DE   Synthetic peptide (SeqID 6) that binds atherosclerotic lesions.
PN   WO200301445-A2.
PD   20-FEB-2003.
PA   (NOVS) NOVARTIS AG.
PA   (NOVS) NOVARTIS PHARMA GMBH.
PA   (SCRI) SCRIPPS RES INST.
     Query Match   6.5%; Score 5; DB 7; Length 7;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1218
ID   ADR69555 standard; peptide; 7 AA.
DE   Novel hybrid antigen-related peptide SeqID345.
PN   WO2004071457-A2.
PD   26-AUG-2004.
PA   (MOJA-) MOJAVE THERAPEUTICS INC.
     Query Match   6.5%; Score 5; DB 8; Length 7;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1219
ID   ADM68731 standard; peptide; 8 AA.
DE   Human MAGE-2-derived antigenic peptide SeqID80.
PN   WO2004029071-A2.
PD   08-APR-2004.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match   6.5%; Score 5; DB 8; Length 8;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1220
ID   ADR69562 standard; peptide; 8 AA.
DE   Novel hybrid antigen-related peptide SeqID501.
PN   WO2004071457-A2.
PD   26-AUG-2004.
PA   (MOJA-) MOJAVE THERAPEUTICS INC.
     Query Match   6.5%; Score 5; DB 8; Length 8;

     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1221
ID   ADR69563 standard; peptide; 8 AA.
DE   Novel hybrid antigen-related peptide SeqID502.
PN   WO2004071457-A2.
PD   26-AUG-2004.
PA   (MOJA-) MOJAVE THERAPEUTICS INC.
     Query Match   6.5%; Score 5; DB 8; Length 8;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1222
ID   ADR69738 standard; peptide; 8 AA.
DE   Novel hybrid antigen-related peptide #1318.
PN   WO2004071457-A2.
PD   26-AUG-2004.
PA   (MOJA-) MOJAVE THERAPEUTICS INC.
     Query Match   6.5%; Score 5; DB 8; Length 8;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1223
ID   AAG88479 standard; peptide; 9 AA.
DE   HER2/NEU DR supermotif binding peptide core sequence #96.
PN   WO200141787-A1.
PD   14-JUN-2001.
PA   (EPIM-) EPIMMUNE INC.
     Query Match   6.5%; Score 5; DB 4; Length 9;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1224
ID   ADE78189 standard; peptide; 9 AA.
DE   Synthetic peptide (SeqID 440) that binds atherosclerotic lesions.
PN   WO200301445-A2.
PD   20-FEB-2003.
PA   (NOVS) NOVARTIS AG.
PA   (NOVS) NOVARTIS PHARMA GMBH.
PA   (SCRI) SCRIPPS RES INST.
     Query Match   6.5%; Score 5; DB 7; Length 9;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1225
ID   ADE77757 standard; peptide; 9 AA.
DE   Synthetic peptide (SeqID 8) that binds atherosclerotic lesions.
PN   WO200301445-A2.
PD   20-FEB-2003.
PA   (NOVS) NOVARTIS AG.
PA   (NOVS) NOVARTIS PHARMA GMBH.
PA   (SCRI) SCRIPPS RES INST.
     Query Match   6.5%; Score 5; DB 7; Length 9;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1226
ID   ADK04181 standard; peptide; 9 AA.
DE   Hepatitis C virus CTL epitope peptide #2011.
PN   WO2004011650-A2.
PD   05-FEB-2004.
PA   (INTE-) INTERCELL AG.
     Query Match   6.5%; Score 5; DB 8; Length 9;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1227
ID   ADM68730 standard; peptide; 9 AA.
DE   Human MAGE-2-derived antigenic peptide SeqID79.
PN   WO2004029071-A2.
PD   08-APR-2004.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match   6.5%; Score 5; DB 8; Length 9;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1228
ID   ADM68729 standard; peptide; 9 AA.
DE   Human MAGE-2-derived antigenic peptide SeqID78.
PN   WO2004029071-A2.
PD   08-APR-2004.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match   6.5%; Score 5; DB 8; Length 9;
     Best Local Similarity   100.0%; Pred. No. 1.8e+06;
RESULT 1229
ID   ADO69362 standard; peptide; 9 AA.
DE   Human 213P1F11 HLA motif bearing epitope #5452.
PN   US2004019915-A1.

PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
     Query Match   6.5%;   Score 5; DB 8; Length 9;
     Best Local Similarity 100.0%;   Pred. No. 1.8e+06;
RESULT 1230
ID   AD065155 standard; peptide; 9 AA.
DE   Human 213P1F11 HLA motif bearing epitope #1245.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
     Query Match   6.5%;   Score 5; DB 8; Length 9;
     Best Local Similarity 100.0%;   Pred. No. 1.8e+06;
RESULT 1231
ID   AAY81292 standard; peptide; 10 AA.
DE   Protein VIII zone-1 library variant peptide, SEQ ID NO:143.
PN   WO200006717-A2.
PD   10-FEB-2000.
PA   (GETH) GENENTECH INC.
     Query Match   6.5%;   Score 5; DB 3; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1232
ID   AAU68189 standard; peptide; 10 AA.
DE   Human Breast cancer-associated protein isoform, BPI-218 peptide.
PN   WO200171357-A2.
PD   27-SEP-2001.
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
     Query Match   6.5%;   Score 5; DB 4; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1233
ID   AAU68047 standard; peptide; 10 AA.
DE   Human Breast cancer-associated protein isoform, BPI-302 peptide #7.
PN   WO200171357-A2.
PD   27-SEP-2001.
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
     Query Match   6.5%;   Score 5; DB 4; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1234
ID   AAU68096 standard; peptide; 10 AA.
DE   Human Breast cancer-associated protein isoform, BPI-311 peptide #6.
PN   WO200171357-A2.
PD   27-SEP-2001.
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
     Query Match   6.5%;   Score 5; DB 4; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1235
ID   AAG88845 standard; peptide; 10 AA.
DE   HER2/neu epitope B7 supermotif peptide #5.
PN   WO200141787-A1.
PD   14-JUN-2001.
PA   (EPIM-) EPIMMUNE INC.
     Query Match   6.5%;   Score 5; DB 4; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1236
ID   AAB76168 standard; peptide; 10 AA.
DE   Tumour associated antigen Her2/neu immunogenic peptide.
PN   WO20010225-A1.
PD   04-JAN-2001.
PA   (EPIM-) EPIMMUNE INC.
     Query Match   6.5%;   Score 5; DB 4; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1237

ID   AAM43188 standard; peptide; 10 AA.
DE   Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 497.
PN   WO200142278-A2.
PD   14-JUN-2001.
PA   (PROT-) PROTEOM LTD.
     Query Match   6.5%;   Score 5; DB 4; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1238
ID   ABR91494 standard; peptide; 10 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:328.
PN   WO200102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5; DB 6; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1239
ID   ADM33152 standard; peptide; 10 AA.
DE   Human MAGE-C2 peptide #9.
PN   US200317256-A1.
PD   11-SEP-2003.
PA   (LUCA/) LUCAS S.
PA   (DSME/) DE SMET C.
PA   (BOON/) BOON-FALLEUR T.
     Query Match   6.5%;   Score 5; DB 7; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1240
ID   ADK04197 standard; peptide; 10 AA.
DE   Hepatitis C virus CTL epitope peptide #2027.
PN   WO2004011650-A2.
PD   05-FEB-2004.
PA   (INTE-) INTERCELL AG.
     Query Match   6.5%;   Score 5; DB 8; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1241
ID   ADM68728 standard; peptide; 10 AA.
DE   Human MAGE-2-derived antigenic peptide SeqID77.
PN   WO2004029071-A2.
PD   08-APR-2004.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match   6.5%;   Score 5; DB 8; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1242
ID   ADM68739 standard; peptide; 10 AA.
DE   Human MAGE-2-derived antigenic peptide SeqID88.
PN   WO2004029071-A2.
PD   08-APR-2004.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match   6.5%;   Score 5; DB 8; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1243
ID   ADN64612 standard; peptide; 10 AA.
DE   HLA binding peptide #1212.
PN   WO2004031211-A2.
PD   15-APR-2004.
PA   (EPIM-) EPIMMUNE INC.
     Query Match   6.5%;   Score 5; DB 8; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1244
ID   AD065924 standard; peptide; 10 AA.
DE   Human 213P1F11 HLA motif bearing epitope #2014.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
     Query Match   6.5%;   Score 5; DB 8; Length 10;
     Best Local Similarity 100.0%;   Pred. No. 3.7e+02;
RESULT 1245
ID   AD074645 standard; peptide; 10 AA.

DE   Human 213P1F11 HLA motif bearing epitope #8744.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
  Query Match   6.5%;   Score 5;   DB 8;   Length 10;
  Best Local Similarity   100.0%;   Pred. No. 3.7e+02;
RESULT 1246
ID   AD065435 standard; peptide; 10 AA.
DE   Human 213P1F11 HLA motif bearing epitope #1525.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
  Query Match   6.5%;   Score 5;   DB 8;   Length 10;
  Best Local Similarity   100.0%;   Pred. No. 3.7e+02;
RESULT 1247
ID   ADP80201 standard; peptide; 10 AA.
DE   Human HLA-B44 epitope vaccine peptide SeqID457.
PN   WO2004052917-A2.
PD   24-JUN-2004.
PA   (EPIM-) EPIMMUNE INC.
  Query Match   6.5%;   Score 5;   DB 8;   Length 10;
  Best Local Similarity   100.0%;   Pred. No. 3.7e+02;
RESULT 1248
ID   ABR91498 standard; peptide; 11 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:332.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
  Query Match   6.5%;   Score 5;   DB 6;   Length 11;
  Best Local Similarity   100.0%;   Pred. No. 4.1e+02;
RESULT 1249
ID   AAY93003 standard; peptide; 12 AA.
DE   Transforming growth factor inhibitory peptide P49.
PN   WO2000031135-A1.
PD   02-JUN-2000.
PA   (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
  Query Match   6.5%;   Score 5;   DB 3;   Length 12;
  Best Local Similarity   100.0%;   Pred. No. 4.4e+02;
RESULT 1250
ID   ABP61679 standard; peptide; 13 AA.
DE   Human KRPI tryptic digest peptide #158.
PN   WO200254081-A2.
PD   11-JUL-2002.
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
  Query Match   6.5%;   Score 5;   DB 5;   Length 13;
  Best Local Similarity   100.0%;   Pred. No. 4.8e+02;
RESULT 1251
ID   AAM00699 standard; peptide; 14 AA.
DE   Human protein fragment SEQ ID NO: 1249.
PN   WO200151670-A2.
PD   19-JUL-2001.
PA   (CURA-) CURAGEN CORP.
  Query Match   6.5%;   Score 5;   DB 4;   Length 14;
  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1252
ID   AAM00411 standard; peptide; 14 AA.
DE   Human protein fragment SEQ ID NO: 959.
PN   WO200151670-A2.
PD   19-JUL-2001.
PA   (CURA-) CURAGEN CORP.
  Query Match   6.5%;   Score 5;   DB 4;   Length 14;

  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1253
ID   AAM00412 standard; peptide; 14 AA.
DE   Human protein fragment SEQ ID NO: 960.
PN   WO200151670-A2.
PD   19-JUL-2001.
PA   (CURA-) CURAGEN CORP.
  Query Match   6.5%;   Score 5;   DB 4;   Length 14;
  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1254
ID   ABR91535 standard; peptide; 14 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:369.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
  Query Match   6.5%;   Score 5;   DB 6;   Length 14;
  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1255
ID   ABR64069 standard; peptide; 14 AA.
DE   E. coli phosphoglyceromutase 1 tryptic peptide #9.
PN   WO2003025006-A2.
PD   27-MAR-2003.
PA   (AFFI-) AFFINIUM PHARM INC.
  Query Match   6.5%;   Score 5;   DB 6;   Length 14;
  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1256
ID   ADB98806 standard; peptide; 14 AA.
DE   LRP5 peptide #4.
PN   WO200292000-A2.
PD   21-NOV-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (AMHP) WYETH.
  Query Match   6.5%;   Score 5;   DB 7;   Length 14;
  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1257
ID   ADD18061 standard; peptide; 14 AA.
DE   Human G-protein coupled receptor phosphorylation peptide SeqID118.
PN   WO2003016478-A2.
PD   27-FEB-2003.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
  Query Match   6.5%;   Score 5;   DB 7;   Length 14;
  Best Local Similarity   100.0%;   Pred. No. 5.1e+02;
RESULT 1258
ID   AAY98848 standard; peptide; 15 AA.
DE   HLA class II binding antigen epitope peptide #37.
PN   WO961916-A1.
PD   02-DEC-1999.
PA   (EPIM-) EPIMMUNE INC.
  Query Match   6.5%;   Score 5;   DB 3;   Length 15;
  Best Local Similarity   100.0%;   Pred. No. 5.4e+02;
RESULT 1259
ID   AAG88490 standard; peptide; 15 AA.
DE   HER2/NEU DR supermotif binding peptide exemplary sequence #101.
PN   WO200141787-A1.
PD   14-JUN-2001.
PA   (EPIM-) EPIMMUNE INC.
  Query Match   6.5%;   Score 5;   DB 4;   Length 15;
  Best Local Similarity   100.0%;   Pred. No. 5.4e+02;
RESULT 1260
ID   AAG89018 standard; peptide; 15 AA.
DE   Her2/neu DR supertype primary binding peptide #12.
PN   WO200141787-A1.
PD   14-JUN-2001.
PA   (EPIM-) EPIMMUNE INC.
  Query Match   6.5%;   Score 5;   DB 4;   Length 15;
  Best Local Similarity   100.0%;   Pred. No. 5.4e+02;
RESULT 1261
ID   AAG88382 standard; peptide; 15 AA.
DE   HER2/NEU DR supermotif binding peptide exemplary sequence #47.
PN   WO200141787-A1.
PD   14-JUN-2001.
PA   (EPIM-) EPIMMUNE INC.
  Query Match   6.5%;   Score 5;   DB 4;   Length 15;

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     Query Match             6.5%;  Score 5; DB 3; Length 16;
     Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
RESULT 1269
ID   ADD90457 standard; protein; 16 AA.
DE   Novel human secreted protein seq id 53 protein feature seq id 272.
PN   US2003199683-A1.
PD   23-OCT-2003.
PA   (RUBE/) RUBEN S M.
PA   (FENG/) FENG P.
PA   (LAFL/) LAFLEUR D W.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (KYAW/) KYAW H.
PA   (LIIY/) LI Y.
PA   (ZENG/) ZENG Z.
PA   (CART/) CARTER K C.
PA   (ENDR/) ENDRESS G A.
PA   (WEIY/) WEI Y.
PA   (FANP/) FAN P.
PA   (ROSE/) ROSEN C A.
     Query Match             6.5%;  Score 5; DB 7; Length 16;
     Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
RESULT 1270
ID   ADF70221 standard; peptide; 16 AA.
DE   Human protease-42 N-myristoylation peptide SeqID51.
PN   WO2003078594-A2.
PD   25-SEP-2003.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
     Query Match             6.5%;  Score 5; DB 7; Length 16;
     Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
RESULT 1271
ID   ADF12260 standard; peptide; 16 AA.
DE   Neurospora crassa poly A element TAD fragment seq id 6.
PN   US2003121063-A1.
PD   26-JUN-2003.
PA   (UYPE-) UNIV PENNSYLVANIA.
     Query Match             6.5%;  Score 5; DB 7; Length 16;
     Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
RESULT 1272
ID   ADG90276 standard; peptide; 16 AA.
DE   Human secreted protein gene 43 extra polypeptide #1.
PN   US2003166541-A1.
PD   04-SEP-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.5%;  Score 5; DB 7; Length 16;
     Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
RESULT 1273
ID   ADM68732 standard; peptide; 16 AA.
DE   Human MAG-2 mingene 14-derived peptide SeqID81.
PN   WO2004029071-A2.
PD   08-APR-2004.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match             6.5%;  Score 5; DB 8; Length 16;
     Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
RESULT 1274
ID   AAB28046 standard; peptide; 17 AA.
DE   Human secreted protein SEQ ID NO: 94.
PN   WO200055177-A2.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.5%;  Score 5; DB 3; Length 17;
     Best Local Similarity   100.0%;  Pred. No. 6.1e+02;
RESULT 1275
ID   AAE19470 standard; peptide; 17 AA.
DE   Limulus polyphemus polyphemusin-like peptide #1.
PN   WO200200687-A2.
PD   03-JAN-2002.
PA   (UYBR-) UNIV BRITISH COLUMBIA.
     Query Match             6.5%;  Score 5; DB 5; Length 17;
     Best Local Similarity   100.0%;  Pred. No. 6.1e+02;
RESULT 1276
ID   AAE19471 standard; peptide; 17 AA.
DE   Limulus polyphemus polyphemusin-like peptide #2.
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     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1262
ID   AAG88480 standard; peptide; 15 AA.
DE   HER2/NEU DR supermotif binding peptide exemplary sequence #96.
PN   WO200141787-A1.
PD   14-JUN-2001.
PA   (EPIM-) EPIMMUNE INC.
     Query Match             6.5%;  Score 5; DB 4; Length 15;
     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1263
ID   ABB05807 standard; peptide; 15 AA.
DE   Human sigma receptor 10.67 N-terminal peptide SEQ ID NO:7.
PN   WO200196524-A2.
PD   20-DEC-2001.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
     Query Match             6.5%;  Score 5; DB 5; Length 15;
     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1264
ID   ABB83075 standard; peptide; 15 AA.
DE   Synoviolin related peptide Syno-P3.
PN   WO200252007-A1.
PD   04-JUL-2002.
PA   (LOCO-) LOCOMOGENE INC.
     Query Match             6.5%;  Score 5; DB 5; Length 15;
     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1265
ID   ADO76610 standard; peptide; 15 AA.
DE   Human 213P1F11 HLA motif bearing epitope #10709.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
     Query Match             6.5%;  Score 5; DB 8; Length 15;
     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1266
ID   ADO76588 standard; peptide; 15 AA.
DE   Human 213P1F11 HLA motif bearing epitope #10687.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
     Query Match             6.5%;  Score 5; DB 8; Length 15;
     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1267
ID   ADO76396 standard; peptide; 15 AA.
DE   Human 213P1F11 HLA motif bearing epitope #10495.
PN   US2004019915-A1.
PD   29-JAN-2004.
PA   (CHAL/) CHALLITA-EID P M.
PA   (RAIT/) RAITANO A B.
PA   (FARI/) FARIS M.
PA   (HUBE/) HUBERT R S.
PA   (MORR/) MORRISON R K.
PA   (GEWW/) GE W.
PA   (JAKO/) JAKOBOVITS A.
     Query Match             6.5%;  Score 5; DB 8; Length 15;
     Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
RESULT 1268
ID   AAY95828 standard; peptide; 16 AA.
DE   Native human MAC-1 (CD11 alpha) signal peptide.
PN   WO200047741-A1.
PD   17-AUG-2000.
PA   (AMGE-) AMGEN INC.
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PN   WO20200687-A2.
PD   03-JAN-2002.
PA   (UYBR-) UNIV BRITISH COLUMBIA.
     Query Match      6.5%;   Score 5;  DB 5;  Length 17;
     Best Local Similarity  100.0%; Pred. No. 6.1e+02;
RESULT 1277
ID   AU90064 standard; peptide; 17 AA.
DE   Insulin/insulin-like growth factor receptor-binding peptide #2020.
PN   WO200172771-A2.
PD   04-OCT-2001.
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
     Query Match      6.5%;   Score 5;  DB 5;  Length 17;
     Best Local Similarity  100.0%; Pred. No. 6.1e+02;
RESULT 1278
ID   AU90053 standard; peptide; 17 AA.
DE   Insulin/insulin-like growth factor receptor-binding peptide #2009.
PN   WO200172771-A2.
PD   04-OCT-2001.
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
     Query Match      6.5%;   Score 5;  DB 5;  Length 17;
     Best Local Similarity  100.0%; Pred. No. 6.1e+02;
RESULT 1279
ID   ABR75732 standard; peptide; 17 AA.
DE   Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:243.
PN   WO2003038444-A2.
PD   08-MAY-2003.
PA   (PFIZ ) PFIZER PROD INC.
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
     Query Match      6.5%;   Score 5;  DB 6;  Length 17;
     Best Local Similarity  100.0%; Pred. No. 6.1e+02;
RESULT 1280
ID   ADN07384 standard; peptide; 17 AA.
DE   Liver response-associated feature LRF223.
PN   US2003228583-A1.
PD   11-DEC-2003.
PA   (AMAC/) AMACHER D E.
PA   (FASU/) FASULO L M.
PA   (HERA/) HERATH H M A C.
PA   (HOLT/) HOLT G D.
PA   (STIG/) STIGER T R.
     Query Match      6.5%;   Score 5;  DB 7;  Length 17;
     Best Local Similarity  100.0%; Pred. No. 6.1e+02;
RESULT 1281
ID   AAW03222 standard; peptide; 18 AA.
DE   BMP-8 fragment 85-102.
PN   EP691349-A2.
PD   10-JAN-1996.
PA   (FARH ) HOECHST JAPAN LTD.
     Query Match      6.5%;   Score 5;  DB 2;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1282
ID   AAW53126 standard; peptide; 18 AA.
DE   Human thrombopoietin C-terminal peptide fragment 1.
PN   WO9806849-A1.
PD   19-FEB-1998.
PA   (ZYMO ) ZYMOGENETICS INC.
     Query Match      6.5%;   Score 5;  DB 2;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1283
ID   ABG32241 standard; peptide; 18 AA.
DE   Tomato lycopene epsilon cyclase catalytic domain.
PN   WO200261050-A2.
PD   08-AUG-2002.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
     Query Match      6.5%;   Score 5;  DB 5;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1284
ID   ABG32239 standard; peptide; 18 AA.
DE   A. thaliana lycopene epsilon cyclase catalytic domain.
PN   WO200261050-A2.
PD   08-AUG-2002.

PA   (UYMA-) UNIV MARYLAND BALTIMORE.
     Query Match      6.5%;   Score 5;  DB 5;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1285
ID   ABG32240 standard; peptide; 18 AA.
DE   Potato lycopene epsilon cyclase catalytic domain.
PN   WO200261050-A2.
PD   08-AUG-2002.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
     Query Match      6.5%;   Score 5;  DB 5;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1286
ID   ABG32242 standard; peptide; 18 AA.
DE   Marigold lycopene epsilon cyclase catalytic domain.
PN   WO200261050-A2.
PD   08-AUG-2002.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
     Query Match      6.5%;   Score 5;  DB 5;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1287
ID   ABR64073 standard; peptide; 18 AA.
DE   E. coli phosphoglyceromutase 1 tryptic peptide #13.
PN   WO2003025006-A2.
PD   27-MAR-2003.
PA   (AFFI-) AFFINIUM PHARM INC.
     Query Match      6.5%;   Score 5;  DB 6;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1288
ID   ADO27348 standard; peptide; 18 AA.
DE   E. coli glycoprotin lead peptide SeqID 50.
PN   WO2004044220-A2.
PD   27-MAY-2004.
PA   (TULA ) TULANE EDUCATIONAL FUND.
PA   (UYRQ ) UNIV ROCKEFELLER.
     Query Match      6.5%;   Score 5;  DB 8;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1289
ID   ADO27347 standard; peptide; 18 AA.
DE   Hepatitis C virus E1 glycoprotin lead peptide SeqID 49.
PN   WO2004044220-A2.
PD   27-MAY-2004.
PA   (TULA ) TULANE EDUCATIONAL FUND.
PA   (UYRQ ) UNIV ROCKEFELLER.
     Query Match      6.5%;   Score 5;  DB 8;  Length 18;
     Best Local Similarity  100.0%; Pred. No. 6.5e+02;
RESULT 1290
ID   AAB51951 standard; protein; 19 AA.
DE   Human secreted protein sequence encoded by gene 23 SEQ ID NO:83.
PN   WO200058334-A1.
PD   05-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match      6.5%;   Score 5;  DB 3;  Length 19;
     Best Local Similarity  100.0%; Pred. No. 6.8e+02;
RESULT 1291
ID   ADB36949 standard; peptide; 19 AA.
DE   Interfacial biomaterial ligand polystyrene binding peptide SEQ ID NO:10.
PN   WO2004071457-A2.
PD   26-AUG-2004.
PA   (UYDU-) UNIV DUKE.
     Query Match      6.5%;   Score 5;  DB 7;  Length 19;
     Best Local Similarity  100.0%; Pred. No. 6.8e+02;
RESULT 1292
ID   ADR69755 standard; peptide; 19 AA.
DE   Novel hybrid antigen-related peptide #1335.
PN   WO2003072542-A2.
PD   04-SEP-2003.
PA   (MOJA-) MOJAVE THERAPEUTICS INC.
     Query Match      6.5%;   Score 5;  DB 7;  Length 19;
     Best Local Similarity  100.0%; Pred. No. 6.8e+02;
RESULT 1293
ID   AAR84422 standard; peptide; 20 AA.
DE   Hepatitis C virus E1 region (265-284) peptide.
PN   WO9512677-A2.
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PD   11-MAY-1995.
PA   (INNO-) INNOGENETICS NV.
     Query Match   6.5%; Score 5; DB 2; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
ID   AAR90973 standard; peptide; 20 AA.
DE   HCV E1 peptide E1-45 for competition studies.
PN   WO9604385-A2.
PD   15-FEB-1996
PA   (INNO-) INNOGENETICS NV.
     Query Match   6.5%; Score 5; DB 2; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1295
ID   AAM20136 standard; protein; 20 AA.
DE   Peptide #6570 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1296
ID   ABB40352 standard; peptide; 20 AA.
DE   Peptide #7858 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1297
ID   ABB24740 standard; protein; 20 AA.
DE   Protein #6739 encoded by probe for measuring placental gene expression.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1298
ID   AAM34057 standard; protein; 20 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 34181.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1299
ID   AAM73875 standard; protein; 20 AA.
DE   Human brain expressed single exon probe, SEQ ID No 34274.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1300
ID   AAM61161 standard; protein; 20 AA.
DE   Protein #6739 encoded by probe for measuring heart cell gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1301
ID   ABG55626 standard; peptide; 20 AA.
DE   Human liver peptide, SEQ ID No 34274.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 4; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1302
ID   ABG43763 standard; peptide; 20 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 33428.
PN   WO200186003-A2.
PD   15-NOV-2001.

PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%; Score 5; DB 5; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1303
ID   AAU71025 standard; peptide; 20 AA.
DE   M. tuberculosis Rv0284 protein immunogenic peptide P38.
PN   WO200179274-A2.
PD   25-OCT-2001.
PA   (STAT-) STATENS SERUM INST.
     Query Match   6.5%; Score 5; DB 5; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1304
ID   AAO18693 standard; peptide; 20 AA.
DE   Hepatitis C virus E1 protein derived peptide E1-45.
PN   WO200255548-A2.
PD   18-JUL-2002.
PA   (INNO-) INNOGENETICS NV.
     Query Match   6.5%; Score 5; DB 5; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1305
ID   ADD55572 standard; peptide; 20 AA.
DE   Hepatitis C virus E1 epitope peptide #14.
PN   WO2003051912-A2.
PD   26-JUN-2003.
PA   (INNO-) INNOGENETICS NV.
     Query Match   6.5%; Score 5; DB 7; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1306
ID   ADP71154 standard; peptide; 20 AA.
DE   HCV E1 protein, peptide E1-45.
PN   US2004126395-A1.
PD   01-JUL-2004.
PA   (MAER/) MAERTENS G.
PA   (DEPL/) DEPLA E.
PA   (BOSM/) BOSMAN F.
     Query Match   6.5%; Score 5; DB 8; Length 20;
     Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1307
ID   AAW88554 standard; protein; 21 AA.
DE   Secreted protein encoded by gene 21 clone HSDGP60.
PN   WO9854963-A2.
PD   10-DEC-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.5%; Score 5; DB 2; Length 21;
     Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1308
ID   ABB50321 standard; protein; 21 AA.
DE   Human secreted protein encoded by gene 21 SEQ ID NO:269.
PN   WO200162891-A2.
PD   30-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.5%; Score 5; DB 4; Length 21;
     Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1309
ID   ABG6496 standard; peptide; 21 AA.
DE   IgE Fcepsilon RI binding peptide IGE134 #37.
PN   WO200226781-A2.
PD   04-APR-2002.
PA   (GETH) GENENTECH INC.
     Query Match   6.5%; Score 5; DB 5; Length 21;
     Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1310
ID   ABO44578 standard; protein; 21 AA.
DE   Novel human secreted protein #21.
PN   US20030365160-A1.
PD   03-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.5%; Score 5; DB 6; Length 21;
     Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1311
ID   ABO26058 standard; protein; 21 AA.
DE   Human protein from novel secreted protein gene 21.
PN   US6525174-B1.

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PD  25-FEB-2003.
PA  (HUMA-) HUMAN GENOME SCI INC.
    Query Match    6.5%;  Score 5;  DB 7;  Length 21;
    Best Local Similarity  100.0%;  Pred. No. 7.5e+02;
RESULT 1312
ID  ADB48087 standard; peptide; 21 AA.
DE  Hyaluronidase fragment #8.
PN  US200309296-A1.
PD  09-JAN-2003.
PA  (INCY-) INCYTE GENOMICS INC.
    Query Match    6.5%;  Score 5;  DB 7;  Length 21;
    Best Local Similarity  100.0%;  Pred. No. 7.5e+02;
RESULT 1313
ID  AB060589 standard; protein; 21 AA.
DE  Human genome derived single exon protein #6823.
PN  US2003194704-A1.
PD  16-OCT-2003.
PA  (PENN/) PENN S G.
PA  (RANK/) RANK D R.
PA  (HANZ/) HANZEL D K.
    Query Match    6.5%;  Score 5;  DB 8;  Length 21;
    Best Local Similarity  100.0%;  Pred. No. 7.5e+02;
RESULT 1314
ID  AAW03582 standard; peptide; 22 AA.
DE  Human m2 muscarinic acetylcholine GPR N-terminal sequence.
PN  US5508384-A.
PD  16-APR-1996.
PA  (UYNY ) UNIV NEW YORK STATE.
    Query Match    6.5%;  Score 5;  DB 2;  Length 22;
    Best Local Similarity  100.0%;  Pred. No. 7.8e+02;
RESULT 1315
ID  AAY52259 standard; peptide; 22 AA.
DE  H. pylori ygiD protein fragment containing conserved motif 3.
PN  WO9954470-A2.
PD  28-OCT-1999.
PA  (GLAX ) GLAXO GROUP LTD.
    Query Match    6.5%;  Score 5;  DB 3;  Length 22;
    Best Local Similarity  100.0%;  Pred. No. 7.8e+02;
RESULT 1316
ID  AAB57740 standard; peptide; 22 AA.
DE  D.melanogaster Jock peptide #6.
PN  US6150160-A.
PD  21-NOV-2000.
PA  (UYJO ) UNIV JOHNS HOPKINS.
PA  (UYPE-) UNIV PENNSYLVANIA.
    Query Match    6.5%;  Score 5;  DB 4;  Length 22;
    Best Local Similarity  100.0%;  Pred. No. 7.8e+02;
RESULT 1317
ID  AAY11429 standard; protein; 23 AA.
DE  Human 5' EST secreed protein SEQ ID No 251.
PN  WO9906551-A2.
PD  11-FEB-1999.
PA  (GEST ) GENSET.
    Query Match    6.5%;  Score 5;  DB 2;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1318
ID  AAU90690 standard; peptide; 23 AA.
DE  Insulin/insulin-like growth factor receptor-binding peptide #2646.
PN  WO200172771-A2.
PD  04-OCT-2001.
PA  (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA  (NOVO ) NOVO NORDISK AS.
    Query Match    6.5%;  Score 5;  DB 5;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1319
ID  AAU88261 standard; peptide; 23 AA.
DE  Insulin/insulin-like growth factor receptor-binding peptide #217.
PN  WO200172771-A2.
PD  04-OCT-2001.
PA  (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA  (NOVO ) NOVO NORDISK AS.
    Query Match    6.5%;  Score 5;  DB 5;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;

RESULT 1320
ID  ADA04526 standard; peptide; 23 AA.
DE  IR/IGF-1R related peptide SEQ ID NO:1157.
PN  WO2003027246-A2.
PD  03-APR-2003.
PA  (NOVO ) NOVO NORDISK AS.
PA  (DGIB-) DGI BIOTECHNOLOGIES.
    Query Match    6.5%;  Score 5;  DB 6;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1321
ID  AAE33949 standard; peptide; 23 AA.
DE  Dilipidated malaria peptide.
PN  WO20276485-A2.
PD  03-OCT-2002.
PA  (BUDZ/) BUDZYNSKI W A.
    Query Match    6.5%;  Score 5;  DB 6;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1322
ID  AAE38456 standard; peptide; 23 AA.
DE  CD2AP peptide #5.
PN  WO200368808-A1.
PD  21-AUG-2003.
PA  (GARV-) GARVAN INST MEDICAL RES.
    Query Match    6.5%;  Score 5;  DB 6;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1323
ID  ADD18049 standard; peptide; 23 AA.
DE  Human G-protein coupled receptor related transmembrane peptide SeqID106.
PN  WO2003016478-A2.
PD  27-FEB-2003.
PA  (BRIM ) BRISTOL-MYERS SQUIBB CO.
    Query Match    6.5%;  Score 5;  DB 7;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1324
ID  ADH95739 standard; protein; 23 AA.
DE  Insulin/insulin-like growth factor receptor binding protein, SEQ ID 1157.
PN  WO2003070747-A2.
PD  28-AUG-2003.
PA  (NOVO ) NOVO NORDISK AS.
PA  (DGIB-) DGI BIOTECHNOLOGIES.
    Query Match    6.5%;  Score 5;  DB 7;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1325
ID  ADL68430 standard; peptide; 23 AA.
DE  IGF-1R/IR binding peptide seq id 1157.
PN  US2004023887-A1.
PD  05-FEB-2004.
PA  (PILL/) PILLUTLA R.
PA  (DEDO/) DEDOVA O.
PA  (BLUM/) BLUME A J.
PA  (GOLD/) GOLDSTEIN N I.
PA  (BRIS/) BRISSETTE R.
PA  (WANG/) WANG P.
PA  (LIUH/) LIU H.
PA  (HSIA/) HSIAO K.
PA  (LENN/) LENNICK M.
PA  (FLET/) FLETCHER P.
    Query Match    6.5%;  Score 5;  DB 8;  Length 23;
    Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
RESULT 1326
ID  ADM38275 standard; peptide; 23 AA.
DE  Representative peptide #3.
PN  US2003236190-A1.
PD  25-DEC-2003.
PA  (PILL/) PILLUTLA R.
PA  (BRIS/) BRISSETTE R.
PA  (BLUM/) BLUME A J.
PA  (SCHA/) SCHAFFER L.
PA  (BRAN/) BRANDT J.
PA  (GOLD/) GOLDSTEIN N I.
PA  (SPET/) SPETZLER J.
PA  (OSTE/) OSTERGAARD S.
PA  (HANS/) HANSEN P H.
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Query Match            6.5%;   Score 5;   DB 8;  Length 23;
Best Local Similarity   100.0%;   Pred. No. 8.1e+02;
RESULT 1327
ID   AAB57698 standard; peptide; 24 AA.
DE   N.crassa TAD peptide #6.
PN   US6150160-A.
PD   21-NOV-2000.
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (UYPE-) UNIV PENNSYLVANIA.
Query Match            6.5%;   Score 5;   DB 4;  Length 24;
Best Local Similarity   100.0%;   Pred. No. 8.5e+02;
RESULT 1328
ID   AAB48671 standard; peptide; 24 AA.
DE   Human CD86 constant domain fragment, SEQ ID NO:20.
PN   WO20006162-A1.
PD   09-NOV-2000.
PA   (UYPE-) UNIV PENNSYLVANIA.
PA   (SEKA/) SEKALY R P.
PA   (HOLT/) HOLTERMAN M.
Query Match            6.5%;   Score 5;   DB 4;  Length 24;
Best Local Similarity   100.0%;   Pred. No. 8.5e+02;
RESULT 1329
ID   ABR91576 standard; peptide; 24 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:410.
PN   WO2002102324-A2.
PD   27-DEC-2002.
Query Match            6.5%;   Score 5;   DB 6;  Length 24;
Best Local Similarity   100.0%;   Pred. No. 8.5e+02;
RESULT 1330
ID   ABO57390 standard; protein; 24 AA.
DE   Human genome derived single exon protein #3624.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
Query Match            6.5%;   Score 5;   DB 8;  Length 24;
Best Local Similarity   100.0%;   Pred. No. 8.5e+02;
RESULT 1331
ID   AAR10510 standard; protein; 25 AA.
DE   Fragment of subtilisine secretion signal.
PN   EP409098-A.
PD   23-JAN-1991.
PA   (ENIE ) ENIRICERCHE SPA.
Query Match            6.5%;   Score 5;   DB 2;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1332
ID   AAM3922 standard; protein; 25 AA.
DE   Melittin delta 14 (deletion analogue).
PN   US5235038-A.
PD   10-AUG-1993.
PA   (TORR-) TORRY PINES INST MOLECULAR STUDIES.
Query Match            6.5%;   Score 5;   DB 2;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1333
ID   AAM13922 standard; protein; 25 AA.
DE   Peptide #356 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1334
ID   ABB32867 standard; peptide; 25 AA.
DE   Peptide #373 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1335
ID   AAM26328 standard; protein; 25 AA.
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DE   Peptide #365 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1336
ID   ABB27696 standard; peptide; 25 AA.
DE   Human peptide #347 encoded by breast cell single exon nucleic acid probe.
PN   WO200157271-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1337
ID   ABB18349 standard; protein; 25 AA.
DE   Protein #348 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1338
ID   AAM66053 standard; protein; 25 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 26359.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1339
ID   AAM53669 standard; protein; 25 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 25774.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1340
ID   ABG47719 standard; peptide; 25 AA.
DE   Human liver peptide, SEQ ID No 26367.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1341
ID   AAM01665 standard; protein; 25 AA.
DE   Peptide #347 encoded by probe for measuring human breast gene expression.
PN   WO200157270-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1342
ID   ABG13692 standard; protein; 25 AA.
DE   Novel human diagnostic protein #13683.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1343
ID   AAB62888 standard; protein; 25 AA.
DE   Mature bovine beta-lactoglobulin (BLG) tryptic digest peptide 3.
PN   WO200118528-A1.
PD   15-MAR-2001.
PA   (IOWA ) UNIV IOWA STATE RES FOUND INC.
Query Match            6.5%;   Score 5;   DB 4;  Length 25;
Best Local Similarity   100.0%;   Pred. No. 8.8e+02;
RESULT 1344
ID   ABG35701 standard; peptide; 25 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 25366.
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PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 5;   Length 25;
     Best Local Similarity 100.0%;   Pred. No. 8.8e+02;
RESULT 1345
ID   ABR91360 standard; peptide; 25 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:194.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5;   DB 6;   Length 25;
     Best Local Similarity 100.0%;   Pred. No. 8.8e+02;
RESULT 1346
ID   ABR91580 standard; peptide; 25 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:414.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5;   DB 6;   Length 25;
     Best Local Similarity 100.0%;   Pred. No. 8.8e+02;
RESULT 1347
ID   ABR91363 standard; peptide; 25 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:197.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5;   DB 6;   Length 25;
     Best Local Similarity 100.0%;   Pred. No. 8.8e+02;
RESULT 1348
ID   AAY70373 standard; peptide; 26 AA.
DE   Maize ZmKCS1 peptide-4.
PN   WO200008172-A1.
PD   17-FEB-2000.
PA   (AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.
     Query Match   6.5%;   Score 5;   DB 3;   Length 26;
     Best Local Similarity 100.0%;   Pred. No. 9.1e+02;
RESULT 1349
ID   ABR91364 standard; peptide; 26 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:198.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5;   DB 6;   Length 26;
     Best Local Similarity 100.0%;   Pred. No. 9.1e+02;
RESULT 1350
ID   ABR91365 standard; peptide; 26 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:199.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5;   DB 6;   Length 26;
     Best Local Similarity 100.0%;   Pred. No. 9.1e+02;
RESULT 1351
ID   ABR91362 standard; peptide; 26 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:196.
PN   WO2002102324-A2.
PD   27-DEC-2002.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
     Query Match   6.5%;   Score 5;   DB 6;   Length 26;
     Best Local Similarity 100.0%;   Pred. No. 9.1e+02;
RESULT 1352
ID   ADM10549 standard; peptide; 26 AA.
DE   Nucleic acid-peptide library peptide sequence #11.
PN   WO2003089454-A2.
PD   30-OCT-2003.
PA   (CALY) CALIFORNIA INST OF TECHNOLOGY.
     Query Match   6.5%;   Score 5;   DB 7;   Length 26;
     Best Local Similarity 100.0%;   Pred. No. 9.1e+02;
RESULT 1353
ID   ADI19974 standard; peptide; 26 AA.
DE   Bovine lactalbumin peptide #3.
PN   US2003219838-A1.

PD   27-NOV-2003.
PA   (JOHN/) JOHNSON R S.
     Query Match   6.5%;   Score 5;   DB 8;   Length 26;
     Best Local Similarity 100.0%;   Pred. No. 9.1e+02;
RESULT 1354
ID   AAW33910 standard; peptide; 27 AA.
DE   Fragment from LITMUS 39 based plasmid pLit.GFP-2A23H-CP.
PN   WO9739134-A1.
PD   23-OCT-1997.
PA   (SCCR-) SCOTTISH CROP RES INST.
     Query Match   6.5%;   Score 5;   DB 2;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1355
ID   AAM20101 standard; protein; 27 AA.
DE   Peptide #6535 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1356
ID   ABB40292 standard; peptide; 27 AA.
DE   Peptide #7798 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1357
ID   AAM33975 standard; protein; 27 AA.
DE   Peptide #8012 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1358
ID   ABB24700 standard; protein; 27 AA.
DE   Protein #6699 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1359
ID   AAM73788 standard; protein; 27 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 34094.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1360
ID   AAM61085 standard; protein; 27 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 33190.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1361
ID   ABG55535 standard; peptide; 27 AA.
DE   Human liver peptide, SEQ ID No 34183.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   6.5%;   Score 5;   DB 4;   Length 27;
     Best Local Similarity 100.0%;   Pred. No. 9.4e+02;
RESULT 1362
ID   ABG43674 standard; peptide; 27 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 33339.
PN   WO200186003-A2.
PD   15-NOV-2001.

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PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match        6.5%;    Score 5;   DB 5;   Length 27;
     Best Local Similarity   100.0%;   Pred. No. 9.4e+02;
RESULT 1363
ID   ABR91366 standard; peptide; 27 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:200.
PN   WO200210324-A2.
PD   27-DEC-2002.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
     Query Match        6.5%;    Score 5;   DB 6;   Length 27;
     Best Local Similarity   100.0%;   Pred. No. 9.4e+02;
RESULT 1364
ID   ADF28635 standard; peptide; 27 AA.
DE   Neural IgCAM-like protein transmembrane domain - SED ID 545.
PN   WO200304832 6-A2.
PD   12-JUN-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match        6.5%;    Score 5;   DB 7;   Length 27;
     Best Local Similarity   100.0%;   Pred. No. 9.4e+02;
RESULT 1365
ID   ABG78097 standard; peptide; 28 AA.
DE   ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG and STMST-related peptide #45.
PN   US200207208 9-A1.
PD   13-JUN-2002.
PA   (HOLT/) HOLTZMAN D A.
PA   (MCCA/) MCCARTHY S A.
PA   (MACB/) MACBETH K J.
PA   (BUSF/) BUSFIELD S J.
PA   (PANY/) PAN Y.
PA   (WHIT/) WHITE D.
PA   (KHOD/) KHODADOUST M M.
PA   (GUWW/) GU W.
     Query Match        6.5%;    Score 5;   DB 5;   Length 28;
     Best Local Similarity   100.0%;   Pred. No. 9.8e+02;
RESULT 1366
ID   ADR45673 standard; peptide; 28 AA.
DE   Human G protein-coupled receptor IL-8RA, transmembrane domain 2.
PN   US200417629 6-A1.
PD   09-SEP-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match        6.5%;    Score 5;   DB 8;   Length 28;
     Best Local Similarity   100.0%;   Pred. No. 9.8e+02;
RESULT 1367
ID   AAR60524 standard; protein; 29 AA.
DE   Secretion sequence.
PN   EP614982-A1.
PD   14-SEP-1994.
PA   (ENIE ) ENIRICERCHE SPA.
     Query Match        6.5%;    Score 5;   DB 2;   Length 29;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1368
ID   AAW94837 standard; peptide; 29 AA.
DE   Dimeric coiled-coil peptide dCoil-adLL29.
PN   US200211957 2-A1.
PD   29-AUG-2002.
PA   (JACO/) JACOBSON J M.
PA   (SCHW/) SCHWARTZ J J.
PA   (HAMA/) HAMAD K.
PA   (ZHAN/) ZHANG S.
     Query Match        6.5%;    Score 5;   DB 2;   Length 29;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1369
ID   ADB25860 standard; peptide; 29 AA.
DE   Dimeric coiled-coil peptide dCoil-adLL29.
PN   WO985692 6 Seq ID 3.
PN   WO985692 6-A1.
PD   17-DEC-1998.
PA   (TAKI ) TAKARA SHUZO CO LTD.
     Query Match        6.5%;    Score 5;   DB 6;   Length 29;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1370
ID   ABM74029 standard; protein; 29 AA.
DE   DNA clone originating in barley containing SNP sequence #439.
PN   WO200305787 7-A1.

PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
     Query Match        6.5%;    Score 5;   DB 7;   Length 29;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1371
ID   AAY64891 standard; protein; 30 AA.
DE   Human 5' EST related polypeptide SEQ ID NO:1052.
PN   WO995305 1-A2.
PD   21-OCT-1999.
PA   (GEST ) GENSET.
     Query Match        6.5%;    Score 5;   DB 3;   Length 30;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1372
ID   AAU84616 standard; peptide; 30 AA.
DE   HCV HepC1a segment 19.
PN   WO200190197-A1.
PD   29-NOV-2001.
PA   (AUSU ) UNIV AUSTRALIAN NAT.
     Query Match        6.5%;    Score 5;   DB 5;   Length 30;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1373
ID   AAU84615 standard; peptide; 30 AA.
DE   HCV HepC1a segment 18.
PN   WO200190197-A1.
PD   29-NOV-2001.
PA   (AUSU ) UNIV AUSTRALIAN NAT.
     Query Match        6.5%;    Score 5;   DB 5;   Length 30;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1374
ID   ABR91368 standard; peptide; 30 AA.
DE   P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:202.
PN   WO200210324-A2.
PD   27-DEC-2002.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
     Query Match        6.5%;    Score 5;   DB 6;   Length 30;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1375
ID   ADH39846 standard; peptide; 30 AA.
DE   Subtilisin E signal peptide.
PN   US200321590 6-A1.
PD   20-NOV-2003.
PA   (LIMB/) LIM B L.
     Query Match        6.5%;    Score 5;   DB 8;   Length 30;
     Best Local Similarity   100.0%;   Pred. No. 1e+03;
RESULT 1376
ID   AAW24746 standard; peptide; 31 AA.
DE   Heel domain of OP-2.
PN   WO964077 1-A1.
PD   19-DEC-1996.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
     Query Match        6.5%;    Score 5;   DB 2;   Length 31;
     Best Local Similarity   100.0%;   Pred. No. 1.1e+03;
RESULT 1377
ID   AAY02266 standard; protein; 31 AA.
DE   A F-box protein sequence.
PN   WO991898 9-A1.
PD   22-APR-1999.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
     Query Match        6.5%;    Score 5;   DB 2;   Length 31;
     Best Local Similarity   100.0%;   Pred. No. 1.1e+03;
RESULT 1378
ID   AAM19230 standard; protein; 31 AA.
DE   Peptide #5664 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match        6.5%;    Score 5;   DB 4;   Length 31;
     Best Local Similarity   100.0%;   Pred. No. 1.1e+03;
RESULT 1379
ID   AAE08038 standard; peptide; 31 AA.
DE   Mouse F-box protein, F13.
PN   US623208 1-B1.
PD   15-MAY-2001.
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PA   (BAYU) BAYLOR COLLEGE MEDICINE.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1380
ID   ABB38458 standard; peptide; 31 AA.
DE   Peptide #5964 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1381
ID   AAM31899 standard; protein; 31 AA.
DE   Peptide #5936 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1382
ID   ABB23622 standard; protein; 31 AA.
DE   Protein #5621 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1383
ID   AAM71602 standard; protein; 31 AA.
DE   Human bone marrow expressed single exon probe encoded protein SEQ ID NO: 31908.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1384
ID   AAM59069 standard; protein; 31 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 31174.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1385
ID   ABG53284 standard; peptide; 31 AA.
DE   Human liver peptide, SEQ ID No 31932.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 4; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1386
ID   ABG41414 standard; protein; 31 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 31079.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match   6.5%; Score 5; DB 5; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1387
ID   AAE39646 standard; peptide; 31 AA.
DE   Mouse F-box protein, F13 (omicron).
PN   US6573094-B1.
PD   03-JUN-2003.
PA   (BAYU) BAYLOR COLLEGE MEDICINE.
   Query Match   6.5%; Score 5; DB 7; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1388
ID   ADR68965 standard; peptide; 31 AA.
DE   Mouse F13 (omicron) F-box domain peptide.
PN   US2004166530-A1.
PD   26-AUG-2004.
PA   (HARP/) HARPER J W.

PA   (ELLE/) ELLEDGE S J.
PA   (WINS/) WINSTON J T.
   Query Match   6.5%; Score 5; DB 8; Length 31;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1389
ID   AAR57991 standard; protein; 32 AA.
DE   B.licheniformis alpha-amylase signal sequence in pBLapr.
PN   WO9418314-A1.
PD   18-AUG-1994.
PA   (GEMV) GENENCOR INT INC.
   Query Match   6.5%; Score 5; DB 2; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1390
ID   AAR85822 standard; peptide; 32 AA.
DE   Peptide rI from the WD-40 domain-contg. YCW2 protein.
PN   WO9521252-A2.
PD   10-AUG-1995.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
   Query Match   6.5%; Score 5; DB 2; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1391
ID   AAW88722 standard; protein; 32 AA.
DE   Secreted protein encoded by gene 189 SEQ ID NO:437.
PN   WO9854963-A2.
PD   10-DEC-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
   Query Match   6.5%; Score 5; DB 2; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1392
ID   ABB50489 standard; protein; 32 AA.
DE   Human secreted protein encoded by gene 55 SEQ ID NO:665.
PN   WO200162891-A2.
PD   30-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
   Query Match   6.5%; Score 5; DB 4; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1393
ID   ABB50714 standard; protein; 32 AA.
DE   Human secreted protein encoded by gene 55 SEQ ID NO:665.
PN   WO200162891-A2.
PD   30-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
   Query Match   6.5%; Score 5; DB 4; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1394
ID   AAG80082 standard; peptide; 32 AA.
DE   Chemokine CCR3 extracellular loop domain #1.
PN   WO200172830-A2.
PD   04-OCT-2001.
PA   (IPFP) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
   Query Match   6.5%; Score 5; DB 4; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1395
ID   AAO13527 standard; protein; 32 AA.
DE   Human polypeptide SEQ ID NO 27419.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE) HYSEQ INC.
   Query Match   6.5%; Score 5; DB 4; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1396
ID   AAG65885 standard; protein; 32 AA.
DE   B. licheniformis alpha-amylase fragment.
PN   US6297037-B1.
PD   02-OCT-2001.
PA   (BARN/) BARNETT C C.
PA   (MITC/) MITCHINSON C.
PA   (POWE/) POWER S D.
PA   (REQU/) REQUADT C A.
   Query Match   6.5%; Score 5; DB 4; Length 32;
   Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1397

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ID   ABO44971 standard; protein; 32 AA.
DE   Novel human secreted protein #55 fragment #2.
PN   US200306516O-A1.
PD   03-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     6.5%;   Score 5;  DB 6;  Length 32;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1398
ID   ABO44746 standard; protein; 32 AA.
DE   Novel human secreted protein #189.
PN   US2003065160-A1.
PD   03-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     6.5%;   Score 5;  DB 6;  Length 32;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1399
ID   ABO26226 standard; protein; 32 AA.
DE   Human protein from novel secreted protein gene 189.
PN   US6525174-B1.
PD   25-FEB-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     6.5%;   Score 5;  DB 7;  Length 32;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1400
ID   ABO26451 standard; protein; 32 AA.
DE   Protein associated with novel secreted protein gene 55 #2.
PN   US6525174-B1.
PD   25-FEB-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     6.5%;   Score 5;  DB 7;  Length 32;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1401
ID   ADF90370 standard; peptide; 32 AA.
DE   ICAM-2 transmembrane domain.
PN   US2003190684-A1.
PD   09-OCT-2003.
PA   (FISH/) FISHER J.
PA   (LORE/) LORENS J.
PA   (PAYA/) PAYAN D.
PA   (ROSS/) ROSSI A.
     Query Match     6.5%;   Score 5;  DB 7;  Length 32;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1402
ID   ABO54160 standard; protein; 32 AA.
DE   Human genome derived single exon protein #394.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (GEMV-) GENENCOR INT INC.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
     Query Match     6.5%;   Score 5;  DB 8;  Length 32;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1403
ID   AAR57989 standard; protein; 33 AA.
DE   B.subtilis alkaline protease aprE signal sequence-mature protein.
PN   WO9418314-A1.
PD   18-AUG-1994.
PA   (GEMV-) GENENCOR INT INC.
     Query Match     6.5%;   Score 5;  DB 2;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1404
ID   AAY49759 standard; peptide; 33 AA.
DE   Compact structure forming exemplification peptide #52.
PN   WO9951625-A2.
PD   14-OCT-1999.
PA   (RIGE-) RIGEL PHARM INC.
     Query Match     6.5%;   Score 5;  DB 2;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1405
ID   AAY43819 standard; peptide; 33 AA.
DE   Transmembrane domain of ICAM-2.
PN   WO9954494-A2.
PD   28-OCT-1999.

PA   (RIGE-) RIGEL PHARM INC.
     Query Match     6.5%;   Score 5;  DB 3;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1406
ID   AAB44770 standard; protein; 33 AA.
DE   Human secreted protein sequence encoded by gene 9 SEQ ID NO:69.
PN   WO20005836-A1.
PD   05-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     6.5%;   Score 5;  DB 3;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1407
ID   AAY88075 standard; peptide; 33 AA.
DE   Human ICAM-2 transmembrane region peptide fragment.
PN   WO20023463-A2.
PD   27-APR-2000.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
     Query Match     6.5%;   Score 5;  DB 3;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1408
ID   AAM19101 standard; protein; 33 AA.
DE   Peptide #5535 encoded by probe for measuring cervical gene expression.
PN   WO20157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match     6.5%;   Score 5;  DB 4;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1409
ID   AAB35066 standard; peptide; 33 AA.
DE   ICAM-2 transmembrane domain.
PN   WO20072008-A2.
PD   30-NOV-2000.
PA   (RIGE-) RIGEL PHARM INC.
     Query Match     6.5%;   Score 5;  DB 4;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1410
ID   AAB45934 standard; peptide; 33 AA.
DE   Transdominant effector peptide associated screening peptide #14.
PN   US6153380-A.
PD   28-NOV-2000.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (RIGE-) RIGEL PHARM INC.
     Query Match     6.5%;   Score 5;  DB 4;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1411
ID   AAB35094 standard; peptide; 33 AA.
DE   Filamentous phage protein display related sequence #1.
PN   WO20071694-A1.
PD   30-NOV-2000.
PA   (SCRI ) SCRIPPS RES INST.
     Query Match     6.5%;   Score 5;  DB 4;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1412
ID   ABB38307 standard; peptide; 33 AA.
DE   Peptide #5813 encoded by human foetal liver single exon probe.
PN   WO20157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match     6.5%;   Score 5;  DB 4;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1413
ID   AAM31744 standard; protein; 33 AA.
DE   Peptide #5781 encoded by probe for measuring placental gene expression.
PN   WO20157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match     6.5%;   Score 5;  DB 4;  Length 33;
     Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
RESULT 1414
ID   ABG99131 standard; peptide; 33 AA.
DE   Human ICAM-2 transmembrane domain.
PN   WO20166565-A2.
PD   13-SEP-2001.
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PA   (RIGE-) RIGEL PHARM INC.
   Query Match     6.5%;   Score 5;   DB 4;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1415
ID   ABB23485 standard; protein; 33 AA.
DE   Protein #5484 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match     6.5%;   Score 5;   DB 4;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1416
ID   AAM71451 standard; protein; 33 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 31757.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match     6.5%;   Score 5;   DB 4;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1417
ID   AAM58927 standard; protein; 33 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 31032.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match     6.5%;   Score 5;   DB 4;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1418
ID   ABG53146 standard; peptide; 33 AA.
DE   Human liver peptide, SEQ ID No 31794.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match     6.5%;   Score 5;   DB 4;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1419
ID   AAG65883 standard; protein; 33 AA.
DE   B. subtilis alkaline protease aprE fragment.
PN   US6297037-B1.
PD   02-OCT-2001.
PA   (BARN/) BARNETT C C.
PA   (MITC/) MITCHINSON C.
PA   (POWE/) POWER S D.
PA   (REQU/) REQUADT C A.
   Query Match     6.5%;   Score 5;   DB 4;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1420
ID   ABG41255 standard; peptide; 33 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 30920.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
   Query Match     6.5%;   Score 5;   DB 5;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1421
ID   ABB07745 standard; peptide; 33 AA.
DE   Transmembrane domain of ICAM.2 protein (residues 224-256).
PN   WO200210417-A2.
PD   07-FEB-2002.
PA   (XENC-) XENCOR INC.
   Query Match     6.5%;   Score 5;   DB 5;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1422
ID   AAU76172 standard; protein; 33 AA.
DE   Intercellular adhesion molecule-2 transmembrane anchoring sequence.
PN   US2002001830-A1.
PD   03-JAN-2002.
PA   (LUOY/) LUO Y.
PA   (YUPW/) YU P W.
PA   (LORE/) LORENS J.
   Query Match     6.5%;   Score 5;   DB 5;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1423

ID   AAE28677 standard; peptide; 33 AA.
DE   Human ICAM-2 transmembrane domain.
PN   WO200268453-A2.
PD   06-SEP-2002.
PA   (XENC-) XENCOR INC.
   Query Match     6.5%;   Score 5;   DB 5;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1424
ID   ABG92957 standard; peptide; 33 AA.
DE   ICAM-2 transmembrane domain sequence peptide.
PN   WO200262822-A2.
PD   15-AUG-2002.
PA   (UYRP ) UNIV ROCHESTER.
   Query Match     6.5%;   Score 5;   DB 5;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1425
ID   ABG98455 standard; peptide; 33 AA.
DE   Transmembrane domain for use in controlling signal pathways #2.
PN   US2002127564-A1.
PD   12-SEP-2002.
PA   (NOLA/) NOLAN G P.
   Query Match     6.5%;   Score 5;   DB 6;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1426
ID   ABU64892 standard; peptide; 33 AA.
DE   Human ICAM-2 transmembrane domain.
PN   US2002172968-A1.
PD   21-NOV-2002.
PA   (LIUH/) LIU H.
PA   (DAHI/) DAHIYAT B I.
PA   (LIMM/) LI M.
   Query Match     6.5%;   Score 5;   DB 6;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1427
ID   ABU64787 standard; peptide; 33 AA.
DE   Human ICAM-2 membrane anchor peptide, #2.
PN   US2002168640-A1.
PD   14-NOV-2002.
PA   (LIMM/) LI M.
PA   (DAHI/) DAHIYAT B I.
   Query Match     6.5%;   Score 5;   DB 6;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1428
ID   ABP56553 standard; peptide; 33 AA.
DE   Human ICAM-2 transmembrane domain SEQ ID NO:19.
PN   WO200286096-A2.
PD   31-OCT-2002.
PA   (UYRP ) UNIV ROCHESTER MEDICAL CENT.
   Query Match     6.5%;   Score 5;   DB 6;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1429
ID   ABR39521 standard; peptide; 33 AA.
DE   ICAM-2 transmembrane domain fragment (residues 224-256).
PN   WO2003017937-A2.
PD   06-MAR-2003.
PA   (UYHA-) UNIV HAWAII.
   Query Match     6.5%;   Score 5;   DB 6;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1430
ID   ABU14020 standard; peptide; 33 AA.
DE   ICAM-2 residues 224-256, transmembrane domain.
PN   US6455247-B1.
PD   24-SEP-2002.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (RIGE-) RIGEL PHARM INC.
   Query Match     6.5%;   Score 5;   DB 6;   Length 33;
   Best Local Similarity  100.0%;   Pred. No. 1.1e+03;
RESULT 1431
ID   ABP72873 standard; peptide; 33 AA.
DE   Human ICAM-2 membrane anchoring signal sequence.
PN   WO2003020896-A2.
PD   13-MAR-2003.
PA   (RIGE-) RIGEL PHARM INC.
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Query Match   6.5%;   Score 5; DB 6; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1432
ID ABU09644 standard; peptide; 33 AA.
DE ICAM-2 transmembrane domain.
PN US2003017601-A1.
PD 23-JAN-2003.
PA (RIGE-) RIGEL PHARM INC.

Query Match   6.5%;   Score 5; DB 6; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1433
ID AAE32695 standard; peptide; 33 AA.
DE ICAM-2 targetting peptide #2.
PN WO200286450-A2.
PD 31-OCT-2002.
PA (HARD) HARVARD COLLEGE.

Query Match   6.5%;   Score 5; DB 6; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1434
ID ADA07047 standard; peptide; 33 AA.
DE ICAM-1 transmembrane domain peptide.
PN WO200290535-A1.
PD 14-NOV-2002.
PA (RIGE-) RIGEL PHARM INC.

Query Match   6.5%;   Score 5; DB 6; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1435
ID ADA06998 standard; peptide; 33 AA.
DE ICAM-2 transmembrane domain.
PN US2003022196-A1.
PD 30-JAN-2003.
PA (LORE/) LORENS J.
PA (KINS/) KINSELLA T M.
PA (MASU/) MASUDA E.
PA (HITO/) HITOSHI Y.
PA (LIAO/) LIAO X C.
PA (PEAR/) PEARSALL D.
PA (FRIE/) FRIERA A.
PA (CHUP/) CHU P.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1436
ID ADA08288 standard; peptide; 33 AA.
DE Human ICAM-2 transmembrane anchoring signal.
PN US656617-B1.
PD 13-MAY-2003.
PA (RIGE-) RIGEL PHARM INC.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1437
ID ADB66843 standard; peptide; 33 AA.
DE Fusion nucleic acid retroviral vector associated peptide #13.
PN US2003099932-A1.
PD 29-MAY-2003.
PA (LORE/) LORENS J B.
PA (FERR/) FERRICK D A.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1438
ID AAE38941 standard; peptide; 33 AA.
DE Human ICAM-2 transmembrane domain.
PN US6548249-B1.
PD 15-APR-2003.
PA (RIGE-) RIGEL PHARM INC.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1439
ID AAE39825 standard; peptide; 33 AA.
DE Human ICAM-2 transmembrane domain peptide.
PN US2003170641-A1.
PD 11-SEP-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match   6.5%;   Score 5; DB 7; Length 33;

Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1440
ID ADD28901 standard; peptide; 33 AA.
DE ICAM-2 transmembrane domain.
PN US2003104384-A1.
PD 05-JUN-2003.
PA (NOLA/) NOLAN G P.
PA (ROTH/) ROTHENBERG S M.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1441
ID ADE10737 standard; peptide; 33 AA.
DE structurally biased peptide library membrane anchoring sequence #4.
PN US2003143562-A1.
PD 31-JUL-2003.
PA (RIGE-) RIGEL PHARM INC.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1442
ID ADF32299 standard; peptide; 33 AA.
DE ICAM-2 membrane anchoring peptide domain.
PN US6548632-B1.
PD 15-APR-2003.
PA (RIGE-) RIGEL PHARM INC.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1443
ID ADJ53812 standard; peptide; 33 AA.
DE ICAM-2 transmembrane domain.
PN US2003211535-A1.
PD 13-NOV-2003.
PA (LORE/) LORENS J.
PA (BOGE/) BOGENBERGER J M.

Query Match   6.5%;   Score 5; DB 7; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1444
ID ADG14185 standard; peptide; 33 AA.
DE Human BMP8/OP2 protein heel region.
PN US2003185792-A1.
PD 02-OCT-2003.
PA (CURI-) CURIS INC.

Query Match   6.5%;   Score 5; DB 8; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1445
ID ADI36216 standard; peptide; 33 AA.
DE Human ICAM-2 transmembrane domain.
PN US2003219723-A1.
PD 27-NOV-2003.
PA (LUHH/) LU H H.
PA (HUAN/) HUANG P.
PA (KINS/) KINSELLA T.
PA (MART/) MARTINEZ A.

Query Match   6.5%;   Score 5; DB 8; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1446
ID ADK15756 standard; peptide; 33 AA.
DE Fusion protein library-related human peptide #10.
PN US2003224412-A1.
PD 04-DEC-2003.
PA (ANDE/) ANDERSON D.
PA (PEEL/) PEELLE B R.
PA (BOGE/) BOGENBERGER J M.

Query Match   6.5%;   Score 5; DB 8; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1447
ID ADM24749 standard; peptide; 33 AA.
DE Human ICAM-2 transmembrane sequence.
PN US2003211462-A1.
PD 13-NOV-2003.
PA (SHEN/) SHEN M.
PA (YUSS/) YU S.
PA (WUXX/) WU X.
PA (PAYA/) PAYAN D.

Query Match   6.5%;   Score 5;   DB 8; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1448
ID ADL23786 standard; peptide; 33 AA.
DE ICAM-2 transmembrane domain sequence.
PN WO2004019890-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match   6.5%;   Score 5;   DB 8; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1449
ID ADN41111 standard; protein; 33 AA.
DE Novel human secreted protein seqid 233.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN R.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match   6.5%;   Score 5;   DB 8; Length 33;
Best Local Similarity 100.0%;   Pred. No. 1.1e+03;
RESULT 1450
ID AAY02700 standard; protein; 34 AA.
DE Human secreted protein encoded by gene 51 clone HUKEX85,
PN WO9902546-A1.
PD 21-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   6.5%;   Score 5;   DB 2; Length 34;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1451
ID ABP66698 standard; protein; 34 AA.
DE Human breast specific protein SEQ ID NO 200.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match   6.5%;   Score 5;   DB 5; Length 34;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1452
ID ADA07379 standard; protein; 34 AA.
DE Human secreted protein from gene 51.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
Query Match   6.5%;   Score 5;   DB 7; Length 34;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1453
ID AAR57990 standard; protein; 35 AA.
DE B.licheniformis alpha-amylase signal sequence in pA4BL.
PN WO9418314-A1.
PD 18-AUG-1994.
PA (GEMV) GENENCOR INT INC.
Query Match   6.5%;   Score 5;   DB 2; Length 35;

Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1454
ID AAW96863 standard; peptide; 35 AA.
DE Nucleic acid binding domain from apoB-100, residues 2353-2387.
PN WO955938-A1.
PD 17-DEC-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match   6.5%;   Score 5;   DB 2; Length 35;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1455
ID AAG55884 standard; protein; 35 AA.
DE B. licheniformis alpha-amylase fragment.
PN US6297037-B1.
PD 02-OCT-2001.
PA (BARN/) BARNETT C C.
PA (MITC/) MITCHINSON C.
PA (POWE/) POWER S D.
PA (REQU/) REQUADT C A.
Query Match   6.5%;   Score 5;   DB 4; Length 35;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1456
ID ABP77794 standard; protein; 35 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2118.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match   6.5%;   Score 5;   DB 6; Length 35;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1457
ID ABP68409 standard; protein; 36 AA.
DE Human colon specific protein, SEQ ID 150.
PN WO200277234-A2.
PD 03-OCT-2002.
PA (DIAD-) DIADEXUS INC.
Query Match   6.5%;   Score 5;   DB 6; Length 36;
Best Local Similarity 100.0%;   Pred. No. 1.2e+03;
RESULT 1458
ID AAW93461 standard; peptide; 37 AA.
DE Human hCG beta-subunit peptide structure XVIa.
PN US5891992-A.
PD 06-APR-1999.
PA (OHIS) UNIV OHIO STATE RES FOUND.
Query Match   6.5%;   Score 5;   DB 2; Length 37;
Best Local Similarity 100.0%;   Pred. No. 1.3e+03;
RESULT 1459
ID AAY87497 standard; peptide; 37 AA.
DE Human chorionic gonadotropin beta subunit-derived peptide XVIa.
PN US6039948-A.
PD 21-MAR-2000.
PA (OHIS) UNIV OHIO STATE.
Query Match   6.5%;   Score 5;   DB 3; Length 37;
Best Local Similarity 100.0%;   Pred. No. 1.3e+03;
RESULT 1460
ID AAB20566 standard; protein; 37 AA.
DE Human chorionic gonadotropin beta subunit derived polypeptide (XVIa).
PN US6096318-A.
PD 01-AUG-2000.
PA (OHIS) UNIV OHIO STATE.
Query Match   6.5%;   Score 5;   DB 3; Length 37;
Best Local Similarity 100.0%;   Pred. No. 1.3e+03;
RESULT 1461
ID AAU21887 standard; protein; 37 AA.
DE Human cardiovascular system antigen polypeptide SEQ ID No 661.
PN WO200015321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   6.5%;   Score 5;   DB 4; Length 37;
Best Local Similarity 100.0%;   Pred. No. 1.3e+03;
RESULT 1462
ID AAU01169 standard; peptide; 37 AA.
DE Structure XVIa, peptide used to produce modified HCG peptides.
PN US6217881-B1.
PD 17-APR-2001.

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PA   (OHIS ) UNIV OHIO STATE RES FOUND.
Query Match             6.5%;    Score 5;   DB 4;   Length 37;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1463
ID   AAB48403 standard; peptide; 37 AA.
DE   Human chorionic gonadotropin beta subunit structure XVIa.
PN   US6143305-A.
PD   07-NOV-2000.
PA   (OHIS ) UNIV OHIO STATE.
Query Match             6.5%;    Score 5;   DB 4;   Length 37;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1464
ID   AAU02865 standard; protein; 37 AA.
DE   Human Chorionic Gonadotrophin (HCG) beta-subunit fragment #14.
PN   WO200124765-A2.
PD   12-APR-2001.
PA   (OHIS ) UNIV OHIO STATE RES FOUND.
Query Match             6.5%;    Score 5;   DB 4;   Length 37;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1465
ID   AAB04141 standard; peptide; 37 AA.
DE   Peptide fragment of beta subunit of human chorionic gonadotropin.
PN   US6146633-A.
PD   14-NOV-2000.
PA   (OHIS ) UNIV OHIO STATE.
Query Match             6.5%;    Score 5;   DB 4;   Length 37;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1466
ID   ADE45855 standard; protein; 37 AA.
DE   Human cardiovascular system related polypeptide #36.
PN   US2003059908-A1.
PD   27-MAR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 7;   Length 37;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1467
ID   ADJ07273 standard; peptide; 37 AA.
DE   Human cardiovascular system associated polypeptide SeqID661.
PN   US2004005575-A1.
PD   08-JAN-2004.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 8;   Length 37;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1468
ID   AAY12631 standard; protein; 39 AA.
DE   Human 5' EST secreted protein SEQ ID NO: 296 from WO 9906553.
PN   WO9906553-A2.
PD   11-FEB-1999.
PA   (GST ) GENSET.
Query Match             6.5%;    Score 5;   DB 2;   Length 39;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1469
ID   AAB52117 standard; protein; 39 AA.
DE   Human secreted protein encoded by cDNA #15.
PN   WO200123546-A1.
PD   19-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 3;   Length 39;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1470
ID   AAU01783 standard; peptide; 39 AA.
DE   Human secreted protein #62.
PN   WO200123546-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 4;   Length 39;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1471
ID   ABJ19737 standard; peptide; 39 AA.
DE   Human secreted protein amino acid sequence - SEQ ID No 205.
PN   WO200277188-A2.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.

Query Match             6.5%;    Score 5;   DB 6;   Length 39;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1472
ID   ABP99831 standard; protein; 39 AA.
DE   Human secreted protein SEQ ID NO 775.
PN   WO200277186-A2.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 6;   Length 39;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1473
ID   ADC20554 standard; protein; 39 AA.
DE   Human secreted protein - amino acid sequence #235.
PN   WO200292787-A2.
PD   21-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 7; Length 39;
Best Local Similarity  100.0%;   Pred. No. 1.3e+03;
RESULT 1474
ID   ABB15215 standard; protein; 41 AA.
DE   Human nervous system related polypeptide SEQ ID NO 3872.
PN   WO200159063-A2.
PD   16-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 4;   Length 41;
Best Local Similarity  100.0%;   Pred. No. 1.4e+03;
RESULT 1475
ID   ABP80379 standard; protein; 41 AA.
DE   N. gonorrhoeae amino acid sequence SEQ ID 7288.
PN   WO200279243-A2.
PD   10-OCT-2002.
PA   (CHIR-) CHIRON SPA.
Query Match             6.5%;    Score 5;   DB 6;   Length 41;
Best Local Similarity  100.0%;   Pred. No. 1.4e+03;
RESULT 1476
ID   AAW27841 standard; protein; 42 AA.
DE   Staphylococcus aureus protein of unknown function.
PN   WO9730070-A1.
PD   21-AUG-1997.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
Query Match             6.5%;    Score 5;   DB 2;   Length 42;
Best Local Similarity  100.0%;   Pred. No. 1.4e+03;
RESULT 1477
ID   AAY19539 standard; protein; 42 AA.
DE   Amino acid sequence of a human secreted protein.
PN   WO992243-A1.
PD   06-MAY-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             6.5%;    Score 5;   DB 2;   Length 42;
Best Local Similarity  100.0%;   Pred. No. 1.4e+03;
RESULT 1478
ID   AAM17255 standard; protein; 42 AA.
DE   Peptide #3689 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match             6.5%;    Score 5;   DB 4;   Length 42;
Best Local Similarity  100.0%;   Pred. No. 1.4e+03;
RESULT 1479
ID   ABB36254 standard; peptide; 42 AA.
DE   Peptide #3760 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match             6.5%;    Score 5;   DB 4;   Length 42;
Best Local Similarity  100.0%;   Pred. No. 1.4e+03;
RESULT 1480
ID   AAM29750 standard; protein; 42 AA.
DE   Peptide #3787 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match             6.5%;    Score 5;   DB 4;   Length 42;
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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1481
ID ABB31065 standard; peptide; 42 AA.
DE Peptide #3716 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1482
ID AAM69421 standard; protein; 42 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29727.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1483
ID AAM57029 standard; protein; 42 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29134.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1484
ID ABG51093 standard; peptide; 42 AA.
DE Human liver peptide, SEQ ID No 29741.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 42;
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RESULT 1485
ID AAM04946 standard; protein; 42 AA.
DE Peptide #3628 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1486
ID ABG39039 standard; peptide; 42 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28704.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 5; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1487
ID ABR91588 standard; peptide; 42 AA.
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:422.
PN WO200210232-4-A2.
PD 27-DEC-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
    Query Match   6.5%;   Score 5; DB 6; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1488
ID ADN04586 standard; protein; 42 AA.
DE Antipsoriatic protein sequence #482.
PN WO200210232-4-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
    Query Match   6.5%;   Score 5; DB 8; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1489
ID ADO19898 standard; protein; 42 AA.
DE Human PRO polypeptide #409.
PN WO200404361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
    Query Match   6.5%;   Score 5; DB 8; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;

RESULT 1490
ID ADP55022 standard; protein; 42 AA.
DE Human PRO protein sequence SEQ ID NO:998.
PN WO200403956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
    Query Match   6.5%;   Score 5; DB 8; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1491
ID ADP24559 standard; protein; 42 AA.
DE PRO polypeptide SEQ ID NO:1737.
PN WO200404170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
    Query Match   6.5%;   Score 5; DB 8; Length 42;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1492
ID AAR28988 standard; protein; 43 AA.
DE Thyroid N-acetyl-glucosamine receptor fragment TGR-CL11.
PN WO9219733-A1.
PD 12-NOV-1992.
PA (CNRS) CENT NAT RECH SCI.
    Query Match   6.5%;   Score 5; DB 2; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1493
ID AAW86581 standard; protein; 43 AA.
DE Secreted protein encoded by gene 48 clone HCNAP62.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   6.5%;   Score 5; DB 2; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1494
ID AAM16809 standard; protein; 43 AA.
DE Peptide #3243 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1495
ID ABB50048 standard; protein; 43 AA.
DE Human secreted protein encoded by gene 48 SEQ ID NO:296.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   6.5%;   Score 5; DB 4; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1496
ID ABB35792 standard; peptide; 43 AA.
DE Peptide #1298 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1497
ID AAM29291 standard; protein; 43 AA.
DE Peptide #3328 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
    Query Match   6.5%;   Score 5; DB 4; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1498
ID ABB11187 standard; peptide; 43 AA.
DE Human pheromone receptor V1RL1 homologue, SEQ ID NO:1557.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSB-) HYSEQ INC.
    Query Match   6.5%;   Score 5; DB 4; Length 43;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1499

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ID    ABB30627 standard; peptide; 43 AA.
DE    Peptide #3278 encoded by breast cell single exon nucleic acid probe.
PN    WO200157271-A2.
PD    09-AUG-2001.
PA    (MOLE-) MOLECULAR DYNAMICS INC.
Query Match             6.5%;  Score 5;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
RESULT 1500
ID    ABB21214 standard; protein; 43 AA.
DE    Protein #3213 encoded by probe for measuring heart cell gene expression.
PN    WO200157274-A2.
PD    09-AUG-2001.
PA    (MOLE-) MOLECULAR DYNAMICS INC.
Query Match             6.5%;  Score 5;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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OM protein - protein search, using sw model


Run on:     April 7, 2005, 04:04:42 ; Search time 41 Seconds
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Title:      US-10-063-563-56
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Searched:   513545 seqs, 74649064 residues

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Post-processing: Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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3	9.1	7	168	4	US-09-270-767-48214	Sequence 48214, A
4	9.1	7	172	4	US-09-270-767-36922	Sequence 36922, A
5	9.1	7	172	4	US-09-270-767-52139	Sequence 52139, A
6	9.1	7	199	4	US-09-489-039A-10661	Sequence 10661, A
7	9.1	7	220	4	US-09-198-452A-461	Sequence 461, App
8	9.1	7	220	4	US-09-438-185A-442	Sequence 442, App
9	7.8	6	27	3	US-08-470-953A-9	Sequence 9, Appli
10	7.8	6	42	4	US-09-270-767-56935	Sequence 56935, A
11	7.8	6	74	4	US-09-270-767-34586	Sequence 34586, A
12	7.8	6	74	4	US-09-270-767-49803	Sequence 49803, A
13	7.8	6	78	4	US-09-248-796A-24206	Sequence 24206, A
14	7.8	6	78	4	US-09-248-796A-26253	Sequence 26253, A
15	7.8	6	91	4	US-09-270-767-41301	Sequence 41301, A
16	7.8	6	91	4	US-09-270-767-56517	Sequence 56517, A
17	7.8	6	96	4	US-09-107-433-4292	Sequence 4292, Ap
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22	7.8	6	124	1	US-08-023-764B-28	Sequence 10, Appl
23	7.8	6	124	3	US-08-904-871-10	Sequence 20, Appl
24	7.8	6	125	1	US-08-225-989-20	Sequence 20, Appl
25	7.8	6	125	1	US-08-570-923-20	Sequence 20, Appl
26	7.8	6	125	1	US-08-580-014-20	Sequence 20, Appl
27	7.8	6	125	3	US-09-079-785-20	Sequence 20, Appl
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34	7.8	6	167	4	US-09-205-258-867	Sequence 867, App
35	7.8	6	171	4	US-09-252-991A-20773	Sequence 20773, A
36	7.8	6	184	4	US-09-902-540-12024	Sequence 12024, A
37	7.8	6	185	4	US-09-328-352-5973	Sequence 5973, Ap
38	7.8	6	196	4	US-09-270-767-38699	Sequence 38699, A
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46	7.8	6	231	4	US-09-248-796A-18348	Sequence 18348, A
47	7.8	6	234	4	US-09-328-352-4885	Sequence 4885, Ap
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56	7.8	6	248	3	US-09-933-999A-7	Sequence 7, Appli
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61	7.8	6	275	4	US-09-489-039A-12987	Sequence 12987, A
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63	7.8	6	276	4	US-09-543-681A-4770	Sequence 4770, Ap
64	7.8	6	290	4	US-09-543-681A-7149	Sequence 7149, Ap
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67	7.8	6	301	4	US-09-489-039A-9236	Sequence 9236, Ap
68	7.8	6	301	4	US-09-248-796A-18346	Sequence 18346, A
69	7.8	6	311	4	US-09-107-433-3296	Sequence 3296, Ap
70	7.8	6	318	4	US-09-489-039A-12748	Sequence 12748, A
71	7.8	6	318	4	US-09-248-796A-20731	Sequence 20731, A
72	7.8	6	319	4	US-09-252-991A-30973	Sequence 30973, A
73	7.8	6	326	4	US-09-270-767-36225	Sequence 36225, A
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76	7.8	6	357	4	US-09-248-796A-14157	Sequence 14157, A
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79	7.8	6	369	4	US-09-535-909-8	Sequence 8, Appli
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84	7.8	6	399	4	US-09-902-540-10970	Sequence 10970, A
85	7.8	6	402	4	US-09-328-352-6411	Sequence 6411, Ap
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87	7.8	6	402	4	US-09-248-796A-18347	Sequence 18347, A
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92	7.8	6	488	4	US-09-489-039A-9445	Sequence 9445, Ap
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95	7.8	6	576	4	US-09-535-909-4	Sequence 4, Appli
96	7.8	6	598	4	US-09-489-039A-13363	Sequence 13363, A
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99	7.8	6		2	US-08-742-923A-2	Sequence 2, Appli
100	7.8	6		4	US-09-540-236-3415	Sequence 3415, Ap

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103	6	7.8	643	4	US-09-198-452A-474	Sequence 474, App
104	6	7.8	712	1	US-08-121-713D-64	Sequence 64, Appl
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106	6	7.8	712	2	US-09-060-692-64	Sequence 64, Appl
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117	6	7.8	1144	3	US-08-726-214-6	Sequence 6, Appli
118	6	7.8	1144	4	US-09-949-016-6446	Sequence 6446, Ap
119	6	7.8	1149	4	US-09-949-016-7682	Sequence 7682, Ap
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121	6	7.8	1165	2	US-08-735-893-2	Sequence 2, Appli
122	6	7.8	1170	4	US-09-561-709B-12	Sequence 12, Appl
123	6	7.8	1170	4	US-09-560-385A-14	Sequence 14, Appl
124	6	7.8	1172	4	US-09-919-172-16	Sequence 16, Appl
125	6	7.8	1286	4	US-09-170-496D-291	Sequence 291, App
126	6	7.8	1286	4	US-09-364-425B-56	Sequence 56, Appl
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130	6	7.8	1437	4	US-09-647-140B-4	Sequence 4, Appli
131	6	7.8	1453	2	US-09-001-273-2	Sequence 2, Appli
132	6	7.8	1453	3	US-08-843-459A-2	Sequence 2, Appli
133	6	7.8	1666	4	US-09-902-540-15792	Sequence 15792, A
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135	6	7.8	1765	4	US-09-354-147C-5	Sequence 5, Appli
136	6	7.8	1857	4	US-09-917-254-91	Sequence 91, Appl
137	6	7.8	1911	4	US-09-854-856-64	Sequence 64, Appl
138	6	7.8	1939	4	US-09-854-856-48	Sequence 48, Appl
139	6	7.8	1971	4	US-09-854-856-32	Sequence 32, Appl
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162	6	7.8	2185	4	US-09-854-856-36	Sequence 36, Appl
163	6	7.8	2201	4	US-09-854-856-24	Sequence 24, Appl
164	6	7.8	2217	4	US-09-854-856-20	Sequence 20, Appl
165	6	7.8	2229	4	US-09-854-856-8	Sequence 8, Appli
166	6	7.8	2245	4	US-09-854-856-4	Sequence 4, Appli
167	6	7.8	2294	5	US-09-854-856-50	Sequence 50, Appl
168	6	7.8	2322	4	US-09-854-856-34	Sequence 34, Appl
169	6	7.8	2354	4	US-09-854-856-18	Sequence 18, Appl
170	6	7.8	2382	4	US-09-854-856-2	Sequence 2, Appli
171	5	6.5	8	1	US-08-214-650-13	Sequence 13, Appl
172	5	6.5	12	4	US-09-082-358B-26	Sequence 26, Appl
173	5	6.5	12	6	5489533-15	Patent No. 5489533

No.					Reference	Label
174	5	6.5	12	6	5512660-15	Patent No. 5512660
175	5	6.5	12	6	5489533-15	Patent No. 5489533
176	5	6.5	12	6	5512660-15	Patent No. 5512660
177	5	6.5	14	1	US-08-232-453A-67	Sequence 67, Appl
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179	5	6.5	17	3	US-09-604-864-2	Sequence 2, Appli
180	5	6.5	17	4	US-10-042-872-1	Sequence 1, Appli
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182	5	6.5	18	3	US-08-612-973-64	Sequence 64, Appl
183	5	6.5	20	3	US-08-927-597-64	Sequence 64, Appl
184	5	6.5	20	3	US-08-635-886C-22	Sequence 22, Appl
185	5	6.5	20	4	US-08-974-690C-22	Sequence 22, Appl
186	5	6.5	21	4	US-08-974-685-22	Sequence 22, Appl
187	5	6.5	23	4	US-09-205-258-269	Sequence 269, App
188	5	6.5	24	3	US-08-847-844A-48	Sequence 48, Appl
189	5	6.5	24	3	US-08-270-767-57029	Sequence 57029, A
190	5	6.5	25	3	US-08-847-844A-6	Sequence 6, Appli
191	5	6.5	27	4	US-09-902-540-15676	Sequence 15676, A
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ALIGNMENTS

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; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT: Gary Breton et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE: 2000-01-27
;  PRIOR APPLICATION NUMBER: US 60/117,747
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 14342
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US-09-489-039A-10091

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;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: Patentin Ver. 2.0
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
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; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-36922

Query Match   9.1%; Score 7; DB 4; Length 172;
Best Local Similarity   100.0%; Pred. No. 14;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   40 GLALIFC 46
           |||||||
Db   47 GLALIFC 53

RESULT 5
US-09-270-767-52139
; Sequence 52139, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52139
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52139

Query Match   9.1%; Score 7; DB 4; Length 172;
Best Local Similarity   100.0%; Pred. No. 14;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   40 GLALIFC 46
           |||||||
Db   47 GLALIFC 53

RESULT 6
US-09-489-039A-10661
; Sequence 10661, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10661
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10661

Query Match   9.1%; Score 7; DB 4; Length 199;
Best Local Similarity   100.0%; Pred. No. 17;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   47 ILQSlAL 53
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Db   16 ILQSlAL 22

RESULT 7
US-09-198-452A-461
; Sequence 461, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 461
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-461

Query Match   9.1%; Score 7; DB 4; Length 220;
Best Local Similarity   100.0%; Pred. No. 18;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 LCFAlTL 30
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Db   62 LCFAlTL 68

RESULT 8
US-09-438-185A-442
; Sequence 442, Application US/09438185A

; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-953A-9

Query Match 7.8%; Score 6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CFALTL 30
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Db 15 CFALTL 20

RESULT 10
US-09-270-767-56935
; Sequence 56935, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56935
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56935

Query Match 7.8%; Score 6; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 PFARDA 67
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Db 8 PFARDA 13

RESULT 11
US-09-270-767-34586
; Sequence 34586, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34586
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-34586

Query Match 7.8%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 RDAVKK 70
  |||||
Db 10 RDAVKK 15

RESULT 12

; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-0004111US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 442
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0440
US-09-438-185A-442

Query Match 9.1%; Score 7; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LCFALTL 30
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Db 62 LCFALTL 68

RESULT 9
US-08-470-953A-9
; Sequence 9, Application US/08470953A
; Patent No. 6346407
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUYL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,953A
; FILING DATE: 6-OCTOBER-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhlem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850

US-09-270-767-49803
; Sequence 49803, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49803
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49803

Query Match   7.8%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 72;
Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   65 RDAVKK 70
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Db   10 RDAVKK 15

RESULT 13
US-09-248-796A-24206
; Sequence 24206, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24206
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24206

Query Match   7.8%; Score 6; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 75;
Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   45 FCILQS 50
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Db   52 FCILQS 57

RESULT 14
US-09-248-796A-26253
; Sequence 26253, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 26253
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26253

Query Match   7.8%; Score 6; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 75;
Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   44 IFCILQ 49
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Db   57 IFCILQ 62

RESULT 15
US-09-270-767-41301
; Sequence 41301, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41301
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41301

Query Match   7.8%; Score 6; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 87;
Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   23 LLCFAL 28
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Db   68 LLCFAL 73

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          Copyright (c) 1993 - 2005 Compugen Ltd.

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
27	77	100.0	77	10	US-09-997-428-283	Sequence 283, App
562	77	100.0	77	14	US-10-174-587-214	Sequence 214, App
626	77	100.0	77	14	US-10-063-742-56	Sequence 56, Appl
741	77	100.0	77	17	US-10-972-317-56	Sequence 56, Appl
742	77	100.0	160	9	US-09-799-777-22	Sequence 22, Appl
743	77	100.0	170	15	US-10-276-774-2357	Sequence 2357, Ap
744	69	89.6	160	11	US-09-978-360A-561	Sequence 561, App
745	8	10.4	65	15	US-10-424-599-156694	Sequence 156694,
746	8	10.4	124	15	US-10-264-237-2023	Sequence 2023, Ap
747	8	10.4	159	9	US-09-731-872-419	Sequence 419, App
748	8	10.4	159	10	US-09-876-997-419	Sequence 419, Appl
749	8	10.4	178	16	US-10-755-889-34	Sequence 34, Appl
750	8	10.4	412	15	US-10-282-122A-73517	Sequence 73517, A
751	8	10.4	436	15	US-10-282-122A-60321	Sequence 60321, A
752	8	10.4	438	15	US-10-282-122A-43328	Sequence 43328, A
753	8	10.4	438	15	US-10-282-122A-76172	Sequence 76172, A
754	8	10.4	830	16	US-10-437-963-198121	Sequence 198121,
755	8	10.4	840	16	US-10-437-963-198124	Sequence 198124,
756	7	9.1	94	16	US-10-767-701-55829	Sequence 55829, A
757	7	9.1	126	15	US-10-424-599-238797	Sequence 238797,
758	7	9.1	197	16	US-10-767-701-35099	Sequence 35099, A
759	7	9.1	212	15	US-10-312-273-357	Sequence 357, App
760	7	9.1	220	15	US-10-289-762-461	Sequence 461, App
761	7	9.1	243	15	US-10-425-114-57246	Sequence 57246, A
762	7	9.1	304	15	US-10-282-122A-71016	Sequence 71016, A
763	7	9.1	314	9	US-09-886-055-263	Sequence 263, App
764	7	9.1	314	10	US-09-804-291-263	Sequence 263, App
765	7	9.1	314	14	US-10-044-643-60	Sequence 60, Appl
766	7	9.1	314	15	US-10-024-212-44	Sequence 44, Appl
767	7	9.1	314	15	US-10-343-650A-184	Sequence 184, App
768	7	9.1	337	15	US-10-424-599-175299	Sequence 175299,
769	7	9.1	448	15	US-10-369-493-500	Sequence 500, App
770	7	9.1	449	15	US-10-369-493-21220	Sequence 21220, A
771	7	9.1	626	16	US-10-437-963-142127	Sequence 142127,
772	7	9.1	891	15	US-10-369-493-10030	Sequence 10030, A
773	7	9.1	1053	15	US-10-369-493-12547	Sequence 12547, A
774	7	9.1	1215	15	US-10-282-122A-69475	Sequence 69475, A
775	7	9.1	3583	16	US-10-437-963-125761	Sequence 125761,
776	6	7.8	11	14	US-10-223-277-37	Sequence 37, Appl
777	6	7.8	15	14	US-10-084-813-1125	Sequence 1125, Ap
778	6	7.8	15	14	US-10-084-813-1142	Sequence 1142, Ap
779	6	7.8	27	9	US-09-909-207-9	Sequence 9, Appli
780	6	7.8	35	15	US-10-424-599-270755	Sequence 270755,
781	6	7.8	45	15	US-10-424-599-147101	Sequence 147101,
782	6	7.8	47	15	US-10-424-599-257077	Sequence 257077,
783	6	7.8	49	15	US-10-424-599-183292	Sequence 183292,
784	6	7.8	52	15	US-10-424-599-149527	Sequence 149527,
785	6	7.8	54	15	US-10-424-599-179097	Sequence 179097,
786	6	7.8	55	15	US-10-424-599-202813	Sequence 202813,
787	6	7.8	55	9	US-09-764-86-1105	Sequence 1105, Ap
788	6	7.8	56	14	US-10-091-504-1105	Sequence 1105, Ap
789	6	7.8	56	15	US-10-227-577-1105	Sequence 1105, Ap
790	6	7.8	62	9	US-09-864-761-40363	Sequence 40363, A
791	6	7.8	66	15	US-10-182-243-54	Sequence 54, Appl
792	6	7.8	70	15	US-10-424-599-179650	Sequence 179650,
793	6	7.8	77	16	US-10-437-963-121827	Sequence 121827,
794	6	7.8	77	16	US-10-437-963-185844	Sequence 185844,
795	6	7.8	78	17	US-10-778-935-6	Sequence 6, Appli
796	6	7.8	79	16	US-10-437-963-137480	Sequence 137480,
797	6	7.8	81	15	US-10-424-599-282526	Sequence 282526,
798	6	7.8	83	15	US-10-276-774-2587	Sequence 2587, Ap
799	6	7.8	85	15	US-10-425-114-54568	Sequence 54568, A
800	6	7.8	85	16	US-10-437-963-131570	Sequence 131570,
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803	6	7.8	89	9	US-09-864-761-49044	Sequence 49044, A
804	6	7.8	89	16	US-10-437-963-151671	Sequence 151671,
805	6	7.8	89	16	US-10-437-963-164607	Sequence 164607,
806	6	7.8	94	15	US-10-424-599-192913	Sequence 192913,
807	6	7.8	94	16	US-10-767-701-33292	Sequence 33292, A
808	6	7.8	95	15	US-10-276-774-1947	Sequence 1947, Ap
809	6	7.8	96	10	US-09-764-891-4819	Sequence 4819, Ap
810	6	7.8	96	14	US-10-091-572-374	Sequence 374, App
811	6	7.8	98	14	US-10-011-585A-176	Sequence 176, App
812	6	7.8	100	15	US-10-424-599-198486	Sequence 198486,
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814	6	7.8	105	15	US-10-424-599-148164	Sequence 148164,
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816	6	7.8	107	15	US-10-424-599-263810	Sequence 263810,
817	6	7.8	113	15	US-10-424-599-184966	Sequence 184966,
818	6	7.8	118	15	US-10-425-114-49227	Sequence 49227, A
819	6	7.8	124	15	US-10-144-194A-18	Sequence 18, Appl
820	6	7.8	124	16	US-10-787-958-20	Sequence 20, Appl
821	6	7.8	124	15	US-10-494-940-4	Sequence 4, Appli
822	6	7.8	126	17	US-10-276-774-1742	Sequence 1742, Ap
823	6	7.8	128	16	US-10-437-963-149697	Sequence 149697,
824	6	7.8	130	9	US-09-738-626-4192	Sequence 4192, Ap

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825	7.8	6	US-10-424-599-198110	15	Sequence 198110,
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827	7.8	6	US-10-437-963-195835	16	Sequence 195835, A
828	7.8	6	US-10-767-701-52652	16	Sequence 52652, A
829	7.8	6	US-10-094-749-2654	15	Sequence 2654, Ap
830	7.8	6	US-10-156-761-10425	14	Sequence 10425, A
831	7.8	6	US-10-282-122A-54173	15	Sequence 54173, A
832	7.8	6	US-10-017-161-1184	15	Sequence 1184, Ap
833	7.8	6	US-10-292-798-1000	15	Sequence 1000, Ap
834	7.8	6	US-10-767-701-44201	16	Sequence 44201, A
835	7.8	6	US-10-767-701-42143	16	Sequence 42143, A
836	7.8	6	US-09-933-767-867	10	Sequence 867, App
837	7.8	6	US-10-004-860-867	14	Sequence 867, App
838	7.8	6	US-10-023-282-867	15	Sequence 867, App
839	7.8	6	US-10-424-599-247179	15	Sequence 247179, Ap
840	7.8	6	US-10-389-566-1073	15	Sequence 1073, Ap
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1374	5	6.5	48	10	US-09-983-802-241	Sequence 241, App
1375	5	6.5	48	10	US-09-984-490-241	Sequence 241, App
1376	5	6.5	48	11	US-09-833-245-673	Sequence 673, App
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1382	5	6.5	49	15	US-10-767-701-54823	Sequence 54823, A
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1429	15	6.5	5	US-10-424-599-234978	Sequence 234978,
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1437	17	6.5	5	US-10-863-332-236	Sequence 236, App
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1479	9	6.5	5	US-09-764-860-551	Sequence 551, App
1480	14	6.5	5	US-10-073-961-203	Sequence 203, App
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1484	61	15	6.5	5	US-10-424-599-221032	Sequence 221032,
1485	61	15	6.5	5	US-10-424-599-253306	Sequence 253306, A
1486	61	15	6.5	5	US-10-424-599-274007	Sequence 274007,
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1489	62	10	6.5	5	US-09-820-649-346	Sequence 346, App
1490	62	14	6.5	5	US-10-160-162-346	Sequence 346, App
1491	62	15	6.5	5	US-10-424-599-202036	Sequence 202036,
1492	62	15	6.5	5	US-10-424-599-211787	Sequence 211787,
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1498	63	9	6.5	5	US-09-864-761-37449	Sequence 37449, A
1499	63	14	6.5	5	US-10-106-698-7005	Sequence 7005, Ap
1500	63	15	6.5	5	US-10-282-122A-69791	Sequence 69791, A

Search completed: April 7, 2005, 04:46:14
Job time : 156 secs

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                 GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    April 7, 2005, 04:35:01 ; Search time 43 Seconds
                                     (without alignments)
                                     172.295 Million cell updates/sec

Title:          US-10-063-563-56
Perfect score:  77
Sequence:       1 MGPVKQLKRMFBPTRLIATI.........LSFIPPARDAVKKCFAVCLA 77

Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0

Searched:       283416 seqs, 96216763 residues

Word size :     0

Total number of hits satisfying chosen parameters:       283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :  PIR_79:*
         1: pir1:*
         2: pir2:*
         3: pir3:*
         4: pir4:*

   *     Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
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SUMMARIES

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1	10.4	8	438	1	WQECFP	L-fucose permease
2	10.4	8	438	2	AI0862	L-fucose permease
3	10.4	8	438	2	E91086	fucose permease [i
4	10.4	8	438	2	G85931	fucose permease [i
5	9.1	7	183	2	A86643	hypothetical prote
6	9.1	7	197	2	D86856	hypothetical prote
7	9.1	7	198	2	AI0970	probable TetR-fami
8	9.1	7	212	2	D91193	probable transcrip
9	9.1	7	212	2	E86040	probable transcrip
10	9.1	7	212	2	C65165	ttk protein - Esch
11	9.1	7	212	2	F86545	hypothetical prote
12	9.1	7	212	2	F72077	hypothetical prote
13	9.1	7	264	2	G83761	polysaccharide dea
14	9.1	7	455	2	AF0215	probable 4-hydroxy
15	9.1	7	458	2	AF0631	probable 4-hydroxy
16	9.1	7	566	2	T46219	hypothetical prote
17	9.1	7	569	2	S74053	similar to transcr
18	9.1	7	672	2	AG1541	transcription regu
19	9.1	7	672	2	AI1183	spindle assembly c
20	9.1	7	1216	2	T09224	hypothetical prote
21	7.8	6	73	2	T25649	hypothetical prote
22	7.8	6	78	2	D29653	hypothetical prote
23	7.8	6	121	2	AH2497	stage 0 sporulatio
24	7.8	6	124	1	SZBS0F	conserved hypothet
25	7.8	6	126	2	AB2905	botrocetin alpha c
26	7.8	6	133	2	A47267	hypothetical prote
27	7.8	6	133	2	D97680	16 kD heat shock p
28	7.8	6	157	2	E84997	hypothetical prote
29	7.8	6	160	2	E83295	hypothetical prote
30	7.8	6	174	2	A64442	hypothetical prote
31	7.8	6	174	2	C83943	hypothetical prote
32	7.8	6	177	2	B64505	hypothetical prote
33	7.8	6	182	2	AC0749	CDPdiacylglycerol-
34	7.8	6	183	2	D70339	conserved hypothet
35	7.8	6	195	2	D88086	protein T11F1.7 [i
36	7.8	6	197	2	T09257	late embryonic abu
37	7.8	6	208	2	B69066	conserved hypothet
38	7.8	6	209	1	F71612	glycosyl transfera
39	7.8	6	220	2	S63051	hypothetical prote
40	7.8	6	234	2	A40710	CD30 ligand - huma
41	7.8	6	240	2	T22850	hypothetical prote
42	7.8	6	241	2	G89925	menaquinone biosyn
43	7.8	6	243	2	AB1191	B. subtilis YhfI p
44	7.8	6	243	2	AB1549	conserved hypothet
45	7.8	6	246	1	NDPS7A	type II site-speci
46	7.8	6	246	2	AG2988	competence protein
47	7.8	6	247	2	AD0757	cobalamin (5'-phos
48	7.8	6	247	2	C90977	cobalamin 5'-phosp
49	7.8	6	247	2	A85824	cobalamin 5'-phosp
50	7.8	6	247	2	G64963	cobalamin (5'-phos
51	7.8	6	253	1	G69109	conserved hypothet
52	7.8	6	257	2	F89783	hypothetical prote
53	7.8	6	259	2	T43102	hypothetical prote
54	7.8	6	261	1	OTCA3	cytochrome-c oxida
55	7.8	6	267	2	A87404	ribosomal protein
56	7.8	6	269	2	H71613	probable multiple
57	7.8	6	270	2	S62760	cytochrome-c oxida
58	7.8	6	273	2	C85966	hypothetical prote
59	7.8	6	273	2	AD0892	bacitracin resista
60	7.8	6	273	2	G65093	bacitracin resista
61	7.8	6	273	2	D91121	bacitracin resista
62	7.8	6	277	2	AF3216	ABC transporter, m
63	7.8	6	285	2	AD3175	hypothetical prote
64	7.8	6	286	2	AG0403	anaerobic dimethyl
65	7.8	6	290	2	T39335	probable SURF-fami
66	7.8	6	291	2	JQ0060	hypothetical 32.7K
67	7.8	6	291	2	A99295	competence protein
68	7.8	6	293	2	S58704	probable membrane
69	7.8	6	296	2	S60637	NADH2 dehydrogenas
70	7.8	6	296	2	I52860	smooth muscle myos
71	7.8	6	299	2	AB3191	hypothetical prote
72	7.8	6	300	2	D83487	hypothetical prote
73	7.8	6	305	2	JC4920	2-oxoacid-ferredox
74	7.8	6	306	2	H86695	ABC transporter pe
75	7.8	6	309	2	E84672	hypothetical prote
76	7.8	6	315	2	B83676	hypothetical prote
77	7.8	6	326	2	S73620	hypothetical prote
78	7.8	6	328	2	A70145	prolipoprotein dia
79	7.8	6	330	2	I65768	smooth muscle myos
80	7.8	6	331	2	AF1324	opine catabolism p
81	7.8	6	331	1	AH1695	opine catabolism p
82	7.8	6	332	1	QRECD1	iron(III) dicitrat
83	7.8	6	335	2	AI3063	hypothetical prote
84	7.8	6	335	2	G98222	hypothetical prote
85	7.8	6	340	2	A36988	replication factor
86	7.8	6	345	2	T14053	NADH2 dehydrogenas
87	7.8	6	345	2	T24659	hypothetical prote
88	7.8	6	345	2	T34998	probable transmemb
89	7.8	6	345	2	AB1448	gp18 (Bacteriophag
90	7.8	6	346	2	S22442	probable 3',5'-cyc
91	7.8	6	349	2	D72292	hypothetical prote
92	7.8	6	350	2	S70672	dehydrogenase homo
93	7.8	6	351	2	T04027	hypothetical prote
94	7.8	6	354	2	AF3614	replication factor
95	7.8	6	357	2	S35318	NADH2 dehydrogenas
96	7.8	6	359	2	I50712	probable undecapre
97	7.8	6	365	2	G72306	hypothetical prote
98	7.8	6	378	2	AF1834	MET22 protein - ye
99	7.8	6	381	2	G83050	TOP AP - chicken
100	7.8	6	382	2	T48109	conserved hypothet
101	7.8	6	382	2	D86720	citrate synthase [
102	7.8	6	389	2	F86268	L-lactate dehydrog

#			Accession			Description
103	7.8	6	T14412	2	389	ethanolaminephosph
104	7.8	6	D69312	2	395	molybdopterin oxid
105	7.8	6	S53391	2	398	probable membrane
106	7.8	6	T00754	2	400	probable integral
107	7.8	6	S06745	2	402	plasminogen activa
108	7.8	6	S74951	1	410	Na+/H+-exchanging
109	7.8	6	S07537	2	412	myosin heavy chain
110	7.8	6	C36144	2	434	cobyrinic acid a,c
111	7.8	6	T24952	2	434	hypothetical prote
112	7.8	6	A32670	2	438	fibrinogen gamma c
113	7.8	6	G84069	2	440	hypothetical prote
114	7.8	6	C69545	2	440	conserved hypothet
115	7.8	6	B98052	2	447	conserved hypothet
116	7.8	6	B70903	2	449	probable oxidoredu
117	7.8	6	A46104	2	450	nucleoprotein N -
118	7.8	6	T28094	2	452	hypothetical prote
119	7.8	6	F86846	2	453	ABC transporter pe
120	7.8	6	D86793	2	454	drug-export protei
121	7.8	6	T33723	2	462	pyruvate dehydroge
122	7.8	6	S17656	1	469	Ca2+/calmodulin-de
123	7.8	6	B86221	2	474	hypothetical prote
124	7.8	6	AC3395	2	478	NADH2 dehydrogenas
125	7.8	6	AC2734	2	480	NADH ubiquinone ox
126	7.8	6	A83497	2	480	probable MFS trans
127	7.8	6	D87489	2	481	NADH dehydrogenase
128	7.8	6	E97515	2	482	NADH-ubiquinone ox
129	7.8	6	S28429	2	482	alanine transamina
130	7.8	6	T41527	2	484	probable trna nucl
131	7.8	6	B33501	2	484	myosin heavy chain
132	7.8	6	S52814	2	486	citrate (si)-synth
133	7.8	6	T52132	2	496	probable sugar tra
134	7.8	6	A47751	2	499	NADH2 dehydrogenas
135	7.8	6	T12894	2	504	probable replicati
136	7.8	6	AG2297	2	514	cobyrinic acid a,c
137	7.8	6	H87274	2	524	conserved hypothet
138	7.8	6	JC4533	2	526	cytochrome P450 4F
139	7.8	6	T43919	2	528	yfuB protein [impo
140	7.8	6	T23419	2	535	hypothetical prote
141	7.8	6	D83109	2	538	probable chemotaxi
142	7.8	6	B71502	2	542	probable apolipopr
143	7.8	6	C88456	2	547	protein W03A5.2 [i
144	7.8	6	T50295	2	549	probable vacuolar
145	7.8	6	C87259	2	552	lysyl-tRNA synthet
146	7.8	6	T05545	2	561	pollen-specific pr
147	7.8	6	A53651	1	573	sulfate adenylyltr
148	7.8	6	A95902	2	577	prbbable glycerol-
149	7.8	6	S74819	2	582	extracellular solu
150	7.8	6	S43718	2	585	malate dehydrogena
151	7.8	6	S18826	1	589	malate dehydrogena
152	7.8	6	S77267	2	590	secreted protein M
153	7.8	6	JC5967	2	592	malate dehydrogena
154	7.8	6	F98150	2	594	probable gamma-glu
155	7.8	6	AF3137	2	594	gamma-glutamyltran
156	7.8	6	T49877	2	595	phosphoenolpyruvat
157	7.8	6	C90426	2	603	myosin heavy chain
158	7.8	6	S10450	2	621	probable lysophosp
159	7.8	6	T38006	2	624	flagellar hook-ass
160	7.8	6	B82108	2	624	major facilitator
161	7.8	6	T38110	1	630	hypothetical prote
162	7.8	6	T05103	2	631	malate dehydrogena
163	7.8	6	DEZMMX	1	636	NADP-dependent mal
164	7.8	6	S46499	2	638	ABC transport syst
165	7.8	6	H81361	2	643	probable malate ox
166	7.8	6	E96828	2	646	malate dehydrogena
167	7.8	6	S42939	2	647	malate dehydrogena
168	7.8	6	S12893	2	648	probable dna-bindi
169	7.8	6	T41580	2	660	probable lysophosp
170	7.8	6	T50281	2	673	serine/threonine k
171	7.8	6	AF2277	2	707	semaphorin I precu
172	7.8	6	A49423	2	711	hypothetical prote
173	7.8	6	T14080	2	714	TonB-dependent rec
174	7.8	6	F87469	2	732	probable sexual cy
175	7.8	6	T43648	2	746	probable sexual cy

Description	Accession					#
beta-glucosidase (	AD0778	2	765	7.8	6	176
beta-D-glucoside g	C91006	2	765	7.8	6	177
beta-glucosidase (	C64981	2	765	7.8	6	178
beta-D-glucoside g	D85850	2	765	7.8	6	179
icmO protein - Leg	T18329	2	783	7.8	6	180
probable DNA ligas	H71300	2	823	7.8	6	181
probable integral	B81282	2	823	7.8	6	182
ATP-dependent RNA	B75073	2	872	7.8	6	183
glutamyl aminopept	T05189	2	873	7.8	6	184
aconitate hydratas	A44153	1	889	7.8	6	185
aconitate hydratas	A44154	2	889	7.8	6	186
aconitate hydratas	S26403	2	889	7.8	6	187
aconitate hydratas	S18720	2	889	7.8	6	188
polymorphic outer	G86546	2	928	7.8	6	189
polymorphic membra	G81591	2	928	7.8	6	190
excinuclease ABC c	D71645	2	953	7.8	6	191
hypothetical prote	H97454	2	971	7.8	6	192
conserved hypothet	AB2673	2	971	7.8	6	193
probable membrane	S57385	2	991	7.8	6	194
hypothetical prote	C84145	2	995	7.8	6	195
hypothetical prote	C75506	2	1070	7.8	6	196
hypothetical prote	T50364	2	1098	7.8	6	197
hypothetical prote	B86423	2	1114	7.8	6	198
adenylate cyclase	A39833	2	1144	7.8	6	199
laminin B1k chain	A53612	2	1170	7.8	6	200
exopolygalacturona	F83711	2	1376	7.8	6	201
hypothetical prote	T20181	2	1449	7.8	6	202
hypothetical prote	T48162	2	1467	7.8	6	203
glutathione-conjug	F84919	2	1516	7.8	6	204
hypothetical prote	T20180	2	1584	7.8	6	205
hypothetical prote	T20179	2	1586	7.8	6	206
similar to late em	T02712	2	1805	7.8	6	207
1-phosphatidylinos	T18273	2	1858	7.8	6	208
smooth muscle myos	JC5421	2	1938	7.8	6	209
smooth muscle myos	A41604	2	1972	7.8	6	210
myosin heavy chain	JC5420	2	1972	7.8	6	211
hypothetical prote	H89960	2	2186	7.8	6	212
translation activa	A48126	2	2672	7.8	6	213
dna-directed RNA p	B71846	2	2890	7.8	6	214
DNA-directed RNA p	F64669	2	2890	7.8	6	215
coat protein C cha	Z7BPF1	1	33	6.5	5	216
coat protein C cha	Z7BPFD	1	33	6.5	5	217
coat protein C cha	Z7BPM3	1	33	6.5	5	218
hypothetical prote	C83780	2	37	6.5	5	219
hypothetical prote	F90439	2	40	6.5	5	220
RNA recognition mo	B47752	2	41	6.5	5	221
H+-transporting tw	S65035	2	48	6.5	5	222
cytochrome-c oxida	S77986	2	49	6.5	5	223
hypothetical prote	T07304	2	49	6.5	5	224
sex-specific prote	A37354	2	52	6.5	5	225
hypothetical prote	G97773	2	53	6.5	5	226
degenerate transpo	C97923	2	53	6.5	5	227
19K truncated Hind	WZVZC1	4	54	6.5	5	228
ATP synthase F0 ch	E90624	2	55	6.5	5	229
hypothetical prote	D90972	2	55	6.5	5	230
unknown protein en	A85820	2	56	6.5	5	231
NADH2 dehydrogenas	S01277	2	56	6.5	5	232
hypothetical prote	G95052	2	57	6.5	5	233
hypothetical prote	C84255	2	61	6.5	5	234
hypothetical prote	A99931	2	62	6.5	5	235
ycf9 protein - Chl	T08028	2	62	6.5	5	236
hypothetical prote	AD0926	2	62	6.5	5	237
hypothetical prote	B89853	2	62	6.5	5	238
hypothetical prote	C86675	2	63	6.5	5	239
hypothetical prote	T07218	2	64	6.5	5	240
hypothetical prote	C81120	2	65	6.5	5	241
hypothetical prote	T11987	2	65	6.5	5	242
hypothetical prote	T28212	2	65	6.5	5	243
hypothetical prote	F90057	2	67	6.5	5	244
pepI protein - Sta	S58357	2	69	6.5	5	245
hypothetical prote	B69223	2	70	6.5	5	246
hypothetical prote	B83730	2	71	6.5	5	247
hypothetical prote	T46623	2	72	6.5	5	248

Left table:

Index	Col A	Col B	Accession	Count	Num	Description
249	6.5	5	B82615	2	72	hypothetical prote
250	6.5	5	T49902	2	73	hypothetical prote
251	6.5	5	E81284	2	74	hypothetical prote
252	6.5	5	H81320	2	75	small hydrophobic
253	6.5	5	AG2371	2	75	hypothetical prote
254	6.5	5	JC5052	2	77	hypothetical 8.9k
255	6.5	5	B90781	2	77	hypothetical prote
256	6.5	5	S25619	2	78	degenerate transpo
257	6.5	5	A97974	2	78	E5 protein - human
258	6.5	5	W5WL35	1	81	elicitor NIP1 prec
259	6.5	5	S58530	2	82	hypothetical prote
260	6.5	5	H84046	2	82	hypothetical prote
261	6.5	5	B97042	2	83	hypothetical prote
262	6.5	5	F64653	2	84	hypothetical prote
263	6.5	5	T14942	2	84	hypothetical prote
264	6.5	5	T26542	2	85	hypothetical prote
265	6.5	5	S63593	2	86	acyl-coenzyme A-bi
266	6.5	5	S63594	2	86	acyl-coenzyme A-bi
267	6.5	5	C71941	2	86	hypothetical prote
268	6.5	5	D97780	2	86	conserved hypothet
269	6.5	5	AB3223	2	87	flagellar biosynth
270	6.5	5	B70134	2	87	hypothetical prote
271	6.5	5	C81890	2	87	probable integral
272	6.5	5	B97161	2	87	hypothetical prote
273	6.5	5	AF2195	2	87	hipB protein - Esc
274	6.5	5	A38112	2	88	probable membrane
275	6.5	5	C36869	1	89	probable export pr
276	6.5	5	D41886	1	89	flagellar biosynth
277	6.5	5	C84939	2	89	flagellar biosynth
278	6.5	5	AE0753	2	89	flagellar biosynth
279	6.5	5	H85812	2	89	probable export pr
280	6.5	5	H90964	2	89	flagellar biosynth
281	6.5	5	S78699	2	89	probable export pr
282	6.5	5	AI0221	2	89	perC protein - Esc
283	6.5	5	S35277	2	89	hypothetical prote
284	6.5	5	I69150	2	89	cryptogene protein
285	6.5	5	S75103	2	89	hypothetical prote
286	6.5	5	S51911	2	89	antigen 7H8/5 - ma
287	6.5	5	G89941	2	89	probable membrane
288	6.5	5	A60396	2	90	flagellar biosynth
289	6.5	5	H97228	2	90	flagellar biosynth
290	6.5	5	AB1159	2	90	hypothetical prote
291	6.5	5	AB1518	1	90	yop secretion and
292	6.5	5	B35392	2	92	hypothetical prote
293	6.5	5	T43587	2	92	hypothetical prote
294	6.5	5	S15321	2	92	probable trp opero
295	6.5	5	S22369	2	93	conserved hypothet
296	6.5	5	H71549	2	94	hypothetical prote
297	6.5	5	B82311	2	96	probable membrane
298	6.5	5	B90831	2	96	hypothetical prote
299	6.5	5	C87024	2	96	hypothetical prote
300	6.5	5	H84381	2	96	hypothetical prote
301	6.5	5	S66582	2	96	hypothetical prote
302	6.5	5	F70578	2	96	hypothetical prote
303	6.5	5	H69197	2	96	hypothetical prote
304	6.5	5	T26525	2	96	ybcO protein - Esc
305	6.5	5	C64787	2	96	conserved hypothet
306	6.5	5	F83200	2	97	hypothetical prote
307	6.5	5	T16463	2	97	NADH2 dehydrogenas
308	6.5	5	T11188	2	98	NADH2 dehydrogenas
309	6.5	5	T11397	2	98	NADH2 dehydrogenas
310	6.5	5	S12189	2	98	mobS protein - Thi
311	6.5	5	S59145	2	99	NADH2 dehydrogenas
312	6.5	5	T11886	2	99	NADH2 dehydrogenas
313	6.5	5	C90472	2	99	hypothetical prote
314	6.5	5	A84949	2	100	NADH2 dehydrogenas
315	6.5	5	C72592	2	100	hypothetical prote
316	6.5	5	A85525	2	100	hypothetical prote
317	6.5	5	F90674	2	100	hypothetical prote
318	6.5	5	B90355	2	101	hypothetical prote
319	6.5	5	H71178	2	101	hypothetical prote
320	6.5	5	E75487	2	101	v-type ATP synthas
321	6.5	5	S65294	2	102	probable membrane

Right table:

Index	Col A	Col B	Num	Count	Accession	Description
322	6.5	5	102	2	B72111	hypothetical prote
323	6.5	5	102	2	G86510	hypothetical prote
324	6.5	5	102	2	F90585	30S ribosomal prot
325	6.5	5	103	2	A69263	conserved hypothet
326	6.5	5	103	2	JC5351	2-nitrotoluene dio
327	6.5	5	104	2	C90958	probable plasmid p
328	6.5	5	104	2	D85806	probable plasmid p
329	6.5	5	104	2	T29918	hypothetical prote
330	6.5	5	105	2	A90560	hypothetical prote
331	6.5	5	106	2	T16378	hypothetical prote
332	6.5	5	106	2	T47814	hypothetical prote
333	6.5	5	107	2	T44493	conserved hypothet
334	6.5	5	107	2	C72779	hypothetical prote
335	6.5	5	107	2	C97859	hypothetical prote
336	6.5	5	107	4	A60600	hypothetical mutan
337	6.5	5	108	2	C75034	hypothetical prote
338	6.5	5	109	2	S54446	prepilin-like prot
339	6.5	5	109	2	C89759	Conserved hypothet
340	6.5	5	109	2	A71191	hypothetical prote
341	6.5	5	110	2	S04643	glutathione transf
342	6.5	5	110	2	S61257	genome polyprotein
343	6.5	5	110	2	S61254	genome polyprotein
344	6.5	5	110	2	S45883	probable membrane
345	6.5	5	111	2	A90144	hypothetical prote
346	6.5	5	111	2	T00688	hypothetical prote
347	6.5	5	111	2	A81673	conserved hypothet
348	6.5	5	112	2	AE0794	probable membrane
349	6.5	5	112	2	B71211	hypothetical prote
350	6.5	5	112	2	A71515	hypothetical prote
351	6.5	5	112	2	D83730	hypothetical prote
352	6.5	5	113	2	E97208	probable permease
353	6.5	5	113	1	S32873	hypA protein - Rhi
354	6.5	5	113	2	A65047	hypothetical prote
355	6.5	5	113	2	H85914	hypothetical prote
356	6.5	5	113	2	E91070	hypothetical prote
357	6.5	5	113	2	F71053	hypothetical prote
358	6.5	5	113	2	B82927	hypothetical prote
359	6.5	5	113	2	AE0629	cell invasion prot
360	6.5	5	114	2	A72486	hypothetical prote
361	6.5	5	114	2	S69320	probable membrane
362	6.5	5	114	2	D71048	hypothetical prote
363	6.5	5	115	2	T29992	hypothetical prote
364	6.5	5	115	1	JN0318	guanylin precursor
365	6.5	5	115	2	T17090	NADH2 dehydrogenas
366	6.5	5	115	2	AD2280	hypothetical prote
367	6.5	5	115	2	S70185	hypothetical prote
368	6.5	5	115	2	F72569	hypothetical prote
369	6.5	5	116	2	AI0332	probable membrane
370	6.5	5	116	2	H58892	NADH2 dehydrogenas
371	6.5	5	116	2	F81796	hypothetical inner
372	6.5	5	116	2	C70656	hypothetical prote
373	6.5	5	116	2	B85070	hypothetical prote
374	6.5	5	116	2	AE0685	NADH2 dehydrogenas
375	6.5	5	116	2	T05517	abscisic acid-indu
376	6.5	5	117	2	A69828	hypothetical prote
377	6.5	5	117	2	C98240	hypothetical prote
378	6.5	5	118	1	CCDV3N	cytochrome c3, tet
379	6.5	5	118	1	PSSNK3	phospholipase A2 (
380	6.5	5	118	2	H34860	phospholipase A2 (
381	6.5	5	118	2	C89861	Na+/H+ antiporter
382	6.5	5	118	2	D89872	conserved hypothet
383	6.5	5	119	2	G69106	transcription regu
384	6.5	5	119	2	S74006	hypothetical prote
385	6.5	5	120	2	A81157	hypothetical prote
386	6.5	5	120	2	AG3195	conserved hypothet
387	6.5	5	121	2	A71508	hypothetical prote
388	6.5	5	121	2	F71451	hypothetical prote
389	6.5	5	122	2	F75351	hypothetical prote
390	6.5	5	122	2	F72636	hypothetical prote
391	6.5	5	123	2	AG0283	probable exported
392	6.5	5	123	2	T32704	hypothetical prote
393	6.5	5	124	2	D71355	probable ribosomal
394	6.5	5	124	2	B75040	hypothetical prote

No.	pH	Len	Description	Accession	Ct
395	6.5	5	hypothetical prote	A71122	2
396	6.5	5	two component resp	AE2704	2
397	6.5	5	hypothetical prote	E97486	2
398	6.5	5	hypothetical prote	T47297	2
399	6.5	5	hypothetical prote	B71185	2
400	6.5	5	hypothetical prote	AF1264	2
401	6.5	5	hypothetical prote	G84615	2
402	6.5	5	cytochrome P450 pr	B95415	2
403	6.5	5	hypothetical prote	PC2270	2
404	6.5	5	hypothetical prote	T44119	2
405	6.5	5	hypothetical prote	H82725	2
406	6.5	5	ribosomal protein	A41839	2
407	6.5	5	ubiquinol oxidase	F87468	2
408	6.5	5	5-carboxymethyl-2-	AD3526	2
409	6.5	5	ribosomal protein	G75312	2
410	6.5	5	nitrogenase (EC 1.	C32057	1
411	6.5	5	conserved hypothet	G70314	2
412	6.5	5	gene 24 protein -	S30969	2
413	6.5	5	hypothetical prote	AE2025	2
414	6.5	5	conserved hypothet	AI3242	2
415	6.5	5	molybdopterin-guan	AG3379	2
416	6.5	5	bfpG protein - Esc	S70967	2
417	6.5	5	conserved hypothet	AI0999	2
418	6.5	5	conserved hypothet	B90260	2
419	6.5	5	interleukin-5 prec	JC5116	2
420	6.5	5	hypothetical prote	C69949	2
421	6.5	5	gp24 protein - Myc	F72802	2
422	6.5	5	protein F54D5.12 [	E88319	2
423	6.5	5	hypothetical prote	E70251	2
424	6.5	5	conserved hypothet	G69802	2
425	6.5	5	NADH2 dehydrogenas	C82821	2
426	6.5	5	ribosomal protein	S78260	2
427	6.5	5	conserved hypothet	A71271	2
428	6.5	5	hypothetical prote	F64034	2
429	6.5	5	hypothetical prote	E75137	2
430	6.5	5	conserved hypothet	F84677	2
431	6.5	5	conserved hypothet	C75465	2
432	6.5	5	succinate dehydrog	A58930	2
433	6.5	5	nucleoside diphosp	H81452	2
434	6.5	5	chromatin-associat	S37870	1
435	6.5	5	nitrogen regulator	A75487	2
436	6.5	5	conserved hypothet	B70123	2
437	6.5	5	conserved hypothet	C69501	2
438	6.5	5	hypothetical prote	T21176	2
439	6.5	5	F23A5.22 [imported	D96841	2
440	6.5	5	conserved hypothet	C83807	2
441	6.5	5	probable membrane	F87018	2
442	6.5	5	hypothetical prote	C97163	2
443	6.5	5	hypothetical prote	D69464	1
444	6.5	5	probable biopolyme	E75518	2
445	6.5	5	MG395 homolog D02_	S73588	2
446	6.5	5	hypothetical prote	AC1280	2
447	6.5	5	hypothetical prote	AC1643	2
448	6.5	5	hypothetical prote	T19083	2
449	6.5	5	hypothetical prote	A86679	2
450	6.5	5	hypothetical prote	G90762	2
451	6.5	5	hypothetical prote	H85625	2
452	6.5	5	hypothetical prote	G90315	2
453	6.5	5	orf US426 - infect	I48552	2
454	6.5	5	PTS system mannito	S73515	2
455	6.5	5	hypothetical prote	H72616	2
456	6.5	5	succinate dehydrog	S78178	2
457	6.5	5	riboflavin synthas	PC1110	2
458	6.5	5	hypothetical prote	F72556	2
459	6.5	5	oviduct-specific p	S69345	2
460	6.5	5	plastocyanin precu	A36569	2
461	6.5	5	ribosomal protein	T11243	2
462	6.5	5	hypothetical prote	H70022	2
463	6.5	5	Hin-1 protein - hu	S30247	2
464	6.5	5	probable periplasm	F81338	2
465	6.5	5	hypothetical prote	T14667	2
466	6.5	5	hypothetical prote	G70020	2
467	6.5	5	spore protein sp21	S74956	2
468	6.5	5	hypothetical prote	H64017	2
469	6.5	5	phosphotransferase	AG0313	2
470	6.5	5	hypothetical prote	AG3578	2
471	6.5	5	hypothetical prote	F87432	2
472	6.5	5	transcription regu	G87362	2
473	6.5	5	conserved hypothet	B81700	2
474	6.5	5	hypothetical prote	H72781	2
475	6.5	5	hypothetical prote	S76922	2
476	6.5	5	homeotic protein -	S21401	2
477	6.5	5	CT667 hypothetical	B86579	2
478	6.5	5	conserved hypothet	E72046	2
479	6.5	5	hypothetical prote	A83045	2
480	6.5	5	guanine nucleotide	JH0249	2
481	6.5	5	hypothetical prote	C86600	2
482	6.5	5	conserved hypothet	C72024	2
483	6.5	5	hypothetical prote	A97536	2
484	6.5	5	pilB homolog K05 o	S73506	1
485	6.5	5	probable transcrip	D83290	2
486	6.5	5	conserved hypothet	G69014	2
487	6.5	5	hypothetical prote	T42950	2
488	6.5	5	hypothetical prote	T14948	2
489	6.5	5	hypothetical prote	T23449	2
490	6.5	5	conserved hypothet	E95845	2
491	6.5	5	ribosomal protein	S48026	2
492	6.5	5	ribosomal L23a-lik	T47667	2
493	6.5	5	60S ribosomal prot	T00556	2
494	6.5	5	hypothetical prote	T37200	2
495	6.5	5	transactivation pr	WMBPP4	1
496	6.5	5	ribosomal protein	R3TW7	1
497	6.5	5	hypothetical prote	A83718	2
498	6.5	5	hypothetical prote	G82080	2
499	6.5	5	hypothetical prote	AI1910	2
500	6.5	5	hypothetical prote	C71406	2
501	6.5	5	probable AsnC-fami	E81919	2
502	6.5	5	hypothetical prote	B89769	2
503	6.5	5	protein-tyrosine k	A39061	2
504	6.5	5	calcium-binding pr	A29557	2
505	6.5	5	beta-lactoglobulin	LGBUI	1
506	6.5	5	colicin V producti	JC7157	2
507	6.5	5	hypothetical prote	E70195	2
508	6.5	5	hypothetical prote	S17806	2
509	6.5	5	hypothetical prote	AF3388	2
510	6.5	5	NADH2 dehydrogenas	T12408	2
511	6.5	5	30S ribosomal prot	F97897	2
512	6.5	5	ribosomal protein	F95026	2
513	6.5	5	transcription regu	G87301	2
514	6.5	5	hydrogenase-2 comp	AB0885	2
515	6.5	5	conserved hypothet	G83606	2
516	6.5	5	hypothetical prote	H64038	2
517	6.5	5	membrane protein y	B64758	2
518	6.5	5	ribosomal protein	R3BS5F	1
519	6.5	5	gp delta - satelli	JW0031	2
520	6.5	5	hypothetical prote	H96519	2
521	6.5	5	hypothetical prote	B72607	2
522	6.5	5	hypothetical prote	F70478	2
523	6.5	5	conserved hypothet	D87360	2
524	6.5	5	hypothetical prote	D82892	2
525	6.5	5	pleiotrophin precu	A37080	1
526	6.5	5	pleiotrophin precu	B37780	1
527	6.5	5	CDP-diacylglycerol	G81665	2
528	6.5	5	probable glycerol-	F71503	2
529	6.5	5	pleiotrophin - mou	I53001	2
530	6.5	5	prophage ps3 prote	H86866	2
531	6.5	5	hypothetical prote	T01482	2
532	6.5	5	outer membrane pro	A82099	2
533	6.5	5	conserved hypothet	G89869	2
534	6.5	5	hypothetical prote	A33141	2
535	6.5	5	hypothetical prote	T17914	2
536	6.5	5	16S rRNA processin	A82848	2
537	6.5	5	protein F58F6.3 [i	A88638	2
538	6.5	5	hypothetical prote	AI3322	2
539	6.5	5	hypothetical prote	T34588	2
540	6.5	5	probable lipoprote	E81312	2

Seq	v1	v2	Idx	Cnt	Accession	Description
541	6.5	5	170	2	AI2857	probable acetyltra
542	6.5	5	170	2	G97634	hypothetical prote
543	6.5	5	171	2	T34587	hypothetical prote
544	6.5	5	171	2	AC1082	hypothetical prote
545	6.5	5	172	2	G87656	conserved hypothet
546	6.5	5	173	2	H84391	hypothetical prote
547	6.5	5	173	2	C82098	riboflavin synthas
548	6.5	5	173	2	T17385	vrlF protein - Dic
549	6.5	5	173	2	F70109	hypothetical prote
550	6.5	5	173	2	S38231	hypothetical prote
551	6.5	5	174	2	C84247	hypothetical prote
552	6.5	5	175	2	AB2942	hypothetical prote
553	6.5	5	175	1	JQ1625	small hydrophobic
554	6.5	5	175	2	T06812	cold acclimation p
555	6.5	5	176	2	B84828	hypothetical prote
556	6.5	5	176	2	F82529	hypothetical prote
557	6.5	5	176	2	T36798	probable transcrip
558	6.5	5	177	2	A90635	probable NAD(P)H o
559	6.5	5	177	2	A85486	probable NAD(P)H o
560	6.5	5	177	2	P84110	hypothetical prote
561	6.5	5	177	2	S39710	hypothetical prote
562	6.5	5	178	2	F96739	hypothetical prote
563	6.5	5	178	2	T37723	probable N-termina
564	6.5	5	178	2	E71211	hypothetical prote
565	6.5	5	178	1	LGBO	beta-lactoglobulin
566	6.5	5	179	2	A71730	ubiquinone biosynt
567	6.5	5	179	2	D81400	hypothetical prote
568	6.5	5	179	2	T19064	hypothetical prote
569	6.5	5	179	2	G81746	ribosome recycling
570	6.5	5	179	2	D71484	ribosome releasing
571	6.5	5	180	2	A42367	spore coat protein
572	6.5	5	180	2	B88028	protein F46F5.16 [
573	6.5	5	180	2	AF1864	hypothetical prote
574	6.5	5	180	1	LGGT	beta-lactoglobulin
575	6.5	5	180	2	S39775	alpha-s2-casein fo
576	6.5	5	181	2	F75073	pyrazinamidase/nic
577	6.5	5	181	2	C97050	phage related prot
578	6.5	5	181	2	E97355	hypothetical prote
579	6.5	5	182	2	D83812	hypothetical prote
580	6.5	5	182	2	B71092	probable pyrazinam
581	6.5	5	182	2	G81122	N-acetylmuramoyl-L
582	6.5	5	182	2	D81135	N-acetylmuramoyl-L
583	6.5	5	182	2	AH2500	peptidase E [impor
584	6.5	5	183	2	T23333	hypothetical prote
585	6.5	5	183	1	XNECPG	CDPdiacylglycerol-
586	6.5	5	183	2	B90960	CDPdiacylglycerol-
587	6.5	5	184	2	C85808	CDPdiacylglycerol-
588	6.5	5	185	2	S77784	probable phosphogl
589	6.5	5	185	2	B70335	conserved hypothet
590	6.5	5	185	2	E72630	hypothetical prote
591	6.5	5	185	2	C86664	hypothetical prote
592	6.5	5	186	2	D82490	hypothetical prote
593	6.5	5	186	2	T25340	hypothetical prote
594	6.5	5	186	2	T44337	hypothetical prote
595	6.5	5	186	2	T22183	hypothetical prote
596	6.5	5	186	2	T40915	probable RNA-bindi
597	6.5	5	187	2	T11924	hypothetical prote
598	6.5	5		2	H98340	C4-dicarboxylate t
599	6.5	5		2	C64592	hypothetical prote
600	6.5	5		2	B87501	TPR domain protein
601	6.5	5		2	AG0747	conserved hypothet
602	6.5	5		2	S64035	hypothetical prote
603	6.5	5		2	A70075	hypothetical prote
604	6.5	5		2	H86835	hypothetical prote
605	6.5	5		2	S76991	hypothetical prote
606	6.5	5		1	R5D09E	ribosomal protein
607	6.5	5		2	S70886	galactosyl transfe
608	6.5	5		2	A44968	surface antigen P2
609	6.5	5		2	AE1850	hypothetical prote
610	6.5	5		2	AE1253	hypothetical prote
611	6.5	5		2	AC1616	hypothetical prote
612	6.5	5		2	G86492	polymorphic outer
613	6.5	5		2	B81441	ribosome recycling

Seq	v1	v2	Idx	Cnt	Accession	Description
614	5	6.5	187	2	T51719	hypothetical prote
615	5	6.5	187	2	B86412	protein F1K23.8 [i
616	5	6.5	187	2	H81182	transcription regu
617	5	6.5	188	2	F75004	hypothetical prote
618	5	6.5	188	2	D70349	conserved hypothet
619	5	6.5	188	2	F82587	dioxygenase XF2210
620	5	6.5	188	2	AD0945	probable DNA-bindi
621	5	6.5	189	2	G69545	malate dehydrogena
622	5	6.5	189	2	T07102	hypothetical prote
623	5	6.5	189	2	B95418	probable KdpC pota
624	5	6.5	190	2	A71569	hypothetical prote
625	5	6.5	190	2	T37168	probable tetR-fami
626	5	6.5	190	2	A64039	hypothetical prote
627	5	6.5	190	2	F82610	hypothetical prote
628	5	6.5	190	2	B95210	hypothetical prote
629	5	6.5	190	2	E98074	hypothetical prote
630	5	6.5	190	2	A87263	hypothetical prote
631	5	6.5	190	2	B89803	conserved hypothet
632	5	6.5	191	2	AE0412	probable 2'-5' RNA
633	5	6.5	191	2	B69462	probable pyruvate
634	5	6.5	191	2	S76838	hypothetical prote
635	5	6.5	191	2	B70788	hypothetical prote
636	5	6.5	192	2	G75419	probable N-termina
637	5	6.5	192	2	B82542	two-component syst
638	5	6.5	192	2	B81911	probable molybdopt
639	5	6.5	192	2	S35630	genome polyprotein
640	5	6.5	193	2	H64174	hypothetical prote
641	5	6.5	193	2	S70279	outer surface prot
642	5	6.5	193	2	S76605	phosphoheptose iso
643	5	6.5	194	1	S19141	beta-coixin, 17K,
644	5	6.5	194	2	T19301	hypothetical prote
645	5	6.5	194	2	T14746	hypothetical prote
646	5	6.5	195	2	S46449	hypothetical prote
647	5	6.5	195	2	D64030	hypothetical prote
648	5	6.5	196	2	AI0270	GTP cyclohydrolase
649	5	6.5	196	2	AD2025	hypothetical prote
650	5	6.5	196	2	P97786	hypothetical prote
651	5	6.5	196	2	D72554	probable cytochrom
652	5	6.5	197	2	G85521	hypothetical prote
653	5	6.5	197	2	C90671	hypothetical prote
654	5	6.5	197	2	JC2320	hypothetical 22K p
655	5	6.5	197	2	I39723	ORF13 - Agrobacter
656	5	6.5	197	2	C64422	hypothetical prote
657	5	6.5	197	2	H97762	hypothetical prote
658	5	6.5	197	2	B83561	probable type II s
659	5	6.5	197	2	B83768	hypothetical prote
660	5	6.5	198	2	S78187	ymf39 protein - Re
661	5	6.5	198	2	T42733	hypothetical prote
662	5	6.5	198	2	I39670	rolD protein - Agr
663	5	6.5	199	2	D64770	yajI protein - Esc
664	5	6.5	199	2	B85537	hypothetical prote
665	5	6.5	199	2	A90687	hypothetical prote
666	5	6.5	199	2	T34610	hypothetical prote
667	5	6.5	199	2	F81421	probable periplasm
668	5	6.5	200	2	B75428	dedA protein - Dei
669	5	6.5	200	2	S64905	hypothetical prote
670	5	6.5	200	2	D96023	probable C-P (carb
671	5	6.5	201	2	B71899	hypothetical prote
672	5	6.5	201	2	B96902	probable NADPH-qui
673	5	6.5	201	2	S74841	hypothetical prote
674	5	6.5	201	2	AH2231	hypothetical prote
675	5	6.5	201	2	F96705	unknown protein, 7
676	5	6.5	201	2	T44594	alcaligin synthesi
677	5	6.5	201	2	T37602	probable excision-
678	5	6.5	202	2	T22543	hypothetical prote
679	5	6.5	202	2	A59099	hypothetical prote
680	5	6.5	202	2	F87697	conserved hypothet
681	5	6.5	203	2	E84135	NAD(P)H oxidoreduc
682	5	6.5	203	2	S53708	N-methyl-D-asparta
683	5	6.5	203	2	AH2428	hypothetical prote
684	5	6.5	203	2	H82327	MSHA pilin protein
685	5	6.5	203	2	T22537	hypothetical prote
686	5	6.5	204	2	H85539	cytochrome o ubiqu

Left column

No.	6.5	5	Num	n	Accession	Description
687	6.5	5	204	2	D90689	cytochrome o ubiqu
688	6.5	5	204	2	C42226	bo-type ubiquinol
689	6.5	5	204	2	C84122	thymidine kinase (
690	6.5	5	204	2	B69764	hypothetical prote
691	6.5	5	204	2	B82166	conserved hypothet
692	6.5	5	204	2	T36295	probable transcrip
693	6.5	5	204	2	S51232	gibberellin-respon
694	6.5	5	205	2	E64369	hypothetical prote
695	6.5	5	205	2	T02662	hinI protein homol
696	6.5	5	205	2	G81354	hypothetical prote
697	6.5	5	205	2	AI1307	conserved hypothet
698	6.5	5	205	2	T14745	hypothetical prote
699	6.5	5	205	2	D95200	conserved hypothet
700	6.5	5	205	2	C98067	hypothetical prote
701	6.5	5	206	2	A86869	transport protein
702	6.5	5	206	2	T50439	probable 60s ribos
703	6.5	5	207	2	H72550	probable inorganic
704	6.5	5	207	2	T02514	hypothetical prote
705	6.5	5	207	2	D82951	conserved hypothet
706	6.5	5	207	2	I55145	neuD protein - Esc
707	6.5	5	208	2	JC5638	pH-sensing regulat
708	6.5	5	208	2	T47735	hypothetical prote
709	6.5	5	208	2	T42545	hypothetical prote
710	6.5	5	208	2	C83014	hypothetical prote
711	6.5	5	208	2	T41555	phenylacetic acid
712	6.5	5	208	2	AH3620	transcription regu
713	6.5	5	208	2	AC1853	hypothetical 23.7K
714	6.5	5	209	2	S54113	conserved hypothet
715	6.5	5	209	2	AI1679	enterobactin synth
716	6.5	5	209	2	A85557	enterochelin synth
717	6.5	5	209	2	F90706	enterobactin synth
718	6.5	5	209	2	E64791	hypothetical prote
719	6.5	5	209	2	E84720	hypothetical prote
720	6.5	5	210	1	S74580	4-alpha-glucanotra
721	6.5	5	210	2	B40203	efflux protein, Ly
722	6.5	5	210	2	E87252	probable periplasm
723	6.5	5	210	2	H81360	hypothetical prote
724	6.5	5	210	2	A85985	hypothetical prote
725	6.5	5	210	2	F91139	hypothetical prote
726	6.5	5	210	2	A65112	hypothetical prote
727	6.5	5	210	2	A82411	probable methyltra
728	6.5	5	211	2	AB3178	glutathione S-tran
729	6.5	5	211	2	AB3089	ATP-phosphoribosyl
730	6.5	5	211	2	I40145	outer surface prot
731	6.5	5	211	2	E85091	hypothetical prote
732	6.5	5	211	2	E82070	transcription regu
733	6.5	5	212	2	T35272	hypothetical prote
734	6.5	5	212	2	F64122	phosphoribosylglyc
735	6.5	5	212	2	D69361	conserved hypothet
736	6.5	5	212	2	G95905	hypothetical prote
737	6.5	5	212	2	AD1958	probable germin ty
738	6.5	5	212	2	H83305	probable radical a
739	6.5	5	212	2	B69493	hypothetical prote
740	6.5	5	213	2	D83929	NAD(P)H nitroreduc
741	6.5	5	213	2	AH2815	50S ribosomal prot
742	6.5	5	213	2	C97594	50S ribosomal prot
743	6.5	5	213	2	S35917	capsid protein VP1
744	6.5	5	214	2	T01370	inorganic diphosph
745	6.5	5	214	2	C69879	hypothetical prote
746	6.5	5	214	2	B86156	hypothetical prote
747	6.5	5	215	2	T04421	probable inorganic
748	6.5	5	215	2	T49657	related to zinc fi
749	6.5	5	215	2	T09248	heat shock protein
750	6.5	5	215	2	I52253	nucleoporin p62 ho
751	6.5	5	216	2	T22446	hypothetical prote
752	6.5	5	216	2	AB2582	glutamine amidotra
753	6.5	5	216	2	AB1052	probable hexulose-
754	6.5	5	216	2	S56421	Probable hexulose-
755	6.5	5	216	2	D91275	probable hexulose-
756	6.5	5	216	2	D86116	probable hexulose-
757	6.5	5	216	2	S75186	hypothetical prote
758	6.5	5	216	2	F84156	hypothetical prote
759	6.5	5	216	2	T06289	hypothetical prote

Right column

No.	6.5	5	Num	n	Accession	Description
760	6.5	5	216	2	H72462	hypothetical prote
761	6.5	5	216	2	E83825	hypothetical prote
762	6.5	5	217	1	GMBPT4	gene 59 protein -
763	6.5	5	217	2	D97529	probable transport
764	6.5	5	217	2	AE2748	hypothetical prote
765	6.5	5	217	2	AB1262	O-methyltransferas
766	6.5	5	217	2	AD1624	O-methyltransferas
767	6.5	5	217	2	D69271	hypothetical prote
768	6.5	5	217	2	D72851	AcOrf-12 protein -
769	6.5	5	217	2	A70123	conserved hypothet
770	6.5	5	217	2	H70123	hypothetical prote
771	6.5	5	217	2	T33353	hypothetical prote
772	6.5	5	218	1	S14133	DNA endonuclease (
773	6.5	5	218	2	T21221	hypothetical prote
774	6.5	5	218	2	B28946	glutathione transf
775	6.5	5	218	2	S33860	glutathione transf
776	6.5	5	218	2	B29231	glutathione transf
777	6.5	5	218	2	G86758	DNA-(apurinic or a
778	6.5	5	218	2	F97021	ABC transporter, p
779	6.5	5	218	2	E75389	hypothetical prote
780	6.5	5	218	2	C72747	probable endonucle
781	6.5	5	218	2	AC3537	dipeptide transpor
782	6.5	5	219	2	A37243	hemopoietic cell s
783	6.5	5	219	1	A39574	leukocyte antigen
784	6.5	5	219	1	RPECYS	tetracycline repre
785	6.5	5	219	2	AE3133	hypothetical prote
786	6.5	5	219	2	G98154	hypothetical prote
787	6.5	5	219	2	S43107	orf2 protein - Yer
788	6.5	5	219	2	T33332	hypothetical prote
789	6.5	5	219	2	AG2124	hypothetical prote
790	6.5	5	219	2	B72291	hypothetical prote
791	6.5	5	219	2	G84388	hypothetical prote
792	6.5	5	219	2	F70149	hypothetical prote
793	6.5	5	219	2	F87444	dethiobiotin synth
794	6.5	5	219	2	AE3215	hypothetical prote
795	6.5	5	220	2	F89823	hypothetical prote
796	6.5	5	220	2	A25513	25K silk protein -
797	6.5	5	220	2	E82381	hypothetical prote
798	6.5	5	220	2	H84447	hypothetical prote
799	6.5	5	220	2	AD0938	hypothetical prote
800	6.5	5	220	2	D71946	hypothetical prote
801	6.5	5	221	2	T31184	amidotransferase h
802	6.5	5	221	2	H97363	hypothetical prote
803	6.5	5	221	2	B85688	hypothetical prote
804	6.5	5	222	2	T31863	hypothetical prote
805	6.5	5	222	2	H90746	arginine 3rd trans
806	6.5	5	222	2	D85597	arginine 3rd trans
807	6.5	5	222	2	E64824	arginine transport
808	6.5	5	222	2	F72572	probable TATA-box
809	6.5	5	222	2	C40745	odorant receptor (
810	6.5	5	222	2	H71408	probable germin ty
811	6.5	5	222	2	T27916	hypothetical prote
812	6.5	5	222	2	A70165	hypothetical prote
813	6.5	5	222	2	F64563	NH(3)-dependent NA
814	6.5	5	222	2	I39192	hypothetical prote
815	6.5	5	223	2	I65769	gene HOXA1 protein
816	6.5	5	223	2	B81867	ribose 5-phosphate
817	6.5	5	223	2	E90795	ribose-5-phosphate
818	6.5	5	223	2	C86707	probable membrane
819	6.5	5	223	2	H86906	ABC transporter AT
820	6.5	5	224	2	AB2428	ABC transporter AT
821	6.5	5	225	2	B72202	transcription regu
822	6.5	5	225	2	F87528	endonuclease V - T
823	6.5	5	225	2	H83750	hypothetical prote
824	6.5	5	226	2	F59153	H+-transporting tw
825	6.5	5	226	2	I65769	smooth muscle myos
826	6.5	5	226	2	G83336	probable two-compo
827	6.5	5	226	2	AC1868	probable two-compo
828	6.5	5	226	2	I48880	hypothetical prote
829	6.5	5	226	2	I49392	X-linked lymphocyt
830	6.5	5	226	2	E70501	gene xlr3b protein
831	6.5	5	226	2	T13783	probable transmemb
832	6.5	5	227	2		cytochrome-c oxida

Index			Accession			Description
833	6.5	5	B90738	2	227	probable transcrip
834	6.5	5	F85433	2	227	hypothetical prote
835	6.5	5	E84403	2	227	hypothetical prote
836	6.5	5	C85588	2	227	probable transcrip
837	6.5	5	D64816	2	227	probable transcrip
838	6.5	5	D70358	2	228	hydrogenase (EC 1.
839	6.5	5	T15325	2	228	hypothetical prote
840	6.5	5	F90130	2	228	probable exported
841	6.5	5	AF0462	2	228	hypothetical prote
842	6.5	5	S46673	2	228	hypothetical prote
843	6.5	5	AB1012	2	229	peptidase E [impor
844	6.5	5	A86094	2	229	peptidase E [impor
845	6.5	5	D65209	2	229	peptidase E - Bsch
846	6.5	5	C91246	2	229	peptidase E [impor
847	6.5	5	A36867	2	229	alpha-aspartyl dip
848	6.5	5	F69096	2	229	hypothetical prote
849	6.5	5	A69006	2	229	triose-phosphate i
850	6.5	5	H83503	2	229	hypothetical prote
851	6.5	5	AF3476	2	229	methyltransferase
852	6.5	5	T41660	2	230	Glutathione S-tran
853	6.5	5	T34892	2	230	probable IS elemen
854	6.5	5	T34854	2	230	hypothetical prote
855	6.5	5	D69983	2	231	conserved hypothet
856	6.5	5	T27803	2	231	hypothetical prote
857	6.5	5	AD2542	2	232	hypothetical prote
858	6.5	5	E84108	2	232	capsular polysacch
859	6.5	5	T25745	2	232	hypothetical prote
860	6.5	5	AH0954	2	232	probable membrane
861	6.5	5	PQBPL	2	233	replication protei
862	6.5	5	B91002	2	233	phage replication
863	6.5	5	B85847	2	233	hypothetical prote
864	6.5	5	F85639	2	233	hypothetical prote
865	6.5	5	D90830	2	233	replication protei
866	6.5	5	B75100	2	233	glycosyltransferas
867	6.5	5	S62063	2	234	H+-exporting ATPas
868	6.5	5	D86313	2	234	T20H2.22 protein -
869	6.5	5	AF0110	2	235	probable hemolysin
870	6.5	5	G70793	2	236	hypothetical prote
871	6.5	5	T22977	2	237	hypothetical prote
872	6.5	5	AI2442	2	237	hypothetical prote
873	6.5	5	CYFFBE	1	237	peptidylprolyl iso
874	6.5	5	AD3474	2	237	transporter BMEI17
875	6.5	5	T44706	1	238	ribonuclease III (
876	6.5	5	S77699	2	238	innet cell wall ma
877	6.5	5	D83141	2	238	probable two-compo
878	6.5	5	C83097	2	238	InaA protein PA437
879	6.5	5	T11925	2	238	hypothetical prote
880	6.5	5	AB1570	2	238	hypothetical prote
881	6.5	5	C70543	2	238	hypothetical prote
882	6.5	5	CYFFBE	1	238	peptidylprolyl iso
883	6.5	5	B64416	2	238	hypothetical prote
884	6.5	5	T31218	2	238	hypothetical prote
885	6.5	5	H95105	2	238	pilin gene inverti
886	6.5	5	B95395	2	238	protein [imported
887	6.5	5	AE2850	2	239	peptidyl tRNA hydr
888	6.5	5	I39845	2	239	orotidine-5'-phosp
889	6.5	5	C64188	2	239	arginine binding p
890	6.5	5	B64961	2	239	probable transcrip
891	6.5	5	B85815	2	239	probable 2-compone
892	6.5	5	C90967	2	239	probable 2-compone
893	6.5	5	C75010	2	239	hypothetical prote
894	6.5	5	H90516	2	240	ABC transporter pe
895	6.5	5	T36206	2	240	hypothetical prote
896	6.5	5	ZIZMD1	1	240	19K zein precursor
897	6.5	5	AI2681	2	240	oxidoreductase Atu
898	6.5	5	E70748	2	240	NADPH-flavin oxido
899	6.5	5	D82288	2	240	probable rnc prote
900	6.5	5	E70362	2	240	UMP kinase - Aquif
901	6.5	5	S75017	2	240	hypothetical prote
902	6.5	5	E87110	2	240	ribonuclease HII [
903	6.5	5	C86194	2	240	hypothetical prote
904	6.5	5	AG1083	2	240	hypothetical prote
905	6.5	5	F97752	2	241	tolQ protein [impo
906	6.5	5	H71686	2	241	tolQ protein (tolQ
907	6.5	5	T05040	2	241	nodulin-26-like pr
908	6.5	5	B87337	2	241	ada regulatory pro
909	6.5	5	D97229	2	242	probable pseudouri
910	6.5	5	T27210	2	242	hypothetical prote
911	6.5	5	JQ0021	1	243	ubiquinol-cycochro
912	6.5	5	F69553	2	243	enoyl-CoA hydratas
913	6.5	5	A69480	2	243	cobalt transport p
914	6.5	5	A70670	2	243	hypothetical prote
915	6.5	5	B82390	2	243	conserved hypothet
916	6.5	5	C82393	2	243	probable amino aci
917	6.5	5	B72757	2	243	probable phosphate
918	6.5	5	B95855	2	243	probable transcrip
919	6.5	5	T12051	2	243	3-oxoacyl-[acyl-ca
920	6.5	5	F69260	2	244	nitrate ABC transp
921	6.5	5	AE1318	2	244	hypothetical prote
922	6.5	5	AB1690	2	244	hypothetical prote
923	6.5	5	T15647	2	244	hypothetical prote
924	6.5	5	F82838	2	244	conserved hypothet
925	6.5	5	F70754	2	244	probable lprA prot
926	6.5	5	D86725	2	244	hypothetical prote
927	6.5	5	E83478	2	244	probable ATP-bindi
928	6.5	5	F69830	2	244	conserved hypothet
929	6.5	5	AB3609	2	244	multidrug resistan
930	6.5	5	AC2751	2	244	transcription regu
931	6.5	5	C97532	2	244	probable transcrip
932	6.5	5	AG1823	2	244	hypothetical prote
933	6.5	5	AI3412	2	245	ribonuclease III (
934	6.5	5	T36127	2	245	probable ribonucle
935	6.5	5	A48598	2	245	kallikrein-like se
936	6.5	5	AG3346	2	245	LSU ribosomal prot
937	6.5	5	I51323	2	245	proteolipid protei
938	6.5	5	D75386	2	245	uridylate kinase -
939	6.5	5	G81032	2	245	DNA polymerase, ba
940	6.5	5	D81977	2	245	hypothetical prote
941	6.5	5	A85656	2	245	hypothetical prote
942	6.5	5	AI0399	2	246	tRNA (guanine-N1-)
943	6.5	5	E89884	2	246	hypothetical prote
944	6.5	5	A81679	2	246	conserved hypothet
945	6.5	5	B72771	2	246	hypothetical prote
946	6.5	5	T50987	2	246	related to prefold
947	6.5	5	H87427	2	246	hypothetical prote
948	6.5	5	T20792	2	246	hypothetical prote
949	6.5	5	AH3072	2	246	transcription regu
950	6.5	5	A72260	2	246	ABC transporter, A
951	6.5	5	LNRBPS	1	247	pulmonary surfacta
952	6.5	5	T22109	2	247	hypothetical prote
953	6.5	5	T06721	2	247	hypothetical prote
954	6.5	5	G64341	2	247	hypothetical prote
955	6.5	5	F90510	2	247	conserved hypothet
956	6.5	5	T27205	2	247	hypothetical prote
957	6.5	5	A98009	2	247	sortase [imported]
958	6.5	5	A86276	2	248	F7A19.31 protein -
959	6.5	5	B30125	2	248	tropomyosin 1, fib
960	6.5	5	AF0775	2	248	probable gntR-fami
961	6.5	5	A98143	2	248	response regulator
962	6.5	5	AB3145	2	248	two component resp
963	6.5	5	F75492	2	248	hypothetical prote
964	6.5	5	AH2339	2	248	probable transcrip
965	6.5	5	E69505	2	248	cytochrome oxidase
966	6.5	5	G81218	2	249	bioH protein, prob
967	6.5	5	T20790	2	249	hypothetical prote
968	6.5	5	B84147	2	249	ABC transporter (p
969	6.5	5	AG3485	2	249	homoserine/homoser
970	6.5	5	T41231	4	249	wtf protein pseudo
971	6.5	5	H85577	2	250	phosphoglyceromuta
972	6.5	5	G90726	2	250	phosphoglyceromuta
973	6.5	5	A80594	2	250	phosphoglycerate m
974	6.5	5	C64811	2	250	phosphoglycerate m
975	6.5	5	AE0139	2	250	phosphoglycerate m
976	6.5	5	G81365	2	250	probable ABC-type
977	6.5	5	AD0240	2	250	probable IS100 tra
978	6.5	5	H97448	2	250	hemolysin [importe

No.			Description	Accession	N	Value
979	6.5	5	hemolysin [importe	AB2667	2	250
980	6.5	5	hypothetical prote	C97812	2	250
981	6.5	5	ABC transporter tr	AB1555	2	250
982	6.5	5	ABC transporter tr	AD1197	2	250
983	6.5	5	2,3-dihydro-2,3-di	AH0575	2	251
984	6.5	5	hypothetical prote	E83885	2	251
985	6.5	5	hypothetical prote	T15307	2	251
986	6.5	5	stage v sporulatio	C97627	2	251
987	6.5	5	RNA polymerase sig	D69861	2	251
988	6.5	5	conserved hypothet	E81155	2	252
989	6.5	5	probable RNA-bindi	F81949	2	252
990	6.5	5	hypothetical prote	T17772	2	252
991	6.5	5	hypothetical prote	B89785	2	252
992	6.5	5	hypothetical prote	A96549	2	252
993	6.5	5	pyrroline-5-carbox	H69219	2	253
994	6.5	5	ubiquinone/menaqui	C82675	2	253
995	6.5	5	photosynthetic rea	T50900	2	253
996	6.5	5	motA protein - Rho	S70170	2	253
997	6.5	5	precorrin-3B C17-m	AG2920	2	253
998	6.5	5	precorrin-3B C17-m	H97694	2	253
999	6.5	5	conserved hypothet	AH3106	2	253
1000	6.5	5	L-fuculose-phospha	A72396	1	254
1001	6.5	5	dihydrodipicolinat	F64583	2	254
1002	6.5	5	polysaccharide ABC	B69255	2	254
1003	6.5	5	hypothetical prote	B72549	2	254
1004	6.5	5	trbC protein homol	T31228	2	254
1005	6.5	5	hypothetical prote	T04067	2	254
1006	6.5	5	nikD protein - Esc	S47698	2	254
1007	6.5	5	hypothetical prote	B91172	2	254
1008	6.5	5	ATP-binding protei	B86018	2	254
1009	6.5	5	thyroliberin precu	RHRTT	1	255
1010	6.5	5	hypothetical prote	T23488	2	255
1011	6.5	5	probable transcrip	AB0523	2	255
1012	6.5	5	flagellar biosynth	H83464	2	255
1013	6.5	5	hypothetical prote	T24364	2	255
1014	6.5	5	conserved hypothet	B87485	2	255
1015	6.5	5	expansin 3 - rice	T03299	2	255
1016	6.5	5	hypothetical prote	A70758	2	255
1017	6.5	5	conserved hypothet	C75527	2	255
1018	6.5	5	transcription regu	AH2479	2	255
1019	6.5	5	alcohol dehydrogen	S20713	1	256
1020	6.5	5	thyroliberin precu	RTMST	1	256
1021	6.5	5	T-cell antigen 4-1	B32393	2	256
1022	6.5	5	unknown [imported]	F85505	2	256
1023	6.5	5	probable biotin sy	F90654	2	256
1024	6.5	5	hypothetical prote	C90443	2	256
1025	6.5	5	hypothetical prote	C83474	2	256
1026	6.5	5	protocatechuate 3,	T35018	2	257
1027	6.5	5	hypothetical prote	H97522	2	257
1028	6.5	5	conserved hypothet	AI2741	2	257
1029	6.5	5	protein-methionine	S55365	2	257
1030	6.5	5	hypothetical prote	D95161	2	257
1031	6.5	5	hypothetical prote	C98027	2	257
1032	6.5	5	rRNA methylase UU3	C82904	2	257
1033	6.5	5	protein K02B2.3 [i	B88700	2	257
1034	6.5	5	conserved hypothet	C69870	2	257
1035	6.5	5	UDP-N-acetyl-D-man	AF2358	2	257
1036	6.5	5	probable oxidoredu	A95945	2	258
1037	6.5	5	UDP-N-acetylglucos	D83190	2	258
1038	6.5	5	exodeoxyribonuclea	AF3165	2	258
1039	6.5	5	hypothetical wtf p	T40850	2	258
1040	6.5	5	conserved hypothet	T08265	2	258
1041	6.5	5	ThiJ/PfpI family p	E87615	2	258
1042	6.5	5	sorbitol-6-phospha	DEECSP	1	259
1043	6.5	5	sorbitol-6-phospha	AF0844	2	259
1044	6.5	5	glucitol (sorbitol	H85918	2	259
1045	6.5	5	glucitol (sorbitol	A98074	2	259
1046	6.5	5	probable isocitrat	T08743	2	259
1047	6.5	5	probable isocitrat	H97708	2	259
1048	6.5	5	hypothetical prote	A70408	2	259
1049	6.5	5	phosphatidate cyti	T18151	2	259
1050	6.5	5	conserved hypothet	C82148	2	259
1051	6.5	5	probable transposa	T14971	2	260

No.	Value			Accession	N	Description
1052	260	6.5	5	AB0031	2	insertion sequence
1053	260	6.5	5	AH0078	2	insertion sequence
1054	260	6.5	5	AI0197	2	insertion sequence
1055	260	6.5	5	AH0356	2	insertion sequence
1056	260	6.5	5	AF0065	2	insertion sequence
1057	260	6.5	5	AC0395	2	insertion sequence
1058	260	6.5	5	AH0047	2	insertion sequence
1059	260	6.5	5	AC0185	2	insertion sequence
1060	260	6.5	5	AD0450	2	insertion sequence
1061	260	6.5	5	AF0254	2	insertion sequence
1062	260	6.5	5	AE0174	2	insertion sequence
1063	260	6.5	5	AC0070	2	insertion sequence
1064	260	6.5	5	AH0231	2	insertion sequence
1065	260	6.5	5	AH0436	2	insertion sequence
1066	260	6.5	5	AE0124	2	insertion sequence
1067	260	6.5	5	AC0139	2	insertion sequence
1068	260	6.5	5	AD0113	2	insertion sequence
1069	260	6.5	5	AC0206	2	insertion sequence
1070	260	6.5	5	AE0133	2	insertion sequence
1071	260	6.5	5	AI0095	2	insertion sequence
1072	260	6.5	5	AH0389	2	insertion sequence
1073	260	6.5	5	AF0307	2	insertion sequence
1074	260	6.5	5	AB0332	2	insertion sequence
1075	260	6.5	5	AD0322	2	insertion sequence
1076	260	6.5	5	AF0292	2	insertion sequence
1077	260	6.5	5	AG0004	2	insertion sequence
1078	260	6.5	5	AH0101	2	insertion sequence
1079	260	6.5	5	AB0247	2	insertion sequence
1080	260	6.5	5	AE0288	2	insertion sequence
1081	260	6.5	5	AE0211	2	insertion sequence
1082	260	6.5	5	AD0342	2	insertion sequence
1083	260	6.5	5	AI0398	2	insertion sequence
1084	260	6.5	5	AI0487	2	insertion sequence
1085	260	6.5	5	AG0213	2	insertion sequence
1086	260	6.5	5	AC0457	2	insertion sequence
1087	260	6.5	5	AE0288	2	insertion sequence
1088	260	6.5	5	AH0430	2	insertion sequence
1089	260	6.5	5	AH0012	2	insertion sequence
1090	260	6.5	5	AI0021	2	insertion sequence
1091	260	6.5	5	AF0163	2	insertion sequence
1092	260	6.5	5	AE0265	2	insertion sequence
1093	260	6.5	5	AE0417	2	insertion sequence
1094	260	6.5	5	AE0438	2	insertion sequence
1095	260	6.5	5	JT0371	2	Resolvase (Protein
1096	261	6.5	5	A82224	2	cobalamin 5'-phosp
1097	261	6.5	5	I64249	2	hypothetical prote
1098	261	6.5	5	C69536	2	hypothetical prote
1099	261	6.5	5	T43579	2	type III secretion
1100	261	6.5	5	T16650	2	hypothetical prote
1101	261	6.5	5	G84376	2	hypothetical prote
1102	261	6.5	5	G86880	2	hypothetical prote
1103	261	6.5	5	T32562	2	hypothetical prote
1104	261	6.5	5	H95991	2	probable sugar upt
1105	262	6.5	5	T24439	2	hypothetical prote
1106	262	6.5	5	T11883	2	cytochrome-c oxida
1107	262	6.5	5	I64139	2	hypothetical prote
1108	262	6.5	5	G82959	2	hypothetical prote
1109	262	6.5	5	G02476	2	lysosomal-associat
1110	262	6.5	5	H84152	2	hypothetical prote
1111	262	6.5	5	E97151	2	ABC transported MD
1112	262	6.5	5	H72107	2	peptide ABC transp
1113	262	6.5	5	B86516	2	oligopeptide trans
1114	262	6.5	5	B71721	2	probable signal pe
1115	264	6.5	5	C72080	2	N-acetylmuramoyl-L
1116	264	6.5	5	G86542	2	N-acetylmuramoyl a
1117	264	6.5	5	T36315	2	probable ABC-type
1118	264	6.5	5	G90695	2	probable ligase [i
1119	264	6.5	5	C85546	2	probable ligase yb
1120	264	6.5	5	A64779	2	ybaP protein - Esc
1121	264	6.5	5	B71448	2	hypothetical prote
1122	264	6.5	5	T13116	2	protein gp30 - pha
1123	264	6.5	5	AD0034	2	probable type III
1124	264	6.5	5	AG3175	2	hypothetical prote

No.	pH	Len	Accession	Count	N	Description
1125	6.5	5	D71037	2	264	hypothetical prote
1126	6.5	5	BVECIT	1	265	istB protein - Esc
1127	6.5	5	A89880	2	265	hypothetical prote
1128	6.5	5	T32316	2	265	hypothetical prote
1129	6.5	5	AH0755	2	265	conserved hypothet
1130	6.5	5	F84071	2	265	hypothetical prote
1131	6.5	5	H69468	2	266	lysophospholipase
1132	6.5	5	D97719	2	266	signal peptidase I
1133	6.5	5	C87367	2	266	flagellar biosynth
1134	6.5	5	T41094	2	266	very hypothetical
1135	6.5	5	T46533	2	266	hypothetical prote
1136	6.5	5	T33411	2	266	hypothetical prote
1137	6.5	5	C87497	2	267	hypothetical prote
1138	6.5	5	E81431	2	267	ABC transporter in
1139	6.5	5	D83313	2	267	probable permease
1140	6.5	5	AE1204	2	267	B. subtilis YoaT p
1141	6.5	5	AD1561	2	267	B. subtilis YoaT p
1142	6.5	5	D72499	2	267	intercellular adhe
1143	6.5	5	F97041	2	267	hypothetical prote
1144	6.5	5	AB2472	2	267	hypothetical prote
1145	6.5	5	S77802	2	267	hypothetical prote
1146	6.5	5	B64644	2	267	hypothetical prote
1147	6.5	5	S07557	2	267	cytochrome-c oxida
1148	6.5	5	B42424	2	268	chitinase (EC 3.2.
1149	6.5	5	B71329	2	268	probable glutamate
1150	6.5	5	D82688	2	268	tryptophan synthas
1151	6.5	5	S45062	2	268	vegetative storage
1152	6.5	5	G90018	2	268	conserved hypothet
1153	6.5	5	T46755	2	268	membrane protein a
1154	6.5	5	G95253	2	268	zinc ABC transport
1155	6.5	5	C90516	2	268	esterase/lipase 1
1156	6.5	5	WMBEW4	1	269	UL24 protein - hum
1157	6.5	5	G87271	2	269	prepilin peptidase
1158	6.5	5	S32427	2	269	triose-phosphate i
1159	6.5	5	H70179	2	269	spermidine/putresc
1160	6.5	5	AH1175	2	269	spermidine/putresc
1161	6.5	5	AF1532	2	269	spermidine/putresc
1162	6.5	5	T41611	2	269	hypothetical repea
1163	6.5	5	G91169	2	269	probable acyltrans
1164	6.5	5	C70142	2	269	hypothetical prote
1165	6.5	5	T49240	2	269	tryptophan synthas
1166	6.5	5	C87068	2	270	tryptophan synthas
1167	6.5	5	C70557	2	270	probable trpA prot
1168	6.5	5	A81684	2	270	triosephosphate is
1169	6.5	5	E72543	2	270	probable ABC trans
1170	6.5	5	AE3627	2	270	maltose transport
1171	6.5	5	H83619	2	270	hypothetical prote
1172	6.5	5	F96675	2	270	T23K8.8 [imported]
1173	6.5	5	AF3088	2	270	serine/threonine p
1174	6.5	5	AC2270	2	270	hypothetical prote
1175	6.5	5	G97463	2	271	probable oxidoredu
1176	6.5	5	A36893	2	271	transcription acti
1177	6.5	5	T36885	2	271	probable membrane
1178	6.5	5	AG0315	2	271	conserved hypothet
1179	6.5	5	H90394	2	271	probable cation tr
1180	6.5	5	B87266	2	271	conserved hypothet
1181	6.5	5	T31314	2	271	hypothetical prote
1182	6.5	5	E97451	2	272	hypothetical prote
1183	6.5	5	AG2669	2	272	enoyl-(acyl-carrie
1184	6.5	5	E64182	2	272	cysZ protein - Hae
1185	6.5	5	G91202	2	272	hypothetical prote
1186	6.5	5	T18915	2	272	hypothetical prote
1187	6.5	5	B86049	2	272	hypothetical prote
1188	6.5	5	H86904	2	273	probable membrane
1189	6.5	5	E90516	2	273	esterase/lipase 1
1190	6.5	5	D90516	2	273	esterase/lipase 1
1191	6.5	5	G86015	2	273	hypothetical prote
1192	6.5	5	A83143	2	273	probable ethanolam
1193	6.5	5	E70742	2	273	hypothetical prote
1194	6.5	5	DCASOE	1	274	orotidine-5'-phosp
1195	6.5	5	S22308	2	274	type II site-speci
1196	6.5	5	E87456	2	274	sterol desaturase
1197	6.5	5	T25783	2	274	hypothetical prote
1198	6.5	5	B89795	2	274	hypothetical prote
1199	6.5	5	JC7604	2	275	CD86 spliced varia
1200	6.5	5	D98180	2	275	hypothetical prote
1201	6.5	5	D83910	2	275	hypothetical prote
1202	6.5	5	C82752	2	275	hypothetical prote
1203	6.5	5	S03967	2	275	intercellular adhe
1204	6.5	5	T16765	2	276	hypothetical prote
1205	6.5	5	E89914	2	276	hypothetical prote
1206	6.5	5	A95881	2	276	probable trehalose
1207	6.5	5	C75414	2	276	hypothetical prote
1208	6.5	5	G75518	2	277	probable beta-lact
1209	6.5	5	AC2967	2	277	hypothetical prote
1210	6.5	5	H87213	2	277	conserved hypothet
1211	6.5	5	E85356	2	277	hypothetical prote
1212	6.5	5	E82400	2	277	hemin ABC transpor
1213	6.5	5	T39538	2	277	probable superoxid
1214	6.5	5	T27275	2	277	hypothetical prote
1215	6.5	5	A46510	2	277	intercellular adhe
1216	6.5	5	C90077	2	277	conserved hypothet
1217	6.5	5	I58150	2	278	membrane glycoprot
1218	6.5	5	I51324	2	278	proteolipid protei
1219	6.5	5	E98118	2	278	hypothetical prote
1220	6.5	5	D83080	2	278	hypothetical prote
1221	6.5	5	AG0247	2	278	probable binding-p
1222	6.5	5	T04707	2	279	L-ascorbate peroxi
1223	6.5	5	B89849	2	279	prolipoprotein dia
1224	6.5	5	F86842	2	279	prephenate dehydra
1225	6.5	5	S76201	2	279	hypothetical prote
1226	6.5	5	S75552	2	279	hypothetical prote
1227	6.5	5	H83504	2	279	hypothetical prote
1228	6.5	5	G72637	2	279	hypothetical prote
1229	6.5	5	AC2164	2	279	glycosyltransferas
1230	6.5	5	T36066	2	280	hypothetical prote
1231	6.5	5	C64471	2	280	hypothetical prote
1232	6.5	5	F70805	2	280	hypothetical prote
1233	6.5	5	C70696	2	280	probable transport
1234	6.5	5	F84765	2	280	hypothetical prote
1235	6.5	5	E98242	2	281	hypothetical prote
1236	6.5	5	C69588	2	281	L-arabinose transp
1237	6.5	5	S60477	2	281	1-acylglycerol-3-p
1238	6.5	5	AF2161	2	281	cation-efflux syst
1239	6.5	5	B95159	2	282	prephenate dehydra
1240	6.5	5	B98025	2	282	prephenate dehydra
1241	6.5	5	B84984	2	282	geranyltransf
1242	6.5	5	D70149	2	282	hypothetical prote
1243	6.5	5	S01072	2	283	hypothetical prote
1244	6.5	5	F82779	2	283	hypothetical prote
1245	6.5	5	AI3027	2	283	transcription regu
1246	6.5	5	B98257	2	283	lysR-type transcri
1247	6.5	5	RGBCH	1	284	RNA polymerase sig
1248	6.5	5	F91167	2	284	RNA polymerase sig
1249	6.5	5	F86013	2	284	RNA polymerase sig
1250	6.5	5	S60166	2	284	transcription init
1251	6.5	5	H86515	2	284	oligopeptide perme
1252	6.5	5	F72107	2	284	peptide ABC transp
1253	6.5	5	AF3531	2	285	high-affinity zinc
1254	6.5	5	YQEC88	1	285	fimbrial adhesin K
1255	6.5	5	AE0966	2	285	probable PTS syste
1256	6.5	5	D90500	2	285	hypothetical prote
1257	6.5	5	S31708	2	285	alginate poly(ManA
1258	6.5	5	AB0106	2	285	probable lipoprote
1259	6.5	5	H85356	2	285	hypothetical prote
1260	6.5	5	S69312	2	285	probable membrane
1261	6.5	5	AF2829	2	286	hydrolase [importe
1262	6.5	5	AE2677	2	286	ABC transporter, m
1263	6.5	5	C97459	2	286	sulfate ABC transp
1264	6.5	5	B70833	2	286	carbon-monoxide de
1265	6.5	5	B42709	2	286	DNA restriction en
1266	6.5	5	T33500	2	286	hypothetical prote
1267	6.5	5	D86163	2	286	F15K9.19 protein -
1268	6.5	5	JS0384	2	286	hypothetical 30.5K
1269	6.5	5	H89003	2	286	protein T24A6.5 [i
1270	6.5	5	G90462	2	286	ABC transporter, p

No					Accession	Description
1271	2	287	6.5	5	G85859	ferredoxin-type pr
1272	2	287	6.5	5	E91015	ferredoxin-type pr
1273	2	287	6.5	5	B64990	ferredoxin-type pr
1274	2	287	6.5	5	G81662	conserved hypothet
1275	2	287	6.5	5	G69766	conserved hypothet
1276	2	287	6.5	5	H90674	hypothetical prote
1277	2	287	6.5	5	D90540	glucokinase (gluco
1278	2	287	6.5	5	G86728	alpha-subuni L-ser
1279	2	287	6.5	5	A86764	hypothetical prote
1280	2	287	6.5	5	H70923	probable hg transp
1281	2	287	6.5	5	C85525	yahE protein - Esc
1282	2	287	6.5	5	G64758	hypothetical prote
1283	2	287	6.5	5	S58648	probable protein -
1284	2	288	6.5	5	C64450	ATP phosphoribosyl
1285	2	288	6.5	5	T51595	phosphate transpor
1286	2	288	6.5	5	D83954	hypothetical prote
1287	2	288	6.5	5	T04671	hypothetical prote
1288	2	288	6.5	5	F71504	hypothetical prote
1289	2	288	6.5	5	D71652	hypothetical prote
1290	2	288	6.5	5	T32212	hypothetical prote
1291	2	288	6.5	5	T26383	hypothetical prote
1292	2	288	6.5	5	AG3260	exodeoxyribonuclea
1293	2	289	6.5	5	A43562	homeotic protein H
1294	2	289	6.5	5	H98315	thuG protein (AF17
1295	2	289	6.5	5	T48108	hypothetical prote
1296	2	289	6.5	5	AC0183	probable LysR-fami
1297	2	289	6.5	5	A81779	hypothetical lysin
1298	2	289	6.5	5	C81203	conserved hypothet
1299	2	289	6.5	5	H69645	myo-inositol catab
1300	2	289	6.5	5	H96588	hypothetical prote
1301	2	290	6.5	5	G70336	hypothetical prote
1302	2	290	6.5	5	AF2907	diaminopimelate ep
1303	2	290	6.5	5	E83990	lactose transport
1304	2	290	6.5	5	C75190	cobalamin biosynth
1305	2	290	6.5	5	AD0367	probable sugar kin
1306	2	290	6.5	5	H97791	hypothetical prote
1307	2	291	6.5	5	B95926	probable amino aci
1308	2	291	6.5	5	B69777	transcription regu
1309	2	291	6.5	5	AH2017	lipoic acid synthe
1310	2	291	6.5	5	A96973	probable phosphate
1311	2	291	6.5	5	T27534	hypothetical prote
1312	2	291	6.5	5	AC2870	ABC transporter, m
1313	2	292	6.5	5	A95163	hypothetical prote
1314	2	292	6.5	5	H98028	hypothetical prote
1315	2	292	6.5	5	S76003	uncharacterized st
1316	2	292	6.5	5	G97111	prolactin receptor
1317	2	292	6.5	5	I77525	phosphotransacetyl
1318	2	292	6.5	5	C82938	probable lacyl-car
1319	2	293	6.5	5	S75355	spermidine synthas
1320	2	293	6.5	5	B64339	glycerol-3-phospha
1321	2	293	6.5	5	H82184	hypothetical prote
1322	2	293	6.5	5	D69355	hypothetical prote
1323	2	293	6.5	5	F64463	hypothetical prote
1324	2	293	6.5	5	T51262	lysozyme (EC 3.2.1
1325	2	293	6.5	5	T09065	NADH2 dehydrogenas
1326	2	294	6.5	5	MUSMM1	probable pirin [im
1327	1	294	6.5	5	T11379	hypothetical prote
1328	2	294	6.5	5	D96542	hypothetical prote
1329	2	294	6.5	5	D85036	hypothetical prote
1330	2	294	6.5	5	T22058	peptide ABC transp
1331	2	294	6.5	5	A96707	sugar transport sy
1332	2	294	6.5	5	T18680	UDP-N-acetylglucos
1333	2	295	6.5	5	D82170	hypothetical prote
1334	2	295	6.5	5	AD3577	probable membrane
1335	2	295	6.5	5	D75010	probable ABC sugar
1336	2	295	6.5	5	F86809	ROK family protein
1337	2	295	6.5	5	AD0306	conserved hypothet
1338	2	296	6.5	5	AB0210	hypothetical prote
1339	2	296	6.5	5	H87554	ATP phosphoribosyl
1340	2	296	6.5	5	H83157	
1341	2	296	6.5	5	F87411	
1342	2	296	6.5	5	C95961	
1343	1	297	6.5	5	XRBY	

No	Accession					Description
1344	T40173	2	297	6.5	5	probable transcrip
1345	G87363	2	297	6.5	5	metallo-beta-lacta
1346	AC1706	2	297	6.5	5	hypothetical prote
1347	AD1335	2	297	6.5	5	hypothetical prote
1348	E97646	2	297	6.5	5	ABC transporter (p
1349	B83553	2	298	6.5	5	probable 3-hydroxy
1350	A69623	2	298	6.5	5	flagellar hook-ass
1351	T33220	2	298	6.5	5	hypothetical prote
1352	AC0166	2	298	6.5	5	probable membrane
1353	D71024	2	298	6.5	5	hypothetical prote
1354	B83836	2	298	6.5	5	reductase BH1493 [
1355	E97032	2	298	6.5	5	probable permease
1356	G89927	2	298	6.5	5	hypothetical prote
1357	F97682	2	298	6.5	5	diaminopimelate ep
1358	G97980	2	299	6.5	5	GTPase/GTP-binding
1359	A95112	2	299	6.5	5	GTP-binding protei
1360	B96012	2	299	6.5	5	probable sugar upt
1361	AB0609	2	299	6.5	5	probable membrane
1362	D85599	2	299	6.5	5	probable surface p
1363	H90748	2	299	6.5	5	probable surface p
1364	S68198	2	299	6.5	5	probable transcrip
1365	T21685	2	299	6.5	5	hypothetical prote
1366	A64580	2	300	6.5	5	site-specific DNA-
1367	T36768	2	300	6.5	5	secreted serine pr
1368	AI0486	2	300	6.5	5	dipeptide transpor
1369	A84111	2	300	6.5	5	sugar transport sy
1370	F81799	2	300	6.5	5	hypothetical integ
1371	G81069	2	300	6.5	5	conserved hypothet
1372	T15690	2	300	6.5	5	hypothetical prote
1373	T47557	2	300	6.5	5	hypothetical prote
1374	AE0970	2	300	6.5	5	probable regulator
1375	G89103	2	301	6.5	5	protein C18B10.2 [
1376	S33042	2	301	6.5	5	hypothetical prote
1377	T15293	2	301	6.5	5	hypothetical prote
1378	H75470	2	301	6.5	5	histone deacetylas
1379	T40593	2	301	6.5	5	cytoplasmic dynein
1380	T25741	2	301	6.5	5	hypothetical prote
1381	H89927	2	301	6.5	5	hypothetical prote
1382	A98214	2	302	6.5	5	ABC transporter (A
1383	A70039	2	302	6.5	5	probable dihydropi
1384	T36903	2	302	6.5	5	hypothetical prote
1385	G90078	2	302	6.5	5	nicotinate-nucleot
1386	AB0416	2	302	6.5	5	4-hydroxybenzoate
1387	B81696	2	302	6.5	5	probable integral
1388	AH3108	2	302	6.5	5	conserved hypothet
1389	G86920	2	302	6.5	5	hypothetical prote
1390	C96531	2	302	6.5	5	probable transcrip
1391	B82968	2	302	6.5	5	hypothetical prote
1392	AC2018	2	302	6.5	5	3a protein - brome
1393	P3BVAM	1	303	6.5	5	phosphotransferase
1394	H71246	2	303	6.5	5	PTS system, mannos
1395	C97904	2	303	6.5	5	hypothetical prote
1396	C95033	2	303	6.5	5	cyclin C - human
1397	T32658	2	303	6.5	5	prolactin receptor
1398	A40268	2	303	6.5	5	probable secreted
1399	I77524	2	303	6.5	5	hypothetical prote
1400	D86998	2	304	6.5	5	GTP-binding regula
1401	B86641	2	304	6.5	5	ribose transport A
1402	T50474	2	304	6.5	5	hypothetical prote
1403	T03558	2	305	6.5	5	hypothetical prote
1404	T36056	2	305	6.5	5	hypothetical prote
1405	T45942	2	305	6.5	5	hypothetical prote
1406	H81257	2	305	6.5	5	hypothetical prote
1407	D98198	2	305	6.5	5	sdsB protein - Pse
1408	JC1120	2	306	6.5	5	protein prrB homol
1409	P83348	2	306	6.5	5	hypothetical prote
1410	S73876	2	306	6.5	5	probable ABC trans
1411	D86194	2	307	6.5	5	probable transcrip
1412	B95417	2	307	6.5	5	hypothetical prote
1413	F83339	2	307	6.5	5	probable pyridoxin
1414	G82385	2	307	6.5	5	conserved hypothet
1415	B86965	2	307	6.5	5	
1416	B90303	2	307	6.5	5	

1417	5	6.5	307	2	T16457	hypothetical prote
1418	5	6.5	308	2	T09169	probable peroxidas
1419	5	6.5	308	2	H85214	nodulin-26-like pr
1420	5	6.5	308	2	G69197	hypothetical prote
1421	5	6.5	308	2	H87306	glycosyl transfera
1422	5	6.5	308	2	AF0461	probable membrane
1423	5	6.5	308	2	D97589	probable ATP-bindi
1424	5	6.5	308	2	AI2810	hypothetical prote
1425	5	6.5	309	1	DNECTS	terminator sequenc
1426	5	6.5	309	2	WMBP10	gene 10 protein -
1427	5	6.5	309	1	WMBPC9	gene.10 protein -
1428	5	6.5	309	2	C83017	probable short cha
1429	5	6.5	309	2	D97607	tropinesterase (at
1431	5	6.5	309	2	I48125	syndecan-1 - Chine
1432	5	6.5	309	2	A36064	basic fibroblast g
1433	5	6.5	309	2	T29452	hypothetical prote
1434	5	6.5	309	2	A81403	probable periplasm
1435	5	6.5	310	2	B72342	conserved hypothet
1436	5	6.5	310	2	A41776	syndecan 1 precurs
1437	5	6.5	310	2	H69465	hypothetical prote
1438	5	6.5	310	2	C83267	hypothetical prote
1439	5	6.5	310	2	AC3238	hypothetical prote
1440	5	6.5	310	2	A29884	prolactin receptor
1441	5	6.5	310	2	G71008	hypothetical prote
1442	5	6.5	311	2	I64082	pantothenate kinas
1443	5	6.5	311	2	E98240	ABC transporter ho
1444	5	6.5	311	2	AG3045	dioxygenase [impor
1445	5	6.5	311	2	C70787	probable lipoic ac
1446	5	6.5	311	2	S06619	syndecan-1 precurs
1447	5	6.5	311	2	AG3526	2-hydroxyhepta-2,4
1448	5	6.5	312	1	S29756	nitrogen fixation
1449	5	6.5	312	2	B28663	nodulation protein
1450	5	6.5	312	2	C81795	probable hydrolase
1451	5	6.5	312	2	B87487	translation elonga
1452	5	6.5	312	2	T10836	nodulation protein
1453	5	6.5	312	2	D90198	transposase ISC123
1454	5	6.5	312	2	H90470	hypothetical prote
1455	5	6.5	312	2	T26085	hypothetical prote
1456	5	6.5	313	1	XYNHCL	site-specific DNA-
1457	5	6.5	313	2	E72516	probable ribokinas
1458	5	6.5	313	2	AH0284	conserved hypothet
1459	5	6.5	313	2	D98178	hypothetical prote
1460	5	6.5	313	2	A42853	syndecan core prot
1461	5	6.5	313	2	S38538	aspartoacylase - h
1462	5	6.5	313	2	A86743	hypothetical prote
1463	5	6.5	313	2	JC5342	Na+/H+ antiporter
1464	5	6.5	313	2	D89954	conserved hypothet
1465	5	6.5	313	2	AD1285	glycerate dehydrog
1466	5	6.5	314	2	T05993	probable peroxidas
1467	5	6.5	314	2	G71367	conserved hypothet
1468	5	6.5	314	2	G83487	hypothetical prote
1469	5	6.5	314	2	B81253	probable peptide A
1470	5	6.5	315	2	B64826	probable membrane
1471	5	6.5	315	2	H89004	protein T24A6.4 [i
1472	5	6.5	315	2	F86655	dihydroxyacetone k
1473	5	6.5	316	2	B83658	phosphoribosyl pyr
1474	5	6.5	316	2	B90282	probable peroxidas
1475	5	6.5	316	2	AB2868	UDP-hexose transfe
1476	5	6.5	316	2	F97644	UDP-hexose transfe
1477	5	6.5	316	2	F81661	methionyl-tRNA for
1478	5	6.5	316	2	A71502	probable methionyl
1479	5	6.5	316	2	T33501	hypothetical prote
1480	5	6.5	316	2	T22197	hypothetical prote
1481	5	6.5	316	2	T10436	probable transposa
1482	5	6.5	317	2	S77827	probable DNA-direc
1483	5	6.5	317	2	AH2729	agmatinase [import
1484	5	6.5	317	2	A97511	hypothetical prote
1485	5	6.5	317	2	G86761	hypothetical prote
1486	5	6.5	317	2	S72457	GTP-binding regula
1487	5	6.5	317	2	S60168	hypothetical prote
1488	5	6.5	317	2	F96810	hypothetical prote
1489	5	6.5	317	2	H83775	hypothetical prote
			317	2	A83783	hypothetical prote

1490	5	6.5	317	2	T28277	ORF MSV116 hypothe
1491	5	6.5	318	2	A58888	NADH2 dehydrogenas
1492	5	6.5	318	2	T11493	NADH2 dehydrogenas
1493	5	6.5	318	2	T10972	NADH2 dehydrogenas
1494	5	6.5	318	2	E70609	dihydropteroate sy
1495	5	6.5	318	2	E64082	methionyl-tRNA for
1496	5	6.5	318	2	A83452	probable cytochrom
1497	5	6.5	318	2	H96535	hypothetical prote
1498	5	6.5	318	2	A32816	hypothetical prote
1499	5	6.5	318	2	H71406	probable reverse t
1500	5	6.5	318	2	B95883	probable transcrip

ALIGNMENTS

RESULT 1
WQECFP
L-fucose permease - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 31-Dec-1989 #sequence revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: JS0184; C33495; S49565; E65062
R;Lu, Z.; Lin, E.C.C.
Nucleic Acids Res. 17, 4883-4884, 1989
A;Title: The nucleotide sequence of Escherichia coli genes for L-fucose dissimilation.
A;Reference number: S04702; MUID:89315234; PMID:2664711
A;Accession: JS0184
A;Molecule type: DNA
A;Residues: 1-438 <LUZ>
A;Cross-references: UNIPROT:P11551; EMBL:X15025; NID:g41501; PIDN:CAA33126.1; PID:g41504
R;Chen, Y.M.; Lu, Z.; Lin, E.C.C.
J. Bacteriol. 171, 6097-6105, 1989
A;Title: Constitutive activation of the fucAO operon and silencing of the divergently tr
A;Reference number: A33495; MUID:90036697; PMID:2553671
A;Accession: C33495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <CHE>
A;Cross-references: GB:M31059; NID:g146040; NID:g146041
R;Gunn, F.J.; Tate, C.G.; Henderson, P.J.F.
Mol. Microbiol. 12, 799-809, 1994
A;Title: Identification of a novel sugar-H(+) symport protein, FucP, for transport of L-f
A;Reference number: S49564; MUID:94328931; PMID:8052131
A;Accession: S49565
A;Molecule type: protein
A;Residues: 2-21 <GDN>
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E65062
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-438 <BLAT>
A;Cross-references: GB:AE000364; GB:U00096; NID:g2367162; PIDN:AAC75843.1; PID:g1789166;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: fucP
A;Map position: 60 min
C;Function:
A;Description: this protein is a permease involved in an inducible catabolic pathway for
C;Superfamily: fucose permease
C;Keywords: L-fucose catabolism; L-fucose utilization; transmembrane protein

Query Match   10.4%; Score 8; DB 1; Length 438;
Best Local Similarity   100.0%; Pred. No. 1.5;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   27 ALTLCSAF 34
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Db   353 ALTLCSAF 360

RESULT 2
AI0862
L-fucose permease [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0862
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02801.1; PID:g16504055; GSPDB:GN00176
C;Genetics:
A;Gene: STY3115
C;Superfamily: fucose permease

Query Match   10.4%;   Score 8; DB 2;   Length 438;
Best Local Similarity   100.0%;   Pred. No. 1.5;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   27 ALTLCSAF 34
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Db   353 ALTLCSAF 360

RESULT 3
E91086
fucose permease [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91086
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21152231; PMID:11258796
A;Accession: E91086
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438 <HAY>
A;Cross-references: UNIPROT:Q8X6R7; GB:BA000007; PIDN:BAB37084.1; PID:g13363133; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3661
C;Superfamily: fucose permease

Query Match   10.4%;   Score 8; DB 2;   Length 438;
Best Local Similarity   100.0%;   Pred. No. 1.5;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   27 ALTLCSAF 34
          ||||||||
Db   353 ALTLCSAF 360

RESULT 4
G85931
fucose permease [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85931
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, U.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85931
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438 <STO>
A;Cross-references: UNIPROT:Q8X6R7; GB:AE005174; NID:g12517280; PIDN:AAG57915.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: fucP
C;Superfamily: fucose permease

Query Match   10.4%;   Score 8; DB 2;   Length 438;
Best Local Similarity   100.0%;   Pred. No. 1.5;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   27 ALTLCSAF 34
          ||||||||
Db   353 ALTLCSAF 360

RESULT 5
A86643
hypothetical protein ybeH [imported] - Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86643
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
A;Cross-references: UNIPROT:Q9CJ61; GB:AE005176; PIDN:AAK04243.1; PID:g12722994; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ybeH

Query Match   9.1%;   Score 7; DB 2;   Length 183;
Best Local Similarity   100.0%;   Pred. No. 8.4;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   17 IATIMVL 23
          |||||||
Db   17 IATIMVL 23

RESULT 6
D86856
hypothetical protein ytcA [imported] - Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86856
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86856
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-197 <STO>
A;Cross-references: UNIPROT:Q9CEI9; GB:AE005176; PIDN:AAK05950.1; PID:g12724883; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ytcA

Query Match   9.1%;   Score 7; DB 2;   Length 197;
Best Local Similarity   100.0%;   Pred. No. 8.9;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   17 IATIMVL 23

iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B86040
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <STO>
A;Cross-references: UNIPROT:Q8X580; GB:AE005174; NID:g12518397; PIDN:AAG58785.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ttk
C;Superfamily: hypothetical protein HI0955

Query Match   9.1%;   Score 7; DB 2;   Length 212;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   47 ILQSLAL 53
            |||||||
Db   29 ILQSLAL 35

RESULT 10
C65165
ttk protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: C65165; S07954; B05110
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65165
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-212 <BLAT>
A;Cross-references: UNIPROT:Q8X580; GB:AE000441; GB:U00096; NID:g1790063; PIDN:AAC76665.1
A;Experimental source: strain K-12, substrain MG1655
R;Lundberg, L.G.; Thoresson, H.O.; Karlstroem, O.H.; Nyman, P.O.
EMBO J. 2, 967-971, 1983
A;Title: Nucleotide sequence of the structural gene for dUTPase of Escherichia coli K-12
A;Reference number: A30388; MUID:84057777; PMID:6139280
A;Accession: S07954
A;Molecule type: DNA
A;Residues: 15-209, 'SCSNMTPDFSSGEFL' <LUN>
A;Cross-references: EMBL:V01578; NID:g41299; PIDN:CAA24898.1; PID:g41301
R;Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.
Eur. J. Biochem. 135, 223-229, 1983
A;Title: Nucleotide sequence of the Escherichia coli pyrB gene and of the DNA in front of
A;Reference number: A05110; MUID:8287414; PMID:6349999
A;Accession: B05110
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 199-209, 'SCSNMTPDFSSGEFL' <POU>
A;Cross-references: EMBL:V01578
C;Genetics:
A;Gene: ttk
C;Superfamily: hypothetical protein HI0955

Query Match   9.1%;   Score 7; DB 2;   Length 212;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   47 ILQSLAL 53
            |||||||
Db   29 ILQSLAL 35

RESULT 11
F86545
hypothetical protein CPj0440 [imported] - Chlamydophila pneumoniae (strain J138)

Db   28 IATIMVL 34
            ||||||

RESULT 7
AI0970
probable TeR-family transcription regulator STY4062 [imported] - Salmonella enterica su
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence revision 18-Nov-2002
C;Accession: AI0970
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
.S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0970
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03261.1; PID:g16504882; GSPDB:GN00176
C;Genetics:
A;Gene: STY4062
C;Superfamily: hypothetical protein HI0955

Query Match   9.1%;   Score 7; DB 2;   Length 198;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   47 ILQSLAL 53
            |||||||
Db   15 ILQSLAL 21

RESULT 8
D91193
probable transcription regulator [imported] - Escherichia coli (strain O157:H7, substrai
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91193
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91193
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <HAY>
A;Cross-references: UNIPROT:Q8X580; GB:BA000007; PIDN:BAB37939.1; PID:g13363991; GSPDB:C
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4516
C;Superfamily: hypothetical protein HI0955

Query Match   9.1%;   Score 7; DB 2;   Length 212;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   47 ILQSLAL 53
            |||||||
Db   29 ILQSLAL 35

RESULT 9
B86040
probable transcription regulator ttk [imported] - Escherichia coli (strain O157:H7, subs
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86545
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <STO>
A;Cross-references: UNIPROT:Q9Z8A3; GB:BA000008; NID:g8978812; PIDN:BAA98648.1; GSPDB:GN
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0440
C;Superfamily: Chlamydophila pneumoniae hypothetical protein CP0313

Query Match   9.1%;   Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 LCFALTL 30
       |||||||
Db   54 LCFALTL 60

RESULT 12
F72077
hypothetical protein CP0313 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: F72077; D81590
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: D81590
A;Molecule type: DNA
A;Residues: 1-212 <ARN>
A;Cross-references: UNIPROT:Q9Z8A3; GB:AE001627; GB:AE001363; NID:g4376721; PIDN:AAD1858
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.J.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: D81590
A;Molecule type: DNA
A;Residues: 1-212 <REA>
A;Cross-references: GB:AE002194; GB:AE002161; NID:g7189238; PIDN:AAF38169.1; PID:g7189924
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0440; CP0313
C;Superfamily: Chlamydophila pneumoniae hypothetical protein CP0313

Query Match   9.1%;   Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 LCFALTL 30
       |||||||
Db   54 LCFALTL 60

RESULT 13
G83761
polysaccharide deacetylase (nodulation protein NodB) BH0895 [imported] - Bacillus halodu
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83761
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

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A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <STO>
A;Cross-references: UNIPROT:Q9KEF7; GB:BA000004; NID:g10173440; PIDN:BAB0461
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0895
C;Superfamily: nodulation protein nodB; nodB homology

Query Match   9.1%;   Score 7; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 11;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   41 LALIFCI 47
       |||||||
Db   7 LALIFCI 13

RESULT 14
AF0215
probable 4-hydroxyphenylacetate permease hpaX [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0215
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; P
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <KUR>
A;Cross-references: UNIPROT:Q8ZFE6; GB:AL590842; PIDN:CAC90586.1; PID:g15979793; GSPDB:GN
C;Genetics:
A;Gene: hpaX

Query Match   9.1%;   Score 7; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 18;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   17 IATIMVL 23
       |||||||
Db   103 IATIMVL 109

RESULT 15
AF0631
probable 4-hydroxyphenylacetate permease hpaX [imported] - Salmonella enterica subsp. ent
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0631
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0631
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08233.1; PID:g16502280; GSPDB:GN00176
C;Genetics:
A;Gene: hpaX

Query Match   9.1%;   Score 7; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 18;

Fri Apr 8 09:08:00 2005

us-10-063-563-56.olig.rpr.spdl

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 IATIMVL 23
      |||||||
Db 103 IATIMVL 109

Search completed: April 7, 2005, 04:48:23
Job time : 83 secs

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                 GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       April 7, 2005, 04:43:34 ; Search time 184 Seconds
                                          (without alignments)
                                          214.294 Million cell updates/sec

Title:        US-10-063-563-56
Perfect score: 77
Sequence:     1 MGPVKQLKRMFEPTRLIATI.........LSFIPFARDAVKKCFAVCLA 77

Scoring table: OLIGO
              Gapop 60.0 , Gapext 60.0
Searched:     1612378 seqs, 512079187 residues
Word size :   0

Total number of hits satisfying chosen parameters:      1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :    UniProt_03:*
              1: uniprot_sprot:*
              2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	77	2	Q6UWR8	homo sapien
2	77	100.0	160	2	O95562	homo sapien
3	22	28.6	159	2	Q8VD57	mus musculu
4	20	26.0	161	2	Q7T375	brachydanio
5	9	11.7	113	2	Q86F94	schistosoma
6	8	10.4	136	2	Q922U5	mus musculu
7	8	10.4	159	2	Q8WV19	homo sapien
8	8	10.4	178	2	Q9UIC7	homo sapien
9	8	10.4	438	1	FUCP_ECOLI	escherichia
10	8	10.4	438	2	Q8Z430	salmonella
11	8	10.4	438	2	Q8FEE8	escherichia
12	8	10.4	438	2	Q83QC8	shigella fl
13	8	10.4	438	2	Q8X6R7	escherichia
14	8	10.4	668	2	Q69WI1	oryza sativ
15	8	10.4	898	2	Q82T85	nitrosomona
16	7	9.1	121	2	Q7R543	giardia lam
17	7	9.1	138	1	Y4BI_RHISN	rhizobium s
18	7	9.1	141	2	Q64B27	uncultured
19	7	9.1	163	2	Q9VPD4	drosophila
20	7	9.1	183	2	Q9CJ61	lactococcus
21	7	9.1	188	2	Q74AN2	geobacter s
22	7	9.1	197	2	Q9CEI9	lactococcus
23	7	9.1	198	1	TTK_ECOLI	escherichia
24	7	9.1	198	2	Q8Z2H4	salmonella
25	7	9.1	198	2	Q8ZL46	salmonella
26	7	9.1	211	2	Q93V18	salmonella
27	7	9.1	212	1	Y440_CHLPN	chlamydia p
28	7	9.1	212	2	Q8FC86	escherichia
29	7	9.1	212	2	Q8X580	escherichia
30	7	9.1	236	2	Q7WFX7	bordetella
31	7	9.1	247	2	Q99Y48	streptococc
32	7	9.1	252	2	Q8NZG8	streptococc
33	7	9.1	252	2	Q7CMT5	streptococc
34	7	9.1	258	2	Q82316	chlamydophi
35	7	9.1	264	2	Q9KEF7	bacillus ha
36	7	9.1	290	2	Q6N3D2	rhodopseudo
37	7	9.1	309	2	Q8RGW4	fusobacteri
38	7	9.1	312	2	Q7JNP8	caenorhabdi
39	7	9.1	314	1	OXI1_HUMAN	homo sapien
40	7	9.1	322	2	Q8N4F4	homo sapien
41	7	9.1	369	2	Q9ANK6	bradyrhizob
42	7	9.1	383	2	Q89TQ9	bradyrhizob
43	7	9.1	399	2	Q9VYR3	drosophila
44	7	9.1	404	2	Q8P7Q1	xanthomonas
45	7	9.1	455	2	Q66BX2	yersinia ps
46	7	9.1	455	2	Q8ZFE6	yersinia pe
47	7	9.1	458	2	Q46984	escherichia
48	7	9.1	458	2	Q9RPV1	salmonella
49	7	9.1	458	2	Q8Z7P8	salmonella
50	7	9.1	458	2	Q8ZQ46	salmonella
51	7	9.1	501	2	Q7N7X0	photorhabdu
52	7	9.1	501	2	Q72T83	leptospira
53	7	9.1	501	2	Q8F257	leptospira
54	7	9.1	516	2	Q82TS0	nitrosomona
55	7	9.1	566	2	Q9SCL5	arabidopsis
56	7	9.1	569	2	P95915	sulfolobus
57	7	9.1	595	2	Q9CA08	arabidopsis
58	7	9.1	672	2	Q8Y8M4	listeria mo
59	7	9.1	672	2	Q92DE2	listeria in
60	7	9.1	672	2	Q721U2	listeria mo
61	7	9.1	760	2	Q8EBB5	shewanella
62	7	9.1	872	2	Q7SBD4	neurospora
63	7	9.1	1148	2	Q6SL97	botrytis ci
64	7	9.1	1216	2	O59901	emericella
65	7	9.1	1229	2	Q881Y1	pseudomonas
66	7	9.1	3590	2	Q84MP8	oryza sativ
67	6	7.8	53	2	O6LCD6	xenopus lae
68	6	7.8	68	2	Q97830	human immun
69	6	7.8	68	2	Q8NXN7	staphylococ
70	6	7.8	68	2	Q6GBB4	staphylococ
71	6	7.8	70	2	Q6GIS6	staphylococ
72	6	7.8	71	2	Q6UB57	hyaloperono
73	6	7.8	73	2	Q8WS64	glossina mo
74	6	7.8	77	2	Q94179	caenorhabdi
75	6	7.8	77	2	Q8LAD7	arabidopsis
76	6	7.8	78	1	YDH2_PLAFS	plasmodium
77	6	7.8	80	2	Q7WXD5	alcaligenes
78	6	7.8	80	2	Q8EBU3	shewanella
79	6	7.8	82	2	Q7PCA6	lycopersico
80	6	7.8	83	2	Q7PCA8	lycopersico
81	6	7.8	92	2	Q75YW1	euhadra dec
82	6	7.8	92	2	Q75YW4	euhadra dec
83	6	7.8	92	2	Q75Z57	euhadra dec
84	6	7.8	92	2	Q75Z78	euhadra dec
85	6	7.8	93	2	O21343	euhadra her
86	6	7.8	93	2	Q75YN9	aegista ele
87	6	7.8	93	2	Q75YQ1	euhadra pel
88	6	7.8	93	2	Q75YQ4	euhadra aom
89	6	7.8	93	2	Q75YQ7	euhadra qua
90	6	7.8	93	2	Q75YR0	euhadra qua
91	6	7.8	93	2	Q75YR3	euhadra qua
92	6	7.8	92	2	Q75YS2	euhadra aom
93	6	7.8	93	2	Q75YS5	euhadra gra
94	6	7.8	93	2	Q75YS8	euhadra aom
95	6	7.8	93	2	Q75YT1	euhadra qua
96	6	7.8	93	2	Q75YT7	euhadra san
97	6	7.8	93	2	Q75YU0	euhadra her
98	6	7.8	93	2	Q75YU3	euhadra san
99	6	7.8	93	2	Q75YU6	euhadra dix
100	6	7.8	93	2	Q75YU9	euhadra qua
101	6	7.8	93	2	Q75YV5	euhadra idz
102	6	7.8	93	2	Q75YX0	euhadra san
103	6	7.8	93	2	Q75YX3	euhadra nac
104	6	7.8	93	2	Q75YY2	euhadra qua

No.	ID	Code	N	Len	pH	x		No.	ID	Code	N	Len	pH	x
105	Q75YY8	Q75YY8 euhadra qua	2	93	7.8	6		178	Q6MAG8	Q6MAG8 parachlamyd	2	153	7.8	6
106	Q75YZ1	Q75YZ1 euhadra aom	2	93	7.8	6		179	Q64S35	Q64S35 bacteroides	2	154	7.8	6
107	Q75YZ4	Q75YZ4 euhadra qua	2	93	7.8	6		180	Q7YVB3	Q7YVB3 trypanosoma	2	155	7.8	6
108	Q75YZ7	Q75YZ7 euhadra sig	2	93	7.8	6		181	Q8CR73	Q8CR73 staphylococ	2	155	7.8	6
109	Q75Z00	Q75Z00 euhadra qua	2	93	7.8	6		182	IBP_BUCAI	P57640 buchnera ap	1	157	7.8	6
110	Q75Z06	Q75Z06 euhadra qua	2	93	7.8	6		183	Q8A843	Q8A843 bacteroides	2	159	7.8	6
111	Q75Z12	Q75Z12 euhadra eoa	2	93	7.8	6		184	Q6MAD7	Q6MAD7 parachlamyd	2	159	7.8	6
112	Q75Z15	Q75Z15 euhadra lat	2	93	7.8	6		185	Q88KX3	Q88KX3 pseudomonas	2	160	7.8	6
113	Q75Z18	Q75Z18 euhadra her	2	93	7.8	6		186	Q91046	Q91046 pseudomonas	2	160	7.8	6
114	Q75Z21	Q75Z21 euhadra lat	2	93	7.8	6		187	Q96XI4	Q96XI4 sulfolobus	2	161	7.8	6
115	Q75Z24	Q75Z24 euhadra san	2	93	7.8	6		188	Q884H5	Q884H5 pseudomonas	2	161	7.8	6
116	Q75Z27	Q75Z27 euhadra idz	2	93	7.8	6		189	Q9NEC2	Q9NEC2 leishmania	2	163	7.8	6
117	Q75Z30	Q75Z30 euhadra gra	2	93	7.8	6		190	Q98G82	Q98G82 rhizobium l	2	164	7.8	6
118	Q75Z33	Q75Z33 euhadra con	2	93	7.8	6		191	Q84XV5	Q84XV5 aloe vera (	2	165	7.8	6
119	Q75Z36	Q75Z36 euhadra sen	2	93	7.8	6		192	SSRP_SYNPX	Q7U9W8 synechococc	1	166	7.8	6
120	Q75Z39	Q75Z39 euhadra her	2	93	7.8	6		193	Q14827	Q14827 homo sapien	2	166	7.8	6
121	Q75Z42	Q75Z42 euhadra sen	2	93	7.8	6		194	Q8FT03	Q8FT03 corynebacte	2	168	7.8	6
122	Q75Z45	Q75Z45 euhadra con	2	93	7.8	6		195	Q8IBI9	Q8IBI9 corynebacte	2	170	7.8	6
123	Q75Z54	Q75Z54 euhadra sen	2	93	7.8	6		196	Q9HEZ6	Q9HEZ6 plasmodium	2	173	7.8	6
124	Q75Z60	Q75Z60 euhadra eoa	2	93	7.8	6		197	YB38_METJA	Q58538 methanococc	1	174	7.8	6
125	Q75Z66	Q75Z66 euhadra qua	2	93	7.8	6		198	Q9KAE2	Q9KAE2 bacillus ha	2	174	7.8	6
126	Q75Z72	Q75Z72 euhadra aom	2	93	7.8	6		199	CX42_THUOB	P80971 thunnus obe	1	176	7.8	6
127	Q75YY5	Q75YY5 euhadra bra	2	94	7.8	6		200	Q9XCM8	Q9XCM8 wolinella s	2	176	7.8	6
128	Q7VXQ1	Q7VXQ1 bordetella	2	94	7.8	6		201	Q9XCN3	Q9XCN3 helicobacte	2	176	7.8	6
129	Q7W649	Q7W649 bordetella	2	94	7.8	6		202	Q8BJJ7	Q8BJJ7 shewanella	2	176	7.8	6
130	Q7WI15	Q7WI15 bordetella	2	94	7.8	6		203	Q9DAP4	Q9DAP4 mus musculu	2	176	7.8	6
131	Q91N51	Q91N51 mokola viru	2	96	7.8	6		204	Q9QUL5	Q9QUL5 mus musculu	2	176	7.8	6
132	Q91N52	Q91N52 mokola viru	2	96	7.8	6		205	Q59038	Q59038 methanococc	2	177	7.8	6
133	Q91N53	Q91N53 mokola viru	2	96	7.8	6		206	YG44_METJA	Q6CDQ8 yarrowia li	1	177	7.8	6
134	Q91N54	Q91N54 mokola viru	2	96	7.8	6		207	Q90QJ3	Q90QJ3 caprine art	2	177	7.8	6
135	Q9QM94	Q9QM94 mokola viru	2	96	7.8	6		208	Q9XCN1	Q9XCN1 helicobacte	2	178	7.8	6
136	Q9QM95	Q9QM95 mokola viru	2	96	7.8	6		209	Q9XCN7	Q9XCN7 helicobacte	2	178	7.8	6
137	Q9QM96	Q9QM96 mokola viru	2	96	7.8	6		210	Q9XCN0	Q9XCN0 helicobacte	2	179	7.8	6
138	Q9QM97	Q9QM97 mokola viru	2	96	7.8	6		211	Q9XCN5	Q9XCN5 helicobacte	2	179	7.8	6
139	Q9QM98	Q9QM98 mokola viru	2	96	7.8	6		212	Q9F3P0	Q9F3P0 streptomyce	2	179	7.8	6
140	Q9QM99	Q9QM99 mokola viru	2	96	7.8	6		213	Q821E7	Q821E7 chlamydophi	2	180	7.8	6
141	Q7R1F2	Q7R1F2 giardia lam	2	106	7.8	6		214	Q8FIU3	Q8FIU3 escherichia	2	181	7.8	6
142	Q6YYC7	Q6YYC7 oryza sativ	2	106	7.8	6		215	Q8FKW6	Q8FKW6 escherichia	2	181	7.8	6
143	Q6NK95	Q6NK95 corynebacte	2	110	7.8	6		216	Q8XFD0	Q8XFD0 escherichia	2	182	7.8	6
144	Q8BS41	Q8BS41 mus musculu	2	110	7.8	6		217	Q7CQB9	Q7CQB9 salmonella	2	182	7.8	6
145	Q8C5D2	Q8C5D2 mus musculu	2	112	7.8	6		218	O66744	O66744 aquifex aeo	2	183	7.8	6
146	Q62KN2	Q62KN2 burkholderi	2	115	7.8	6		219	Q7YIM3	Q7YIM3 carassius a	2	185	7.8	6
147	Q6GXQ5	Q6GXQ5 human immun	2	121	7.8	6		220	Q8E8K2	Q8E8K2 shewanella	2	188	7.8	6
148	Q8YKX8	Q8YKX8 anabaena sp	2	124	7.8	6		221	Q8CAG5	Q8CAG5 mus musculu	2	188	7.8	6
149	SP0F_BACSU	P06628 bacillus su	1	126	7.8	6		222	Q6CUF7	Q6CUF7 kluyveromyc	2	189	7.8	6
150	Q86G62	Q86G62 heterodera	2	126	7.8	6		223	Q6CXY9	Q6CXY9 kluyveromyc	2	189	7.8	6
151	Q9TG20	Q9TG20 phenacobius	2	126	7.8	6		224	Q6AAY6	Q6AAY6 propionibac	2	189	7.8	6
152	Q8UC23	Q8UC23 agrobacteri	2	130	7.8	6		225	Q7N0B3	Q7N0B3 photorhabdu	2	190	7.8	6
153	Q93QX3	Q93QX3 corynebacte	2	130	7.8	6		226	Q40853	Q40853 picea glauc	2	197	7.8	6
154	Q8NSP7	Q8NSP7 corynebacte	2	133	7.8	6		227	Q7MX69	Q7MX69 porphyromon	2	197	7.8	6
155	BOTA_BOTJA	P22029 bothrops ja	1	133	7.8	6		228	Q7NYF4	Q7NYF4 chromobacte	2	198	7.8	6
156	Q6TAR2	Q6TAR2 homo sapien	2	133	7.8	6		229	Q6EB39	Q6EB39 campylobact	2	199	7.8	6
157	Q7CWI0	Q7CWI0 agrobacteri	2	133	7.8	6		230	Q716N8	Q716N8 mycobacteri	2	199	7.8	6
158	Q64SN8	Q64SN8 bacteroides	2	133	7.8	6		231	Q8CWB2	Q8CWB2 escherichia	2	199	7.8	6
159	Q89T51	Q89T51 bradyrhizob	2	134	7.8	6		232	Q6ZSX4	Q6ZSX4 homo sapien	2	201	7.8	6
160	Q96MR4	Q96MR4 homo sapien	2	136	7.8	6		233	Q88F43	Q88F43 pseudomonas	2	202	7.8	6
161	Q82J77	Q82J77 streptomyce	2	137	7.8	6		234	Q8WWA1	Q8WWA1 homo sapien	2	203	7.8	6
162	Q90QJ4	Q90QJ4 caprine art	2	138	7.8	6		235	Q9NUZ4	Q9NUZ4 homo sapien	2	203	7.8	6
163	Q7PYU9	Q7PYU9 anopheles g	2	142	7.8	6		236	Q8ID59	Q8ID59 plasmodium	2	205	7.8	6
164	Q6ARU7	Q6ARU7 desulfotale	2	142	7.8	6		237	Q6GDT4	Q6GDT4 staphylococ	2	205	7.8	6
165	Q9PSM6	Q9PSM6 bothrops ja	2	144	7.8	6		238	Q7QS93	Q7QS93 giardia lam	2	206	7.8	6
166	Q9RHG3	Q9RHG3 mycobacteri	2	144	7.8	6		239	Q8Z0A2	Q8Z0A2 nitrosomona	2	206	7.8	6
167	Q64BI5	Q64BI5 uncultured	2	145	7.8	6		240	Q8I2G3	Q8I2G3 plasmodium	2	207	7.8	6
168	Q6L166	Q6L166 picrophilus	2	145	7.8	6		241	Q7QID5	Q7QID5 anopheles g	2	207	7.8	6
169	Q706N8	Q706N8 pseudomonas	2	146	7.8	6		242	Q7V0B2	Q7V0B2 prochloroco	2	208	7.8	6
170	Q9D546	Q9D546 mus musculu	2	146	7.8	6		243	RHO1_ENTHI	P31021 entamoeba h	1	208	7.8	6
171	Q63CD3	Q63CD3 bacillus ce	2	148	7.8	6		244	O27538	O27538 methanobact	2	208	7.8	6
172	Q81RL1	Q81RL1 bacillus an	2	148	7.8	6		245	Q894K8	Q894K8 clostridium	2	208	7.8	6
173	Q64B21	Q64B21 uncultured	2	149	7.8	6		246	Q8EET3	Q8EET3 shewanella	2	209	7.8	6
174	Q6AQX3	Q6AQX3 desulfotale	2	151	7.8	6		247	Q8IZ66	Q8IZ66 homo sapien	2	209	7.8	6
175	Q8CA26	Q8CA26 mus musculu	2	152	7.8	6		248	Q96196	Q96196 plasmodium	2	209	7.8	6
176	Q6BV00	Q6BV00 debaryomyce	2	153	7.8	6		249	Q6YSX2	Q6YSX2 oryza sativ	2	209	7.8	6
177	Q6WU84	Q6WU84 lactobacill	2	153	7.8	6		250	Q8VCT8	Q8VCT8 mus musculu	2	209	7.8	6

No.			Organism	Code	ID	Cnt	Num
251	7.8	6	entamoeba h	Q8i890	Q8I890	2	210
252	7.8	6	drosophila	Q71df1	Q71DF1	2	211
253	7.8	6	acinetobact	Q6f9t3	Q6F9T3	2	212
254	7.8	6	entamoeba h	Q8i892	Q8I892	2	212
255	7.8	6	entamoeba h	Q8i893	Q8I893	2	212
256	7.8	6	entamoeba h	Q8i894	Q8I894	2	212
257	7.8	6	entamoeba h	Q95td4	Q95TD4	2	213
258	7.8	6	drosophila	Q9vx96	Q9VX96	2	215
259	7.8	6	drosophila	Q9v8a7	Q9V8A7	2	216
260	7.8	6	homo sapien	Q9h1c6	Q9H1C6	2	218
261	7.8	6	citrobacter	Q7x242	Q7X242	2	220
262	7.8	6	mus musculu	035660	GTM6_MOUSE	1	220
263	7.8	6	saccharomyc	P53927	YNL0_YEAST	1	220
264	7.8	6	bartonella	Q6g0j1	Q6G0J1	2	221
265	7.8	6	bartonella	Q6g4p4	Q6G4P4	2	222
266	7.8	6	entamoeba h	Q8i891	Q8I891	2	225
267	7.8	6	mycobacteri	Q9lbq2	Q9LBQ2	2	225
268	7.8	6	tenebrio mo	Q27013	Q27013	2	225
269	7.8	6	tenebrio mo	Q27014	Q27014	2	227
270	7.8	6	escherichia	Q8fcy7	Q8FCY7	2	228
271	7.8	6	mus musculu	Q8vcr5	Q8VCR5	2	228
272	7.8	6	prochloroco	Q7v8w1	Q7V8W1	2	231
273	7.8	6	acinetobact	Q6ffn5	Q6FFN5	2	232
274	7.8	6	geobacter s	Q748p3	Q748P3	2	232
275	7.8	6	wolinella s	Q7mrj9	Q7MRJ9	2	233
276	7.8	6	streptomyce	Q93j82	Q93J82	2	234
277	7.8	6	mus musculu	Q9d5j8	Q9D5J8	2	234
278	7.8	6	homo sapien	Q8nal4	Q8NAL4	2	234
279	7.8	6	homo sapien	P32971	TNF8_HUMAN	1	236
280	7.8	6	sulfolobus	Q96yp6	Q96YP6	2	238
281	7.8	6	prochloroco	Q7v2q7	Q7V2Q7	2	238
282	7.8	6	xylella fas	Q87bc9	Q87BC9	2	239
283	7.8	6	symbiobacte	Q67lc3	Q67LC3	2	240
284	7.8	6	bradyrhizob	Q89j84	RL3_BRAJA	1	240
285	7.8	6	legionella	Q8rtn7	Q8RTN7	2	240
286	7.8	6	legionella	Q9s4s9	Q9S4S9	2	240
287	7.8	6	pyrobaculum	Q8zuz3	Q8ZUZ3	2	241
288	7.8	6	caenorhabdi	Q9xxt4	Q9XXT4	2	241
289	7.8	6	bdellovibri	Q6mil1	Q6MIL1	2	241
290	7.8	6	wolbachia p	Q73h87	Q73H87	2	241
291	7.8	6	gallus gall	Q800j1	Q800J1	2	243
292	7.8	6	rhodopseudo	P60456	RLJ_RHOPA	1	243
293	7.8	6	staphylococc	P67061	UBIE_STAAN	1	244
294	7.8	6	staphylococc	P67062	UBIE_STAAN	1	245
295	7.8	6	staphylococc	P67063	UBIE_STAAW	1	245
296	7.8	6	staphylococc	Q6g992	Q6G992	2	245
297	7.8	6	staphylococc	Q6ggu0	Q6GGU0	2	246
298	7.8	6	arabidopsis	Q9lvh9	Q9LVH9	2	246
299	7.8	6	listeria mo	Q8y8h4	Q8Y8H4	2	247
300	7.8	6	listeria in	Q92d87	Q92D87	2	247
301	7.8	6	enterococcu	Q82zj9	Q82ZJ9	2	247
302	7.8	6	pseudomonas	P05104	T2P7_PSEAE	1	247
303	7.8	6	homo sapien	Q8ncl8	Q8NCL8	2	247
304	7.8	6	homo sapien	Q6nsh5	Q6NSH5	2	247
305	7.8	6	streptococc	Q7wt43	Q7WT43	2	247
306	7.8	6	agrobacteri	Q8ua62	Q8UA62	2	247
307	7.8	6	streptococc	Q8cm62	Q8CM62	2	247
308	7.8	6	escherichia	Q8x8u9	COBS_ECO57	1	247
309	7.8	6	escherichia	Q8fga4	COBS_ECOL6	1	247
310	7.8	6	escherichia	P36561	COBS_ECOLI	1	247
311	7.8	6	salmonella	Q8z5n8	COBS_SALTI	1	247
312	7.8	6	salmonella	Q05602	COBS_SALTY	1	253
313	7.8	6	shigella fl	Q83r13	COBS_SHIFL	1	253
314	7.8	6	schizosacch	P78834	P78834	2	253
315	7.8	6	oryzias lat	Q9mx51	Q9MX51	2	255
316	7.8	6	oryza sativ	Q8lir7	Q8LIR7	2	255
317	7.8	6	shewanella	Q8eccs	Q8ECC5	2	256
318	7.8	6	methanobact	027844	Y116_METTH	1	256
319	7.8	6	wautersia o	Q84eg6	Q84E06	2	256
320	7.8	6	brachydanio	Q6nx94	Q6NX94	2	256
321	7.8	6	caulobacter	Q9a8v3	RLJ_CAUCR	1	256
322	7.8	6	vibrio mimi	Q76bt0	Q76BT0	2	256
323	7.8	6	homo sapien	Q96i22	Q96I22	2	256

No.			Organism	Code	ID	Cnt	Num
324	7.8	6	shewanella	Q8egg3	Q8EGG3	2	256
325	7.8	6	staphylococc	Q8nyk8	Q8NYK8	2	257
326	7.8	6	staphylococc	Q932k6	Q932K6	2	257
327	7.8	6	staphylococc	Q99x12	Q99X12	2	257
328	7.8	6	leptospira	Q75ff8	Q75FF8	2	257
329	7.8	6	leptospira	Q8exb2	Q8EXB2	2	257
330	7.8	6	pasteurella	Q9cjx6	Q9CJX6	2	257
331	7.8	6	staphylococc	Q6gcr5	Q6GCR5	2	259
332	7.8	6	lactococcus	087232	087232	2	259
333	7.8	6	enterococcu	Q837y4	Q837Y4	2	260
334	7.8	6	corynebacte	Q8nt23	Q8NT23	2	260
335	7.8	6	corynebacte	Q8fs88	Q8FS88	2	260
336	7.8	6	rhesus cyto	Q7tfn5	Q7TFN5	2	261
337	7.8	6	brachydanio	Q9miy4	COX3_BRARE	1	261
338	7.8	6	carassius a	Q96133	COX3_CARAU	1	261
339	7.8	6	cyprinus ca	P15952	COX3_CYPCA	1	261
340	7.8	6	crenimugil	Q94pr1	Q94PR1	2	261
341	7.8	6	arctoscopus	Q94qg5	Q94QG5	2	261
342	7.8	6	platichthys	Q94s84	Q94S84	2	261
343	7.8	6	gasterosteu	Q94sh5	Q94SH5	2	261
344	7.8	6	rondeletia	Q94sr6	Q94SR6	2	261
345	7.8	6	percopsis t	Q94t27	Q94T27	2	261
346	7.8	6	zu cristatu	Q94t48	Q94T48	2	261
347	7.8	6	trachipteru	Q94t61	Q94T61	2	261
348	7.8	6	diaphus spl	Q94t87	Q94T87	2	261
349	7.8	6	pantodon bu	Q94yn9	Q94YN9	2	261
350	7.8	6	carassius c	Q68ga7	Q68GA7	2	261
351	7.8	6	acanthogobi	Q69aw8	Q69AW8	2	261
352	7.8	6	carassius a	Q6b0m1	Q6B0M1	2	261
353	7.8	6	sebastes sc	Q6rui1	Q6RUI1	2	261
354	7.8	6	elops sauru	Q6z7z3	Q6Z7Z3	2	261
355	7.8	6	bufo melano	Q70ec9	Q70EC9	2	261
356	7.8	6	ambystoma m	Q70ee2	Q70EE2	2	261
357	7.8	6	carpiodes c	Q75uf4	Q75UF4	2	261
358	7.8	6	pagrus auri	Q75vm6	Q75VM6	2	261
359	7.8	6	auxis thaza	Q76f99	Q76F99	2	261
360	7.8	6	auxis roche	Q76g43	Q76G43	2	261
361	7.8	6	thunnus ala	Q76hg7	Q76HG7	2	261
362	7.8	6	katsuwonus	Q76hi0	Q76HI0	2	261
363	7.8	6	elops hawai	Q76md5	Q76MD5	2	261
364	7.8	6	saccopharyn	Q76mh4	Q76MH4	2	261
365	7.8	6	mugil cepha	Q7hjl3	Q7HJL3	2	261
366	7.8	6	thunnus thy	Q7y7f7	Q7Y7F7	2	261
367	7.8	6	etheostoma	Q7yc36	Q7YC36	2	261
368	7.8	6	pseudobagru	Q85d40	Q85D40	2	261
369	7.8	6	galaxias ma	Q85e41	Q85E41	2	261
370	7.8	6	cobitis str	Q85e67	Q85E67	2	261
371	7.8	6	sarcocheili	Q85e80	Q85E80	2	261
372	7.8	6	euthynnus a	Q85ue5	Q85UE5	2	261
373	7.8	6	caranx mela	Q8hl09	Q8HL09	2	261
374	7.8	6	carangoides	Q8h122	Q8H122	2	261
375	7.8	6	cottus rein	Q8hl48	Q8HL48	2	261
376	7.8	6	satyrichthy	Q8hl61	Q8HL61	2	261
377	7.8	6	hypoptychus	Q8hlb2	Q8HLB2	2	261
378	7.8	6	anoplogaste	Q8hlr8	Q8HLR8	2	261
379	7.8	6	melanotaeni	Q8hlz5	Q8HLZ5	2	261
380	7.8	6	diplacantho	Q8hmd7	Q8HMD7	2	261
381	7.8	6	cataetyx ru	Q8hmf0	Q8HMF0	2	261
382	7.8	6	bassozetus	Q8hmh6	Q8HMH6	2	261
383	7.8	6	carassius c	Q9b614	Q9B614	2	261
384	7.8	6	diplophos t	Q9g6q7	Q9G6Q7	2	261
385	7.8	6	ambystoma l	Q644x8	Q644X8	2	262
386	7.8	6	albula glos	Q6zlz2	Q6ZLZ2	2	264
387	7.8	6	plasmodium	Q7rlz2	Q7RLZ2	2	265
388	7.8	6	parachlamyd	Q6ma31	Q6MA31	2	265
389	7.8	6	cyanidium c	P48873	COX3_CYACA	1	270
390	7.8	6	desulfovibr	Q8kz99	Q8KZ99	2	270
391	7.8	6	ralstonia s	Q8xzh9	LPXA_RALSO	1	271
392	7.8	6	shigella fl	Q9al46	Q9AL46	2	271
393	7.8	6	bartonella	Q6g1j1	Q6G1J1	2	271
394	7.8	6	bartonella	Q6g5c5	Q6G5C5	2	272
395	7.8	6	photorhabdu	Q7n0b9	UPPP_PHOLL	1	272
396	7.8	6	escherichia	Q8vqp9	Q8VQP9	2	272

Left block

No.			Len	Mult	Accession	Organism
397	6	7.8	272	2	Q8VQR4	escherichia
398	6	7.8	272	2	Q93FJ0	citrobacter
399	6	7.8	272	2	Q7D3V0	agrobacteri
400	6	7.8	272	2	Q9AJ35	escherichia
401	6	7.8	272	2	Q6D159	erwinia car
402	6	7.8	273	1	UPPP_ECO57	escherichia
403	6	7.8	273	1	UPPP_ECOL6	escherichia
404	6	7.8	273	1	UPPP_ECOLI	escherichia
405	6	7.8	273	1	UPPP_SALTI	salmonella
406	6	7.8	273	1	UPPP_SALTY	salmonella
407	6	7.8	273	1	UPPP_SHIFL	shigella fl
408	6	7.8	273	2	Q7TFX5	rhesus cyto
409	6	7.8	274	2	Q6D760	erwinia car
410	6	7.8	276	2	Q95NZ4	sarcocystis
411	6	7.8	276	2	Q7YSU2	sarcocystis
412	6	7.8	276	2	Q6LK38	photobacter
413	6	7.8	276	2	Q82BB4	streptomyce
414	6	7.8	277	2	Q6N902	rhodopseudo
415	6	7.8	277	2	Q8UJL5	agrobacteri
416	6	7.8	279	2	Q758X7	ashbya goss
417	6	7.8	279	2	Q7Z0V1	sarcocystis
418	6	7.8	279	2	Q86M54	sarcocystis
419	6	7.8	283	2	Q702E8	uncultured
420	6	7.8	283	2	Q8XNP7	clostridium
421	6	7.8	284	2	Q83JP0	shigella fl
422	6	7.8	285	2	O32731	agrobacteri
423	6	7.8	285	2	Q7CP39	agrobacteri
424	6	7.8	286	2	Q66E86	yersinia ps
425	6	7.8	286	2	Q82HK5	streptomyce
426	6	7.8	286	2	Q9X6B4	yersinia pe
427	6	7.8	288	2	Q65TR7	mannheimia
428	6	7.8	288	2	Q9DG22	gallus gall
429	6	7.8	289	2	Q9KZ73	streptomyce
430	6	7.8	290	1	SHY1_SCHPO	schizosacch
431	6	7.8	290	1	Y32K_MCMV	maize chlor
432	6	7.8	290	2	Q70JY7	bacillus am
433	6	7.8	291	2	Q7CSN3	agrobacteri
434	6	7.8	293	1	P40558	saccharomyc
435	6	7.8	293	1	YIA3_YEAST	saccharomyc
436	6	7.8	296	1	NU2M_ARTSF	artemia san
437	6	7.8	296	2	Q16085	homo sapien
438	6	7.8	298	2	Q7Y5V4	bacteriopha
439	6	7.8	299	2	Q8SB85	oryza sativ
440	6	7.8	299	2	Q8UK68	agrobacteri
441	6	7.8	300	2	Q91479	pseudomonas
442	6	7.8	301	2	Q89R49	bradyrhizob
443	6	7.8	301	2	Q6UDL6	psittacid h
444	6	7.8	302	2	Q84W69	arabidopsis
445	6	7.8	302	2	Q9FN16	arabidopsis
446	6	7.8	302	2	Q65P02	bacillus li
447	6	7.8	303	2	Q9I8S9	oncorhynchu
448	6	7.8	304	2	Q8LHB6	xenopus lae
449	6	7.8	305	2	P72579	oryza sativ
450	6	7.8	305	2	Q96Y68	sulfolobus
451	6	7.8	306	2	Q9CI00	sulfolobus
452	6	7.8	307	2	Q8D190	lactococcus
453	6	7.8	309	2	Q9XIP5	yersinia pe
454	6	7.8	310	1	PANC_ARATH	arabidopsis
455	6	7.8	310	2	Q8LEA6	arabidopsis
456	6	7.8	311	2	Q7WXS3	arabidopsis
457	6	7.8	312	1	Q7RA93	alcaligenes
458	6	7.8	312	2	P18929	plasmodium
459	6	7.8	312	2	Q9MI09	drosophila
460	6	7.8	312	1	NU1M_DROME	drosophila
461	6	7.8	314	2	Q9MI11	drosophila
462	6	7.8	315	2	Q9KKH3	yersinia en
463	6	7.8	315	2	Q662B0	borrelia ga
464	6	7.8	315	2	Q6BJA0	debaryomyce
465	6	7.8	315	2	Q6IGT5	drosophila
466	6	7.8	315	2	Q72ST8	leptospira
467	6	7.8	315	2	Q8F2P2	leptospira
468	6	7.8	315	2	Q9KGA2	bacillus ha
469	6	7.8	316	2	Q72UZ0	leptospira

Right block

No.			Len	Mult	Accession	Organism
470	6	7.8	316	2	Q6UYB9	bovine herp
471	6	7.8	316	2	Q6JWV9	brachydanio
472	6	7.8	317	2	Q8GXR5	arabidopsis
473	6	7.8	317	2	Q68EV0	xenopus lae
474	6	7.8	318	2	Q7D3I4	agrobacteri
475	6	7.8	318	2	Q82MD4	streptomyce
476	6	7.8	319	2	Q740U3	mycobacteri
477	6	7.8	320	2	Q7Q4X6	anopheles g
478	6	7.8	320	2	Q64VQ7	bacteroides
479	6	7.8	321	2	Q9VMP1	drosophila
480	6	7.8	325	2	Q966M0	caenorhabdi
481	6	7.8	325	2	Q7Q728	anopheles g
482	6	7.8	325	2	Q93F20	shigella fl
483	6	7.8	326	1	Y370_MYCPN	mycoplasma
484	6	7.8	326	2	Q8XYG0	ralstonia s
485	6	7.8	326	2	Q98UW4	hepatitis c
486	6	7.8	328	1	LGT_BORBU	borrelia bu
487	6	7.8	328	2	Q63HP2	homo sapien
488	6	7.8	328	2	Q661Q7	borrelia ga
489	6	7.8	328	2	Q8XU53	ralstonia s
490	6	7.8	329	2	Q6CNE4	kluyveromyc
491	6	7.8	329	2	Q65MR6	bacillus li
492	6	7.8	329	2	Q7NQ17	chromobacte
493	6	7.8	330	2	Q16086	homo sapien
494	6	7.8	331	2	Q8Y5Q8	listeria mo
495	6	7.8	331	2	Q92A16	listeria in
496	6	7.8	331	2	Q71Y24	listeria mo
497	6	7.8	332	1	FBCC_ECOLI	escherichia
498	6	7.8	332	2	Q8EJ33	shewanella
499	6	7.8	333	2	Q7R4X8	giardia lam
500	6	7.8	333	2	Q9MNJ4	helobdella
501	6	7.8	334	2	Q752L0	ashbya goss
502	6	7.8	335	2	Q8MXL9	dictyosteli
503	6	7.8	335	2	Q8U8G5	agrobacteri
504	6	7.8	336	2	Q943X2	oryza sativ
505	6	7.8	337	2	Q6BNF0	debaryomyce
506	6	7.8	338	2	Q6RWH1	uncultured
507	6	7.8	340	1	RFC3_YEAST	saccharomyc
508	6	7.8	344	2	Q8PFH6	xanthomonas
509	6	7.8	345	1	DDL_WOLSU	wolinella s
510	6	7.8	345	1	PPAN_ARATH	arabidopsis
511	6	7.8	345	2	Q9ASU7	arabidopsis
512	6	7.8	345	2	P92653	euprepis au
513	6	7.8	345	2	Q92FI4	listeria in
514	6	7.8	346	1	CNA1_SCHPO	schizosacch
515	6	7.8	346	2	Q9ZBW2	streptomyce
516	6	7.8	346	2	Q6CDZ0	yarrowia li
517	6	7.8	346	2	Q644Z6	eurycea bis
518	6	7.8	347	2	Q82M16	streptomyce
519	6	7.8	348	2	Q94RK1	chimaera mo
520	6	7.8	348	2	Q8HM26	caulophryne
521	6	7.8	348	2	Q8VNZ6	bordetella
522	6	7.8	349	2	Q8EKB4	shewanella
523	6	7.8	350	2	Q9X0K3	shewanella
524	6	7.8	350	2	Q9VQ77	drosophila
525	6	7.8	350	2	Q6HW78	bacillus an
526	6	7.8	350	2	Q638N3	bacillus ce
527	6	7.8	350	2	Q734N1	bacillus ce
528	6	7.8	350	2	Q79H45	bordetella
529	6	7.8	350	2	Q81N18	bacillus an
530	6	7.8	350	2	Q6HG64	bacillus th
531	6	7.8	351	2	Q9SZ95	arabidopsis
532	6	7.8	354	2	Q9SES1	arabidopsis
533	6	7.8	354	2	Q8XKQ3	clostridium
534	6	7.8	354	2	Q8YBQ5	brucella me
535	6	7.8	355	2	Q8R0N5	mus musculu
536	6	7.8	357	1	HAL2_YEAST	saccharomyc
537	6	7.8	357	2	Q6RFY5	saccharomyc
538	6	7.8	357	2	Q69XT6	oryza sativ
539	6	7.8	357	2	Q9DG23	gallus gall
540	6	7.8	359	2	Q9BWF8	homo sapien
541	6	7.8	359	2	Q90634	gallus gall
542	6	7.8	360	1	MRAY_SHEON	shewanella

No.			Len	N	ID	Accession	Organism
543	6	7.8	360	1	MRAY_SHEVI	Q9fin3	shewanella
544	6	7.8	361	1	P2Y4_MOUSE	Q9jj87	mus musculu
545	6	7.8	363	2	Q6CIQ8	Q6ciq8	kluyveromyc
546	6	7.8	364	2	Q9X092	Q9x092	streptococc
547	6	7.8	365	2	Q9X092	Q9x092	thermotoga
548	6	7.8	366	2	Q6BNJ1	Q6bnj1	debaryomyce
549	6	7.8	366	2	Q7NVB3	Q7nvb3	chromobacte
550	6	7.8	366	2	Q7TUW1	Q7tuw1	prochloroco
551	6	7.8	368	2	Q9H841	Q9h841	homo sapien
552	6	7.8	368	2	Q932E5	Q932e5	staphylococ
553	6	7.8	369	2	Q6QHI5	Q6qhi5	thiobacillu
554	6	7.8	371	2	Q8NXL0	Q8nxl0	staphylococ
555	6	7.8	373	2	Q937R1	Q937r1	brucella me
556	6	7.8	374	2	Q7MAT1	Q7mat1	wolinella s
557	6	7.8	374	2	Q8FWM3	Q8fwm3	brucella su
558	6	7.8	375	2	Q87XJ3	Q87xj3	pseudomonas
559	6	7.8	376	2	Q92ER5	Q92er5	anabaena sp
560	6	7.8	378	2	Q9R6Y4	Q9r6y4	anabaena sp
561	6	7.8	378	1	ARGE_MYXXA	Q68873	myxococcus
562	6	7.8	380	2	Q88DT3	Q88dt3	pseudomonas
563	6	7.8	381	2	Q9HV37	Q9hv37	pseudomonas
564	6	7.8	381	2	Q9M1W9	Q9m1w9	arabidopsis
565	6	7.8	382	2	Q9CHG7	Q9chg7	lactococcus
566	6	7.8	383	2	Q72SZ8	Q72sz8	leptospira
567	6	7.8	383	2	Q8F2H1	Q8f2h1	leptospira
568	6	7.8	384	2	Q93ZQ3	Q93zq3	arabidopsis
569	6	7.8	386	1	ICEA_XENLA	P55865	xenopus lae
570	6	7.8	386	2	Q6H7L8	Q6h7l8	oryza sativ
571	6	7.8	386	2	Q8A2B6	Q8a2b6	bacteroides
572	6	7.8	387	2	Q65Y10	Q65y10	butyrivibri
573	6	7.8	388	2	O04178	O04178	brassica ca
574	6	7.8	389	2	O82567	O82567	arabidopsis
575	6	7.8	389	2	Q74IF5	Q74if5	lactobacill
576	6	7.8	390	2	Q64Y28	Q64y28	bacteroides
577	6	7.8	392	2	Q6CPH2	Q6cph2	kluyveromyc
578	6	7.8	393	2	Q22305	Q22305	caenorhabdi
579	6	7.8	393	2	Q8LEE8	Q8lee8	arabidopsis
580	6	7.8	394	2	Q6C2Q9	Q6c2q9	yarrowia li
581	6	7.8	394	2	Q8LSZ8	Q8lsz8	arabidopsis
582	6	7.8	395	1	HMEB_ARCFU	O29750	archaeoglob
583	6	7.8	395	2	Q8L5J1	Q8l5j1	lycopersico
584	6	7.8	395	2	Q8RVL3	Q8rvl3	lycopersico
585	6	7.8	397	1	PGK_BORBR	Q7wmk9	bordetella
586	6	7.8	397	1	PGK_BORPA	Q7wb43	bordetella
587	6	7.8	397	1	PGK_BORPE	Q7vzb8	bordetella
588	6	7.8	398	2	Q06IS9	Q06is9	saccharomyc
589	6	7.8	400	2	O22204	O22204	arabidopsis
590	6	7.8	400	2	Q8FL54	Q8fl54	escherichia
591	6	7.8	401	2	Q7Y5N8	Q7y5n8	bacteriopha
592	6	7.8	401	2	Q69Y51	Q69y51	oryza sativ
593	6	7.8	402	1	PAI1_BOVIN	P13909	bos taurus
594	6	7.8	402	2	Q7X6V4	Q7x6v4	oryza sativ
595	6	7.8	402	2	Q886K0	Q886k0	streptomyce
596	6	7.8	403	2	Q913V2	Q913v2	burkholderi
597	6	7.8	403	2	Q7W236	Q7w236	bordetella
598	6	7.8	408	2	O85454	O85454	pasteurella
599	6	7.8	408	2	Q83AP2	Q83ap2	coxiella bu
600	6	7.8	408	2	Q9CMP3	Q9cmp3	pasteurella
601	6	7.8	409	2	Q8CDW9	Q8cdw9	mus musculu
602	6	7.8	409	2	Q9D408	Q9d408	mus musculu
603	6	7.8	410	2	P72973	P72973	synechocyst
604	6	7.8	411	2	Q6BYS9	Q6bys9	debaryomyce
605	6	7.8	411	2	Q62KL3	Q62kl3	burkholderi
606	6	7.8	411	2	Q63TQ2	Q63tq2	burkholderi
607	6	7.8	412	2	Q73ZB4	Q73zb4	mycobacteri
608	6	7.8	412	2	Q7Z630	Q7z630	homo sapien
609	6	7.8	414	2	Q8SR58	Q8sr58	encephalito
610	6	7.8	414	2	Q8XNH5	Q8xnh5	clostridium
611	6	7.8	417	2	Q96VU7	Q96vu7	neurospora
612	6	7.8	420	2	Q69FG3	Q69fg3	debaryomyce
613	6	7.8	422	2	Q21298	Q21298	caenorhabdi
614	6	7.8	422	2	Q6MUG5	Q6mug5	mycoplasma
615	6	7.8	423	2	Q9P417	Q9p417	cephalospor
616	6	7.8	429	2	Q8Y0K6	Q8y0k6	ralstonia s
617	6	7.8	431	2	Q6D500	Q6d500	erwinia car
618	6	7.8	433	1	COBB_PSEDE	P21632	pseudomonas
619	6	7.8	434	2	Q9XUP8	Q9xup8	caenorhabdi
620	6	7.8	434	2	Q64VY8	Q87n91	vibrio para
621	6	7.8	435	2	Q87N91	Q64vy8	bacteroides
622	6	7.8	436	2	Q86285	Q86285	diadromus p
623	6	7.8	437	2	Q75SS7	Q75ss7	rabies viru
624	6	7.8	438	1	FIBG_XENLA	P17634	xenopus lae
625	6	7.8	439	2	Q8A1L2	Q8a112	bacteroides
626	6	7.8	439	2	Q9F2N1	Q9f2n1	streptomyce
627	6	7.8	439	2	Q7SZ13	Q7sz13	xenopus lae
628	6	7.8	440	2	O30307	O30307	archaeoglob
629	6	7.8	440	2	Q9K7K2	Q9k7k2	bacillus ha
630	6	7.8	444	2	Q73NC8	Q73nc8	treponema d
631	6	7.8	444	2	Q6D8P7	Q6d8p7	erwinia car
632	6	7.8	444	2	Q72WJ6	Q72wj6	desulfovibr
633	6	7.8	445	2	Q8GQX0	Q8gqx0	selenomonas
634	6	7.8	447	2	Q8DNZ9	Q8dnz9	streptococc
635	6	7.8	447	2	Q8EKI3	Q8eki3	shewanella
636	6	7.8	448	2	Q83CC1	Q83cc1	coxiella bu
637	6	7.8	449	2	O07406	O07406	mycobacteri
638	6	7.8	449	2	Q7U2P7	Q7u2p7	mycobacteri
639	6	7.8	450	2	Q82994	Q82994	lagos bat v
640	6	7.8	450	2	Q83544	Q83544	mokola viru
641	6	7.8	450	2	Q86593	Q86593	mokola viru
642	6	7.8	450	2	Q9WJY5	Q9wjy5	rabies viru
643	6	7.8	451	2	O7NGW2	O7ngw2	gloeobacter
644	6	7.8	451	2	O66453	O66453	duvenhage v
645	6	7.8	451	2	O66532	O66532	european ba
646	6	7.8	451	2	O66533	O66533	european ba
647	6	7.8	451	2	O66534	O66534	european ba
648	6	7.8	451	2	O66535	O66535	european ba
649	6	7.8	451	2	Q6X1D4	Q6x1d4	european ba
650	6	7.8	451	2	Q6X1D8	Q6x1d8	khujand lys
651	6	7.8	451	2	O76K69	O76k69	aravan lyss
652	6	7.8	452	2	Q23660	Q23660	aravan lyss
653	6	7.8	454	2	Q9CER2	Q9cer2	caenorhabdi
654	6	7.8	454	2	Q9CFW6	Q9cfw6	lactococcus
655	6	7.8	455	2	Q91NB1	Q91nb1	lactococcus
656	6	7.8	456	2	Q7VBQ7	Q7vbq7	arabidopsis
657	6	7.8	456	2	Q8KQJ0	Q8kqj0	prochloroco
658	6	7.8	458	2	Q74CL4	Q74cl4	haemophilus
659	6	7.8	461	2	Q6ZE25	Q6ze25	geobacter s
660	6	7.8	461	2	Q8GFB5	Q8gfb5	oryza sativ
661	6	7.8	461	2	Q90Z63	Q90z63	oryza sativ
662	6	7.8	462	1	ODPB_ZYMMO	O66113	zymomonas m
663	6	7.8	462	2	Q6YD7	Q6yd7	oryza sativ
664	6	7.8	462	2	Q64Y27	Q64y27	bacteroides
665	6	7.8	463	2	Q8TNH6	Q8tnh6	methanosarc
666	6	7.8	463	2	Q9CLQ0	Q9clq0	rickettsia
667	6	7.8	465	2	Q7P902	Q7p902	shewanella
668	6	7.8	465	2	Q8ECK2	Q8eck2	mus musculu
669	6	7.8	469	1	KCC4_MOUSE	P08414	mannheimia
670	6	7.8	470	2	Q5R88	Q5r88	pseudomonas
671	6	7.8	470	2	Q8BF87	Q8bf87	paenibacill
672	6	7.8	472	2	Q6VUHO	Q6vuh0	arabidopsis
673	6	7.8	474	2	O04036	O04036	oryza sativ
674	6	7.8	476	2	Q8LQV5	Q8lqv5	oryza sativ
675	6	7.8	476	2	Q7B9Y7	Q7b9y7	brucella me
676	6	7.8	476	2	Q6DRJ6	Q6drj6	brachydanio
677	6	7.8	477	2	Q8MS56	Q8ms56	drosophila
678	6	7.8	477	2	Q9FT94	Q9ft94	arabidopsis
679	6	7.8	478	1	NUON_RHOCA	P50973	rhodobacter
680	6	7.8	478	2	Q69Y52	Q69y52	oryza sativ
681	6	7.8	478	2	Q84UY9	Q84uy9	oryza sativ
682	6	7.8	478	2	Q8YGL3	Q8ygl3	brucella me
683	6	7.8	478	2	Q8G1A4	Q8g1a4	lactobacill
684	6	7.8	480	2	Q8UFW4	Q8ufw4	brucella su
685	6	7.8	480	2	Q92QN9	Q92qn9	agrobacteri
686	6	7.8	480	2	Q6MIS6	Q6mis6	rhizobium m
687	6	7.8	480	2	Q9I482	Q9i482	bdellovibri
688	6	7.8	480	2	Q6AJ25	Q6aj25	desulfotale

Seq			ID	Ct	No	Acc	Organism
689	7.8	6	Q6FU28	2	481	Q6FU28	candida gla
690	7.8	6	Q9A6Y9	2	481	Q9A6Y9	caulobacter
691	7.8	6	ALA2_PANMI	1	482	P34106	panicum mil
692	7.8	6	Q7CZK9	2	482	Q7CZK9	agrobacteri
693	7.8	6	Q8G4U6	2	482	Q8G4U6	bifidobacte
694	7.8	6	Q9BW35	2	483	Q9BW35	homo sapien
695	7.8	6	Q9S768	2	483	Q9S768	oryza sativ
696	7.8	6	Q7UET7	2	483	Q7UET7	rhodopirell
697	7.8	6	Q9Y7U9	2	484	Q9Y7U9	schizosacch
698	7.8	6	Q28713	2	484	Q28713	oryctolagus
699	7.8	6	Q94HC5	2	484	Q94HC5	oryza sativ
700	7.8	6	Q7XF06	2	484	Q7XF06	oryza sativ
701	7.8	6	Q6FZX8	2	484	Q6FZX8	bartonella
702	7.8	6	Q6G3A1	2	485	Q6G3A1	bartonella
703	7.8	6	Q8SCI0	2	485	Q8SCI0	propionibac
704	7.8	6	Q9PWC0	2	485	Q9PWC0	gallus gall
705	7.8	6	CISX_YEAST	1	486	P43635	saccharomyc
706	7.8	6	Q60O97	2	491	Q60O97	drosophila
707	7.8	6	Q8PYS7	2	494	Q8PYS7	methanosarc
708	7.8	6	Q7X740	2	495	Q7X740	oryza sativ
709	7.8	6	O65799	2	496	O65799	arabidopsis
710	7.8	6	Q66K75	2	498	Q66K75	homo sapien
711	7.8	6	NQOE_PARDE	1	499	P29926	paracoccus
712	7.8	6	Q8T9D2	2	500	Q8T9D2	drosophila
713	7.8	6	Q7WBN8	2	502	Q7WBN8	bordetella
714	7.8	6	Q7WPM7	2	502	Q7WPM7	bordetella
715	7.8	6	O64143	2	504	O64143	bacteriopha
716	7.8	6	O31905	2	504	O31905	bacillus su
717	7.8	6	LNT_HAEDU	1	505	Q7VM56	haemophilus
718	7.8	6	Q6C654	2	505	Q6C654	yarrowia li
719	7.8	6	Q89G09	2	506	Q89G09	bradyrhizob
720	7.8	6	Q6GPJ1	2	507	Q6GPJ1	xenopus lae
721	7.8	6	Q9VTH6	2	509	Q9VTH6	drosophila
722	7.8	6	Q8XIG3	2	509	Q8XIG3	clostridium
723	7.8	6	Q7S6W6	2	510	Q7S6W6	neurospora
724	7.8	6	Q9GCM9	2	510	Q9GCM9	pieris napi
725	7.8	6	Q7QJZ4	2	511	Q7QJZ4	anopheles g
726	7.8	6	Q8YQ99	2	514	Q8YQ99	anabaena sp
727	7.8	6	Q6LEJ5	2	518	Q6LEJ5	oryctolagus
728	7.8	6	Q9Y7C0	2	520	Q9Y7C0	neurospora
729	7.8	6	Q8IYS4	2	520	Q8IYS4	homo sapien
730	7.8	6	Q8NCV0	2	520	Q8NCV0	homo sapien
731	7.8	6	PME_PRUPE	1	522	Q43062	prunus pers
732	7.8	6	Q8MNX4	2	523	Q8MNX4	caenorhabdi
733	7.8	6	Q9ABL8	2	524	Q9ABL8	caulobacter
734	7.8	6	Q9W0L9	2	525	Q9W0L9	drosophila
735	7.8	6	CPF5_RAT	1	526	P51870	rattus norv
736	7.8	6	Q7Q135	2	526	Q7Q135	anopheles g
737	7.8	6	Q755C0	2	526	Q755C0	ashbya goss
738	7.8	6	Q52405	2	528	Q52405	pseudomonas
739	7.8	6	Q7BGS5	2	533	Q7BGS5	bacillus st
740	7.8	6	Q9EQ70	2	535	Q9EQ70	rattus norv
741	7.8	6	Q56926	2	535	Q56926	yersinia en
742	7.8	6	Q7SA99	2	537	Q7SA99	neurospora
743	7.8	6	Q6NXG4	2	538	Q6NXG4	homo sapien
744	7.8	6	Q95JW1	2	539	Q95JW1	macaca fasc
745	7.8	6	Q7Q135	2	541	Q7Q135	anopheles g
746	7.8	6	Q9HWB0	2	541	Q9HWB0	pseudomonas
747	7.8	6	Q7S4I3	2	542	Q7S4I3	neurospora
748	7.8	6	Q651N3	2	543	Q651N3	oryza sativ
749	7.8	6	Q6FBD3	2	543	Q6FBD3	acinetobact
750	7.8	6	LNT_CHLTR	1	543	O84539	chlamydia t
751	7.8	6	Q8PXV0	2	544	Q8PXV0	methanosarc
752	7.8	6	Q876L1	2	544	Q876L1	saccharomyc
753	7.8	6	Q7RRP5	2	545	Q7RRP5	plasmodium
754	7.8	6	Q9H882	2	545	Q9H882	homo sapien
755	7.8	6	Q9VMI4	2	546	Q9VMI4	drosophila
756	7.8	6	Q7QA61	2	549	Q7QA61	anopheles g
757	7.8	6	Q9URW7	2	551	Q9URW7	schizosacch
758	7.8	6	Q6BFF2	2	551	Q6BFF2	paramecium
759	7.8	6	SYK_CAUCR	1	552	Q9ABY6	caulobacter
760	7.8	6	Q8IKQ4	2	553	Q8IKQ4	plasmodium
761	7.8	6	Q6ZFW3	2	554	Q6ZFW3	oryza sativ

Seq			ID	Ct	No	Acc	Organism
762	7.8	6	Q7QGW6	2	558	Q7QGW6	anopheles g
763	7.8	6	Q6MF08	2	558	Q6MF08	parachlamyd
764	7.8	6	Q7WZL7	2	560	Q7WZL7	xanthomonas
765	7.8	6	Q8Y0H0	2	568	Q8Y0H0	ralstonia s
766	7.8	6	GLT2_MOUSE	1	570	Q6PB93	m polypepti
767	7.8	6	Q6T5D1	2	570	Q6T5D1	oryza sativ
768	7.8	6	Q9SDL2	2	570	Q9SDL2	apium grave
769	7.8	6	MET3_PENCH	1	572	Q12650	penicillium
770	7.8	6	Q8JMN1	2	574	Q8JMN1	human respi
771	7.8	6	Q6PMI1	2	575	Q6PMI1	hydrilla ve
772	7.8	6	Q85221	2	575	Q85221	human parai
773	7.8	6	Q85222	2	575	Q85222	human parai
774	7.8	6	Q8H0E8	2	577	Q8H0E8	lithospermu
775	7.8	6	Q92W64	2	577	Q92W64	rhizobium m
776	7.8	6	Q8NHH8	2	579	Q8NHH8	homo sapien
777	7.8	6	Q7PXR2	2	581	Q7PXR2	anopheles g
778	7.8	6	P73732	2	582	P73732	synechocyst
779	7.8	6	Q8NHH9	2	583	Q8NHH9	homo sapien
780	7.8	6	MAOX_MESCR	1	585	P37223	mesembryant
781	7.8	6	Q9ZWJ4	2	585	Q9ZWJ4	aloe arbore
782	7.8	6	Q943H8	2	586	Q943H8	arabidopsis
783	7.8	6	Q75CQ4	2	588	Q75CQ4	ashbya goss
784	7.8	6	O14729	2	588	O14729	homo sapien
785	7.8	6	Q9PVX4	2	588	Q9PVX4	cynops pyrr
786	7.8	6	SKS1_ARATH	1	589	Q94G02	arabidopsis
787	7.8	6	Q94G02	2	589	Q94G02	flaveria pr
788	7.8	6	Q94G03	2	589	Q94G03	flaveria pr
789	7.8	6	Q7Q8B5	2	590	Q7Q8B5	anopheles g
790	7.8	6	P73561	2	590	P73561	synechocyst
791	7.8	6	MAOX_POPTR	1	591	P34105	populus tri
792	7.8	6	MAOX_VITVI	1	591	P51615	vitis vinif
793	7.8	6	O48656	2	592	O48656	aloe arbore
794	7.8	6	O71S51	2	593	O71S51	ophiopholis
795	7.8	6	Q9ZXM5	2	594	Q9ZXM5	bacteriopha
796	7.8	6	Q6YZH8	2	594	Q6YZH8	oryza sativ
797	7.8	6	Q8DKN0	2	594	Q8DKN0	synechococc
798	7.8	6	Q8U6T4	2	594	Q8U6T4	agrobacteri
799	7.8	6	Q7S925	2	595	Q7S925	neurospora
800	7.8	6	Q9LY22	2	595	Q9LY22	arabidopsis
801	7.8	6	Q7MJJ1	2	596	Q7MJJ1	vibrio vuln
802	7.8	6	Q8DAJ1	2	596	Q8DAJ1	vibrio vuln
803	7.8	6	VIN3_ARATH	1	600	Q9FIE3	arabidopsis
804	7.8	6	Q6C6Y8	2	602	Q6C6Y8	yarrowia li
805	7.8	6	PPCK_SULSO	1	603	Q97VS5	sulfolobus
806	7.8	6	Q644W1	2	604	Q644W1	rhyacotrito
807	7.8	6	Q7R3S2	2	607	Q7R3S2	giardia lam
808	7.8	6	Q9PVX3	2	608	Q9PVX3	cynops pyrr
809	7.8	6	Q85CV8	2	611	Q85CV8	opisthoproc
810	7.8	6	Q69MX4	2	612	Q69MX4	oryza sativ
811	7.8	6	Q8IBE6	2	613	Q8IBE6	plasmodium
812	7.8	6	Q85D10	2	615	Q85D10	nansenia ar
813	7.8	6	Q85D23	2	615	Q85D23	glossanodon
814	7.8	6	Q85D75	2	615	Q85D75	bathylagus
815	7.8	6	Q8EF90	2	617	Q8EF90	shewanella
816	7.8	6	Q8RZA4	2	618	Q8RZA4	oryza sativ
817	7.8	6	Q6BXU2	2	619	Q6BXU2	debaryomyce
818	7.8	6	Q6LFR9	2	619	Q6LFR9	photobacter
819	7.8	6	Q93F38	2	620	Q93F38	shigella fl
820	7.8	6	Q6BVV1	2	621	Q6BVV1	debaryomyce
821	7.8	6	O14794	2	622	O14794	homo sapien
822	7.8	6	Q6A4K8	2	623	Q6A4K8	mus musculu
823	7.8	6	PLB2_SCHPO	1	624	O13857	schizosacch
824	7.8	6	Q8G5P3	2	624	Q8G5P3	bifidobacte
825	7.8	6	Q9KQ16	2	624	Q9KQ16	vibrio chol
826	7.8	6	Q94GB3	2	628	Q94GB3	oryza sativ
827	7.8	6	Q7XGT5	2	628	Q7XGT5	oryza sativ
828	7.8	6	Q6J1Y6	2	629	Q6J1Y6	bacteriopha
829	7.8	6	Q92341	2	630	Q92341	schizosacch
830	7.8	6	STR3_SCHPO	1	630	O81780	schizosacch
831	7.8	6	Q67XW5	2	631	Q67XW5	arabidopsis
832	7.8	6	Q682A0	2	631	Q682A0	arabidopsis
833	7.8	6	Q8J0D5	2	632	Q8J0D5	microsporum
834	7.8	6	Q6WIH7	2	632	Q6WIH7	microsporum

#	Accession	Description	Accession	N	Length		
835	Q8J0D6	microsporum	Q8J0D6	2	633	7.8	6
836	Q9UVW4	aspergillus	Q9UVW4	2	634	7.8	6
837	Q7RPR9	plasmodium	Q7RPR9	2	634	7.8	6
838	Q8NIB6	trichophyto	Q8NIB6	2	635	7.8	6
839	Q6WIH5	arthroderma	Q6WIH5	2	635	7.8	6
840	MAOC_MAIZE	zea mays	P16243	1	636	7.8	6
841	Q84LP6	zea mays (m	Q84LP6	2	636	7.8	6
842	Q84LQ5	sorghum bic	Q84LQ5	2	638	7.8	6
843	MAOC_ORYSA	oryza sativ	P43279	1	639	7.8	6
844	Q9LDH7	oryza sativ	Q9LDH7	2	640	7.8	6
845	O24550	vitis vinif	O24550	2	640	7.8	6
846	Q8W348	oryza sativ	Q8W348	2	640	7.8	6
847	Q7XGZ1	oryza sativ	Q7XGZ1	2	641	7.8	6
848	Q9M4Q9	ricinus com	Q9M4Q9	2	643	7.8	6
849	Q9PP43	campylobact	Q9PP43	2	644	7.8	6
850	Q8W000	zea mays (m	Q8W000	2	646	7.8	6
851	Q7QS13	giardia lam	Q7QS13	2	646	7.8	6
852	Q9CA83	arabidopsis	Q9CA83	2	647	7.8	6
853	MAOC_FLAPR	flaveria pr	P36444	1	647	7.8	6
854	Q7QDZ1	anopheles g	Q7QDZ1	2	657	7.8	6
855	MAOC_FLATR	flaveria tr	P22178	1	648	7.8	6
856	Q871Q7	neurospora	Q871Q7	2	658	7.8	6
857	Q8XYA3	ralstonia s	Q8XYA3	2	660	7.8	6
858	O94247	schizosacch	O94247	2	662	7.8	6
859	Q9ZRH5	zea mays (m	Q9ZRH5	2	663	7.8	6
860	Q9MA03	arabidopsis	Q9MA03	2	666	7.8	6
861	Q6BFC0	paramecium	Q6BFC0	2	671	7.8	6
862	Q9C547	arabidopsis	Q9C547	2	672	7.8	6
863	Q9W7B7	brachydanio	Q9W7B7	2	673	7.8	6
864	PLB4_SCHPO	schizosacch	O13327	1	676	7.8	6
865	Q6NV02	brachydanio	Q6NV02	2	677	7.8	6
866	Q7ZTU9	brachydanio	Q7ZTU9	2	678	7.8	6
867	Q8MTI5	leishmania	Q8MTI5	2	679	7.8	6
868	Q6N925	rhodopseudo	Q6N925	2	681	7.8	6
869	Q9H7W4	homo sapien	Q9H7W4	2	684	7.8	6
870	Q6CVB6	kluyveromyc	Q6CVB6	2	684	7.8	6
871	Q8IUH8	homo sapien	Q8IUH8	2	684	7.8	6
872	Q8TC67	homo sapien	Q8TC67	2	685	7.8	6
873	Q7R173	giardia lam	Q7R173	2	687	7.8	6
874	Q8GUH6	arabidopsis	Q8GUH6	2	687	7.8	6
875	Q84ZD7	oryza sativ	Q84ZD7	2	688	7.8	6
876	Q9IAL0	brachydanio	Q9IAL0	2	688	7.8	6
877	Q9IBC8	xenopus lae	Q9IBC8	2	690	7.8	6
878	Q9W7R7	xenopus lae	Q9W7R7	2	693	7.8	6
879	Q8WVZ6	homo sapien	Q8WVZ6	2	696	7.8	6
880	Q9DG20	gallus gall	Q9DG20	2	698	7.8	6
881	Q8GVW4	oryza sativ	Q8GVW4	2	704	7.8	6
882	O96078	ephydatia f	O96078	2	707	7.8	6
883	Q7VGG3	helicobacte	Q7VGG3	2	712	7.8	6
884	Q8YQP7	anabaena sp	Q8YQP7	2	713	7.8	6
885	O26972	tribolium c	O26972	1	713	7.8	6
886	SM1A_TRICF	plasmodium	Q9SUM4?	1	714	7.8	6
887	Q8IJF1	plasmodium	Q8IJF1	2	718	7.8	6
888	Q9SUM4	arabidopsis	Q9SUM4	2	719	7.8	6
889	O92614	ophiostoma	O92614	2	720	7.8	6
890	Q838H7	enterococcu	Q838H7	2	731	7.8	6
891	Q8OR01	sclerotinia	Q8OR01	2	731	7.8	6
892	Q6YYL1	oryza sativ	Q6YYL1	2	732	7.8	6
893	Q7UQK4	rhodopirell	Q7UQK4	2	732	7.8	6
894	Q8VQM5	klebsiella	Q8VQM5	2	737	7.8	6
895	Q9A7E5	caulobacter	Q9A7E5	2	739	7.8	6
896	Q9LVD7	arabidopsis	Q9LVD7	2	741	7.8	6
897	Q99AQ3	tt virus. o	Q99AQ3	2	741	7.8	6
898	Q658T4	homo sapien	Q658T4	2	746	7.8	6
899	Q9C6V7	arabidopsis	Q9C6V7	2	747	7.8	6
900	RNG3_SCHPO	schizosacch	Q6SGI1?	1	748	7.8	6
901	Q6SGI1	uncultured	Q6SGI1	2	749	7.8	6
902	Q6A6C2	propionibac	Q6A6C2	2	753	7.8	6
903	Q67IU4	oryza sativ	Q67IU4	2	765	7.8	6
904	Q7PVN0	anopheles g	Q7PVN0	2	765	7.8	6
905	BGLX_ECOLI	escherichia	P33363	1	765	7.8	6
906	BGLX_SALTY	salmonella	Q56078	1	765	7.8	6
907	Q8X668	escherichia	Q8X668	2	765	7.8	6

#	Accession	Description	Accession	N	Length		
908	Q8Z5B5	salmonella	Q8Z5B5	2	765	7.8	6
909	Q8CVX0	escherichia	Q8CVX0	2	765	7.8	6
910	Q83KF8	shigella fl	Q83KF8	2	765	7.8	6
911	CUL3_CAEEL	caenorhabdi	Q17391	1	777	7.8	6
912	O54524	legionella	O54524	2	783	7.8	6
913	Q6SLA6	gibberella	Q6SLA6	2	785	7.8	6
914	Q9HBB2	homo sapien	Q9HBB2	2	790	7.8	6
915	Q7RQA3	plasmodium	Q7RQA3	2	796	7.8	6
916	Q9VVM8	drosophila	Q9VVM8	2	798	7.8	6
917	Q65GD3	bacillus li	Q65GD3	2	804	7.8	6
918	Q62PM4	mus musculu	Q62PM4	2	813	7.8	6
919	Q8D3K7	vibrio vuln	Q8D3K7	2	816	7.8	6
920	Q6BGJ1	paramecium	Q6BGJ1	2	822	7.8	6
921	DNLJ_TREPA	treponema p	O83642	1	823	7.8	6
922	Q9PMS7	campylobact	Q9PMS7	2	823	7.8	6
923	Q6CLZ8	kluyveromyc	Q6CLZ8	2	825	7.8	6
924	Q7UU73	rhodopirell	Q7UU73	2	825	7.8	6
925	Q7MF19	vibrio vuln	Q7MF19	2	827	7.8	6
926	Q23136	caenorhabdi	Q23136	2	832	7.8	6
927	Q8X0X9	neurospora	Q8X0X9	2	841	7.8	6
928	Q8RWY4	arabidopsis	Q8RWY4	2	841	7.8	6
929	Q8H105	arabidopsis	Q8H105	2	841	7.8	6
930	Q9XZS7	drosophila	Q9XZS7	2	844	7.8	6
931	Q9SGW2	arabidopsis	Q9SGW2	2	847	7.8	6
932	Q9DKV4	caprine art	Q9DKV4	2	849	7.8	6
933	Q28SY1	nitrosomona	Q28SY1	2	850	7.8	6
934	Q8TMG3	methanosarc	Q8TMG3	2	851	7.8	6
935	Q6CVG2	kluyveromyc	Q6CVG2	2	857	7.8	6
936	Q8BDF7	jamestown c	Q8BDF7	2	864	7.8	6
937	Q6PZO0	mus musculu	Q6PZO0	2	866	7.8	6
938	Q752E8	ashbya goss	Q752E8	2	869	7.8	6
939	Q9V019	pyrococcus	Q9V019	2	872	7.8	6
940	Q9SN00	arabidopsis	Q9SN00	2	873	7.8	6
941	Q8ILP6	plasmodium	Q8ILP6	2	879	7.8	6
942	Q8VZH2	arabidopsis	Q8VZH2	2	879	7.8	6
943	Q8H8H0	arabidopsis	Q8H8H0	2	884	7.8	6
944	Q6GNK8	xenopus lae	Q6GNK8	2	886	7.8	6
945	Q7ZX16	xenopus lae	Q7ZX16	2	886	7.8	6
946	Q804C7	homo sapien	Q804C7	2	886	7.8	6
947	IRE1_HUMAN	homo sapien	P21399	1	889	7.8	6
948	IRE1_MOUSE	mus musculu	P28271	1	889	7.8	6
949	IRE1_RABIT	oryctolagus	O01059	1	889	7.8	6
950	IRE1_RAT	rattus norv	O63270	1	889	7.8	6
951	IREB_CHICK	gallus gall	Q90875	1	889	7.8	6
952	Q87SQ5	saccharomyc	Q87SQ5	2	889	7.8	6
953	Q9FLX6	arabidopsis	Q9FLX6	2	893	7.8	6
954	Q8VDC3	mus musculu	Q8VDC3	2	899	7.8	6
955	Q6CUN9	kluyveromyc	Q6CUN9	2	900	7.8	6
956	Q7NLM6	gloeobacter	Q7NLM6	2	913	7.8	6
957	PM10_CHLPN	chlamydia p	Q9RB65	1	928	7.8	6
958	CDG5_HUMAN	homo sapien	Q9Y5G8	1	931	7.8	6
959	Q7NU34	chromobacte	Q7NU34	2	935	7.8	6
960	Q8CGH5	mus musculu	Q8CGH5	2	939	7.8	6
961	UVRA_RICPR	rickettsia	Q9ZCC3	1	953	7.8	6
962	Q68YI2	rickettsia	Q68YI2	2	953	7.8	6
963	Q6BKM3	debaryomyce	Q6BKM3	2	969	7.8	6
964	Q8UH99	agrobacteri	Q8UH99	2	971	7.8	6
965	Q7Z3P2	homo sapien	Q7Z3P2	2	978	7.8	6
966	Q95KE0	macaca fasc	Q95KE0	2	978	7.8	6
967	Q12252	saccharomyc	Q12252	2	991	7.8	6
968	Q9K5X4	bacillus ha	Q9K5X4	2	995	7.8	6
969	Q9AXB1	oryza sativ	Q9AXB1	2	1002	7.8	6
970	Q6PG12	mus musculu	Q6PG12	2	1005	7.8	6
971	Q9P8F2	zygosacchar	Q9P8F2	2	1030	7.8	6
972	Q8X0X6	neurospora	Q8X0X6	2	1032	7.8	6
973	Q6FD21	chromobacte	Q6FD21	2	1035	7.8	6
974	Q7P0T4	acinetobact	Q7P0T4	2	1040	7.8	6
975	Q7Z7R0	homo sapien	Q7Z7R0	2	1052	7.8	6
976	Q7PT99	anopheles g	Q7PT99	2	1070	7.8	6
977	Q9RWX7	deinococcus	Q9RWX7	2	1070	7.8	6
978	Q8MLA4	drosophila	Q8MLA4	2	1078	7.8	6
979	Q7QTS9	giardia lam	Q7QTS9	2	1084	7.8	6
980	Q9P7K5	schizosacch	Q9P7K5	2	1098	7.8	6

Left-hand block (entries 981–1053):

No.			SeqNo	N	Accession	Name	Species
981	6	7.8	1098	2	Q64719		bos taurus
982	6	7.8	1102	2	Q75AR3		ashbya goss
983	6	7.8	1104	2	Q62888		oryza sativ
984	6	7.8	1114	2	Q9C8S4		arabidopsis
985	6	7.8	1120	2	Q6B8R8		gracilaria
986	6	7.8	1120	2	Q6SES8		uncultured
987	6	7.8	1131	2	Q9V7A5		drosophila
988	6	7.8	1134	2	Q8P378		xanthomonas
989	6	7.8	1134	2	Q8PEL2		xanthomonas
990	6	7.8	1136	2	Q75HY6		oryza sativ
991	6	7.8	1144	1	O60266	CYA3_HUMAN	homo sapien
992	6	7.8	1144	2	P21932	CYA3_RAT	rattus norv
993	6	7.8	1144	2	Q6PGC0	CYA3_MOUSE	mus musculu
994	6	7.8	1145	2	Q80TY9		mus musculu
995	6	7.8	1150	2	Q6SLC9		cochliobolu
996	6	7.8	1159	2	Q7SBL3		neurospora
997	6	7.8	1160	2	Q9LPQ7		arabidopsis
998	6	7.8	1168	2	Q7SDF3		neurospora
999	6	7.8	1172	1	Q13751	LMB3_HUMAN	homo sapien
1000	6	7.8	1185	2	Q9HCJ9		homo sapien
1001	6	7.8	1189	2	Q7UPG0		rhodopirell
1002	6	7.8	1196	2	Q6FIK1		candida gla
1003	6	7.8	1213	2	Q95PH2		dictyosteli
1004	6	7.8	1213	2	Q86CZ2		dictyosteli
1005	6	7.8	1233	2	Q9FXG4		arabidopsis
1006	6	7.8	1234	1	Q6BZU0	RPOB_THETN	thermoanaer
1007	6	7.8	1246	2	Q67JT3		yarrowia li
1008	6	7.8	1250	2	Q9XZC5		symbiobacte
1009	6	7.8	1260	2	Q6C740		cryptospori
1010	6	7.8	1269	2	Q75B00		yarrowia li
1011	6	7.8	1271	2	Q6PDJ1		ashbya goss
1012	6	7.8	1288	2	Q9V604		mus musculu
1013	6	7.8	1297	2	Q9U3L2		drosophila
1014	6	7.8	1304	2	Q9U3L2		caenorhabdi
1015	6	7.8	1327	1	MYHB_RAT	MYHB_RAT	rattus norv
1016	6	7.8	1329	2	Q8N3P4		homo sapien
1017	6	7.8	1348	2	Q9VCM6		drosophila
1018	6	7.8	1376	2	Q9KF15		bacillus ha
1019	6	7.8	1394	2	Q86UX3		homo sapien
1020	6	7.8	1399	2	Q6APK0		desulfotale
1021	6	7.8	1406	2	Q80TR5		mus musculu
1022	6	7.8	1422	2	Q6MJ09		bdellovibri
1023	6	7.8	1425	2	Q7S802		neurospora
1024	6	7.8	1436	1	MRP5_MOUSE	MRP5_MOUSE	mus musculu
1025	6	7.8	1436	2	MRP5_RAT	MRP5_RAT	rattus norv
1026	6	7.8	1437	1	MRP5_HUMAN	MRP5_HUMAN	homo sapien
1027	6	7.8	1443	2	057106		inkoo virus
1028	6	7.8	1443	2	057107		inkoo virus
1029	6	7.8	1444	2	Q9QKE5		south river
1030	6	7.8	1449	2	Q8LSR0		oryza sativ
1031	6	7.8	1467	2	Q9M033		arabidopsis
1032	6	7.8	1500	2	Q8IHH0		drosophila
1033	6	7.8	1503	2	Q9V6P4		drosophila
1034	6	7.8	1516	2	Q6BUY8		arabidopsis
1035	6	7.8	1521	2	Q8GU64		debaryomyce
1036	6	7.8	1527	2	Q76B62		oryza sativ
1037	6	7.8	1571	2	Q7JM28		homo sapien
1038	6	7.8	1584	2	Q18798		caenorhabdi
1039	6	7.8	1586	2	—		shewanella
1040	6	7.8	1599	2	Q854N0		mycobacteri
1041	6	7.8	1657	1	IQG1_MOUSE	IQG1_MOUSE	mus musculu
1042	6	7.8	1657	2	Q80UW7		mus musculu
1043	6	7.8	1681	2	Q6ZQK2		mus musculu
1044	6	7.8	1726	2	Q6C012		yarrowia li
1045	6	7.8	1765	2	Q9JMD4		mus musculu
1046	6	7.8	1765	2	Q9R053		mus musculu
1047	6	7.8	1768	2	Q9N8K7		trypanosoma
1048	6	7.8	1774	2	Q75418		ashbya goss
1049	6	7.8	1784	2	Q7UPX3		rhodopirell
1050	6	7.8	1805	2	081060		arabidopsis
1051	6	7.8	1858	1	P54674	P3K2_DICDI	dictyosteli
1052	6	7.8	1924	2	Q67654		garlic late
1053	6	7.8					

Right-hand block (entries 1054–1126):

No.			SeqNo	N	Accession	Name	Species
1054	6	7.8	1972	1	P35749	MYHB_HUMAN	homo sapien
1055	6	7.8	1972	1	O08638	MYHB_MOUSE	mus musculu
1056	6	7.8	1972	2	P35748	MYHB_RABIT	oryctolagus
1057	6	7.8	1972	2	Q9LUD7		arabidopsis
1058	6	7.8	1972	2	Q7WY92		staphylococ
1059	6	7.8	1972	2	Q8R384		mus musculu
1060	6	7.8	1983	2	Q931N9		staphylococ
1061	6	7.8	1984	2	Q69ZX3		mus musculu
1062	6	7.8	1995	2	Q72406		homo sapien
1063	6	7.8	2030	2	Q9VXV3		drosophila
1064	6	7.8	2043	2	Q8WQ87		chironomus
1065	6	7.8	2124	2	Q7WRR9		staphylococ
1066	6	7.8	2126	1	Q9JIH7	WNK1_RAT	rattus norv
1067	6	7.8	2131	2	Q6SLK2		mus musculu
1068	6	7.8	2152	2	Q7WRQ2		staphylococ
1069	6	7.8	2186	2	Q9ALM5		saccharopol
1070	6	7.8	2186	2	Q7WS91		staphylococ
1071	6	7.8	2186	2	Q8NW19		staphylococ
1072	6	7.8	2186	2	Q99TB0		staphylococ
1073	6	7.8	2189	2	Q6G8H1		staphylococ
1074	6	7.8	2241	2	Q6GFU5		staphylococ
1075	6	7.8	2253	2	Q7XRJ2		staphylococ
1076	6	7.8	2377	2	Q7QW26		oryza sativ
1077	6	7.8	2382	2	Q9FR96		arabidopsis
1078	6	7.8	2454	1	P83741	WNK1_MOUSE	mus musculu
1079	6	7.8	2581	1	Q9H4A3	WNK1_HUMAN	homo sapien
1080	6	7.8	2672	2	Q86B02		dictyosteli
1081	6	7.8	2883	2	Q9N4C8		caenorhabdi
1082	6	7.8	2890	1	P33892	GCN1_YEAST	saccharomyc
1083	6	7.8	2890	1	—	RPBC_WOLSU	w bifunctio
1084	6	7.8	2894	1	Q9ZK23	RPBC_HELPJ	h bifunctio
1085	6	7.8	2898	1	O25806	RPBC_HELPY	h bifunctio
1086	6	7.8	2898	1	Q7VJ82	RPBC_HELHP	h bifunctio
1087	6	7.8	3099	2	Q872P1		neurospora
1088	6	7.8	3218	2	Q7R5I4		giardia lam
1089	6	7.8	3379	2	Q8ILX0		plasmodium
1090	6	7.8	4335	2	Q9JAD5		rio bravo v
1091	5	6.5	6473	2	Q6NA45		rhodopseudo
1092	5	6.5	14	2	Q8IKH9		plasmodium
1093	5	6.5	14	2	Q7SCJ3		neurospora
1094	5	6.5	18	2	Q6SEH0		umbra limi
1095	5	6.5	24	2	Q6SEH1		novumbra hu
1096	5	6.5	25	2	Q9WUQ6		mus musculu
1097	5	6.5	26	2	Q788Q0		xenopus lae
1098	5	6.5	27	2	Q64FD9		mus musculu
1099	5	6.5	29	2	Q64FE3		toxoplasma
1100	5	6.5	29	2	Q94448		toxoplasma
1101	5	6.5	30	2	Q71UZ8		chaetopteru
1102	5	6.5	31	2	Q93IG2		sus scrofa
1103	5	6.5	32	2	Q86SJ1		thiobacillu
1104	5	6.5	33	2	Q6NJM4		homo sapien
1105	5	6.5	33	2	Q65W75		corynebacte
1106	5	6.5	33	1	P03675	COA1_BPFD	mannheimia
1107	5	6.5	34	2	Q67B72		bacteriopha
1108	5	6.5	35	2	Q7VCT4		dehalococco
1109	5	6.5	36	2	Q83EB8		prochloroco
1110	5	6.5	37	2	Q6UJJ9		coxiella bu
1111	5	6.5	37	2	O87904		carphodacty
1112	5	6.5	37	2	Q696V2		coxiella bu
1113	5	6.5	38	2	Q8EIQ2		rissa trida
1114	5	6.5	38	2	Q8F5H3		shewanella
1115	5	6.5	38	2	Q9KE15		leptospira
1116	5	6.5	38	2	Q6DNC6		bacillus ha
1117	5	6.5	40	2	Q9PV13		rattus norv
1118	5	6.5	40	2	Q8HKI7		triakis sp.
1119	5	6.5	41	2	Q6M3Y2		amblyomma v
1120	5	6.5	42	2	Q90X31		corynebacte
1121	5	6.5		2	Q90XL9		typhlonecte
1122	5	6.5		2	Q9PV12		latimeria m
1123	5	6.5		2	Q97VH1		lepisosteus
1124	5	6.5		2	Q73PJ4		sulfolobus
1125	5	6.5		2	Q26281		treponema d
1126	5	6.5		2	Q86YY8		drosophila / homo sapien

No.	Len	pH	V	N	Entry	ID	Organism
1127	5	6.5	42	2	Q9BMA1	Q9bma1	asphondylia
1128	5	6.5	42	2	Q8VIR6	Q8vir6	mycobacteri
1129	5	6.5	42	2	Q7VJU8	Q7vju8	helicobacte
1130	5	6.5	42	2	Q8EX68	Q8ex68	leptospira
1131	5	6.5	42	2	Q8ZZV9	Q8zzv9	pyrobaculum
1132	5	6.5	44	2	Q8T954	Q8t954	drosophila
1133	5	6.5	44	2	Q9T2T3	Q9t2t3	brassica na
1134	5	6.5	44	2	Q7PBZ7	Q7pbz7	rickettsia
1135	5	6.5	45	2	Q8NNU6	Q8nnu6	corynebacte
1136	5	6.5	46	2	Q8FBK6	Q8fbk6	escherichia
1137	5	6.5	46	2	042535	042535	brachydanio
1138	5	6.5	47	2	Q69YT9	Q69yt9	homo sapien
1139	5	6.5	47	2	O77777	O77777	bos taurus
1140	5	6.5	47	2	Q853T3	Q853t3	mycobacteri
1141	5	6.5	47	2	Q7MPS2	Q7mps2	vibrio vuln
1142	5	6.5	48	1	ATP8_TRIRU	Q7UAC6	trichophyto
1143	5	6.5	48	2	Q7UAC6	Q7uac6	shigella fl
1144	5	6.5	48	2	Q8F357	Q8f357	leptospira
1145	5	6.5	48	2	Q8FEQ8	Q8feq8	escherichia
1146	5	6.5	49	1	COXH_THUOB	P80977	thunnus obe
1147	5	6.5	49	2	Q8EZK6	Q8ezk6	leptospira
1148	5	6.5	50	2	Q9XLF4	Q9xlf4	crax globul
1149	5	6.5	50	2	Q8KMU5	Q8kmu5	enterococcu
1150	5	6.5	51	2	Q6KGD9	Q6kgd9	bacteriopha
1151	5	6.5	52	1	A95E_DROME	P16548	drosophila
1152	5	6.5	52	2	Q6T0Y8	Q6t0y8	ducula bico
1153	5	6.5	53	2	Q6T0W6	Q6t0w6	metriopelia
1154	5	6.5	53	2	Q6T0W7	Q6t0w7	metriopelia
1155	5	6.5	53	2	Q6T0Y2	Q6t0y2	chalcophaps
1156	5	6.5	53	2	Q6T0Y4	Q6t0y4	turtur chal
1157	5	6.5	53	2	Q6T0Y6	Q6t0y6	phapitreron
1158	5	6.5	53	2	Q6T0Y9	Q6t0y9	ducula pist
1159	5	6.5	53	2	Q6T0Z0	Q6t0z0	ducula rubr
1160	5	6.5	53	2	Q6T0Z1	Q6t0z1	ducula paci
1161	5	6.5	53	2	Q6T0Z7	Q6t0z7	ptilinopus
1162	5	6.5	53	2	Q6T102	Q6t102	leptotila m
1163	5	6.5	53	2	Q6T103	Q6t103	leptotila r
1164	5	6.5	53	2	Q6T104	Q6t104	leptotila p
1165	5	6.5	53	2	Q6T105	Q6t105	leptotila c
1166	5	6.5	53	2	Q6T106	Q6t106	zenaida aur
1167	5	6.5	53	2	Q6T107	Q6t107	zenaida aur
1168	5	6.5	53	2	Q6T108	Q6t108	zenaida mac
1169	5	6.5	53	2	Q6T109	Q6t109	zenaida gal
1170	5	6.5	53	2	Q6T110	Q6t110	zenaida mel
1171	5	6.5	53	2	Q6T111	Q6t111	zenaida asi
1172	5	6.5	53	2	Q6T112	Q6t112	geotrygon c
1173	5	6.5	53	2	Q6T113	Q6t113	geotrygon c
1174	5	6.5	53	2	Q6T115	Q6t115	reinwardtoe
1175	5	6.5	53	2	Q6T117	Q6t117	macropygia
1176	5	6.5	53	2	Q6T118	Q6t118	columba fas
1177	5	6.5	53	2	Q6T121	Q6t121	columba sub
1178	5	6.5	53	2	Q6T123	Q6t123	columba spe
1179	5	6.5	53	2	Q6T124	Q6t124	columba oen
1180	5	6.5	53	2	Q6T125	Q6t125	columba fla
1181	5	6.5	53	2	Q6T134	Q6t134	streptopeli
1182	5	6.5	53	2	Q6T135	Q6t135	nesoenas ma
1183	5	6.5	53	2	Q6QXQ2	Q6qxq2	oryza sativ
1184	5	6.5	53	2	Q8K749	Q8k749	streptococc
1185	5	6.5	53	2	Q92I29	Q92i29	rickettsia
1186	5	6.5	53	2	Q8DQZ9	Q8dqz9	streptococc
1187	5	6.5	53	2	Q8E102	Q8e102	streptococc
1188	5	6.5	54	2	Q85332	Q85332	vaccinia vi
1189	5	6.5	54	1	SECG_SULSO	P60465	sulfolobus
1190	5	6.5	55	1	SKK4_MESMA	Q95NJ8	mesobuthus
1191	5	6.5	55	2	Q957Z3	Q957z3	casuarius c
1192	5	6.5	55	2	Q6Y0F6	Q6y0f6	amazona far
1193	5	6.5	55	2	Q9TBJ0	Q9tbj0	neomorphus
1194	5	6.5	55	2	Q64U35	Q64u35	bacteroides
1195	5	6.5	55	2	Q8PJ07	Q8pj07	xanthomonas
1196	5	6.5	55	2	Q98E41	Q98e41	rhizobium l
1197	5	6.5	55	2	Q7V1Y0	Q7v1y0	prochloroco
1198	5	6.5	55	2	Q8X283	Q8x283	escherichia
1199	5	6.5	55	2	Q8JUH9	Q8juh9	foot-and-mo
1200	5	6.5	55	2	Q8JUI7	Q8jui7	foot-and-mo
1201	5	6.5	55	2	Q8JUI8	Q8jui8	foot-and-mo
1202	5	6.5	55	2	Q8JUJ1	Q8juj1	foot-and-mo
1203	5	6.5	55	2	Q913N4	Q913n4	foot-and-mo
1204	5	6.5	55	2	Q913N5	Q913n5	foot-and-mo
1205	5	6.5	55	2	Q913N6	Q913n6	foot-and-mo
1206	5	6.5	55	2	Q913N7	Q913n7	foot-and-mo
1207	5	6.5	55	2	Q913N8	Q913n8	foot-and-mo
1208	5	6.5	55	2	Q913P0	Q913p0	foot-and-mo
1209	5	6.5	55	2	Q913P1	Q913p1	foot-and-mo
1210	5	6.5	55	2	Q913P2	Q913p2	foot-and-mo
1211	5	6.5	55	2	Q913P6	Q913p6	foot-and-mo
1212	5	6.5	55	2	Q913P7	Q913p7	foot-and-mo
1213	5	6.5	55	2	Q913P9	Q913p9	foot-and-mo
1214	5	6.5	55	2	Q913Q0	Q913q0	foot-and-mo
1215	5	6.5	55	2	Q913Q1	Q913q1	foot-and-mo
1216	5	6.5	55	2	Q913Q3	Q913q3	foot-and-mo
1217	5	6.5	55	2	Q913Q5	Q913q5	foot-and-mo
1218	5	6.5	55	2	Q913Q7	Q913q7	foot-and-mo
1219	5	6.5	55	2	Q913Q8	Q913q8	foot-and-mo
1220	5	6.5	55	2	Q913Q9	Q913q9	foot-and-mo
1221	5	6.5	55	2	Q913R0	Q913r0	foot-and-mo
1222	5	6.5	55	2	Q913R1	Q913r1	foot-and-mo
1223	5	6.5	55	2	Q913R2	Q913r2	foot-and-mo
1224	5	6.5	55	2	Q913R3	Q913r3	foot-and-mo
1225	5	6.5	55	2	Q913R5	Q913r5	foot-and-mo
1226	5	6.5	55	2	Q913R7	Q913r7	foot-and-mo
1227	5	6.5	55	2	Q913R8	Q913r8	foot-and-mo
1228	5	6.5	55	2	Q913R9	Q913r9	foot-and-mo
1229	5	6.5	55	2	Q913S0	Q913s0	foot-and-mo
1230	5	6.5	55	2	Q913S2	Q913s2	foot-and-mo
1231	5	6.5	55	2	Q913S4	Q913s4	foot-and-mo
1232	5	6.5	55	2	Q913S9	Q913s9	foot-and-mo
1233	5	6.5	55	2	Q913T1	Q913t1	foot-and-mo
1234	5	6.5	55	2	Q913T4	Q913t4	foot-and-mo
1235	5	6.5	55	2	Q913T7	Q913t7	foot-and-mo
1236	5	6.5	55	2	Q913T9	Q913t9	foot-and-mo
1237	5	6.5	55	2	Q913U0	Q913u0	foot-and-mo
1238	5	6.5	55	2	Q913U1	Q913u1	foot-and-mo
1239	5	6.5	55	2	Q913U2	Q913u2	foot-and-mo
1240	5	6.5	55	2	Q913U3	Q913u3	foot-and-mo
1241	5	6.5	55	2	Q913U8	Q913u8	foot-and-mo
1242	5	6.5	55	2	Q913U9	Q913u9	foot-and-mo
1243	5	6.5	55	2	Q91H71	Q91h71	foot-and-mo
1244	5	6.5	55	2	Q9DJ54	Q9dj54	foot-and-mo
1245	5	6.5	55	2	Q9DJ62	Q9dj62	foot-and-mo
1246	5	6.5	55	2	Q9DJ84	Q9dj84	foot-and-mo
1247	5	6.5	55	2	Q9DJ85	Q9dj85	foot-and-mo
1248	5	6.5	55	2	Q9DJ87	Q9dj87	foot-and-mo
1249	5	6.5	55	2	Q9DJ88	Q9dj88	foot-and-mo
1250	5	6.5	55	2	Q9DJ90	Q9dj90	foot-and-mo
1251	5	6.5	55	2	Q9DJA0	Q9dja0	foot-and-mo
1252	5	6.5	55	2	Q9DSB7	Q9dsb7	foot-and-mo
1253	5	6.5	55	2	Q9DSN7	Q9dsn7	foot-and-mo
1254	5	6.5	56	2	Q34398	Q34398	drosophila
1255	5	6.5	56	2	Q6PU88	Q6pu88	vibrio harv
1256	5	6.5	56	2	Q97SC9	Q97sc9	streptococc
1257	5	6.5	56	2	Q73D06	Q73d06	bacillus ce
1258	5	6.5	56	2	Q81HH5	Q81hh5	bacillus ce
1259	5	6.5	56	2	Q81UP6	Q81up6	bacillus an
1260	5	6.5	56	2	Q9DJ46	Q9dj46	foot-and-mo
1261	5	6.5	56	2	Q9DJ80	Q9dj80	foot-and-mo
1262	5	6.5	57	2	Q9HQV4	Q9hqv4	halobacteri
1263	5	6.5	57	2	Q9BDG3	Q9bdg3	bos taurus
1264	5	6.5	57	2	Q6J1Y5	Q6j1y5	bacteriopha
1265	5	6.5	57	2	Q7X1Q4	Q7x1q4	pseudomonas
1266	5	6.5	57	2	Q7X1R0	Q7x1r0	pseudomonas
1267	5	6.5	57	2	Q7X1T1	Q7x1t1	pseudomonas
1268	5	6.5	57	2	Q64TR7	Q64tr7	bacteroides
1269	5	6.5	57	2	Q879H2	Q879h2	streptococc
1270	5	6.5	57	2	Q913Q4	Q913q4	foot-and-mo
1271	5	6.5	57	2	Q913T8	Q913t8	foot-and-mo
1272	5	6.5	57	2	Q67LI1	Q67li1	chlorella v

Left table — columns: Index | ID | ID2 | Organism | count | score | col | col

Index	ID	ID2	Organism	count	score		
1273	Q65lj9		oryza sativ	2	58	6.5	5
1274	Q7x1s3		pseudomonas	2	58	6.5	5
1275	Q7usq5		rhodopirell	2	58	6.5	5
1276	Q9dj47		foot-and-mo	2	58	6.5	5
1277	Q9pv03		mugil cepha	2	58	6.5	5
1278	Q8ea5	Y9G1_PSEPK	pseudomonas	1	59	6.5	5
1279	Q9vuj6		drosophila	2	59	6.5	5
1280	Q46663		enterobacte	2	59	6.5	5
1281	O39847		foot-and-mo	2	59	6.5	5
1282	Q671h4		chlorella v	2	59	6.5	5
1283	Q8vsn6		shigella fl	2	60	6.5	5
1284	Q7mbp0		vibrio vuln	2	60	6.5	5
1285	Q7z2r6		homo sapien	2	61	6.5	5
1286	Q967u2		branchiosto	2	61	6.5	5
1287	Q7qvc1		giardia lam	2	61	6.5	5
1288	Q8sc27		stx2 conver	2	61	6.5	5
1289	Q94cr6		oryza sativ	2	61	6.5	5
1290	Q7ws68		pseudomonas	2	61	6.5	5
1291	Q7x1r5		pseudomonas	2	61	6.5	5
1292	Q99rv5		staphylococ	2	61	6.5	5
1293	Q7a405		staphylococ	2	61	6.5	5
1294	Q6geb5		staphylococ	2	61	6.5	5
1295	Q8juh6		foot-and-mo	2	61	6.5	5
1296	Q84148		orf virus.	2	61	6.5	5
1297	PSBZ_CHLRE		chlamydomon	1	62	6.5	5
1298	Y100_XANAC		xanthomonas	1	62	6.5	5
1299	Q8zms5		salmonella	2	62	6.5	5
1300	Q99vi6		salmonella	2	62	6.5	5
1301	Q7a1f0		staphylococ	2	62	6.5	5
1302	Q7a6n7		staphylococ	2	62	6.5	5
1303	Q886x8		staphylococ	2	62	6.5	5
1304	Q6akv1		pseudomonas	2	62	6.5	5
1305	Q6gb36		desulfotale	2	62	6.5	5
1306	Q6gij6		staphylococ	2	62	6.5	5
1307	Q88613		staphylococ	2	62	6.5	5
1308	YF96_PSESM		pseudomonas	1	63	6.5	5
1309	Q8esn6		oceanobaci	2	63	6.5	5
1310	Q8f6f8		leptospira	2	63	6.5	5
1311	Q9cif9		lactococcus	2	63	6.5	5
1312	Q9l5p0		salmonella	2	63	6.5	5
1313	Q67li3		chlorella v	2	63	6.5	5
1314	V07K_LSV		lily sympto	1	64	6.5	5
1315	Q42196		arabidopsis	2	64	6.5	5
1316	Q8fke7		escherichia	2	64	6.5	5
1317	Q913s3		foot-and-mo	2	64	6.5	5
1318	Q70wl4		lily sympto	2	64	6.5	5
1319	Q83088		lily sympto	2	64	6.5	5
1320	Q9pv06		plecoglossu	2	64	6.5	5
1321	Q9c4y1		sulfolobus	2	65	6.5	5
1322	O19919		cyanidium c	2	65	6.5	5
1323	Q6u9j9		bacteriopha	2	65	6.5	5
1324	Q707k3		escherichia	2	65	6.5	5
1325	Q63ej8		bacillus ce	2	65	6.5	5
1326	Q64ul0		bacillus an	2	65	6.5	5
1327	Q73by5		bacillus ce	2	65	6.5	5
1328	Q7niw2		bacillus ce	2	65	6.5	5
1329	Q81gm8		gloeobacter	2	65	6.5	5
1330	Q81tt8		bacillus ce	2	66	6.5	5
1331	Q9js68		bacillus an	2	66	6.5	5
1332	Q6hm16		neisseria m	2	66	6.5	5
1333	Q9yw41		bacillus th	2	66	6.5	5
1334	Q9pt45		melanoplus	2	66	6.5	5
1335	Q9pt25		pantodon bu	2	66	6.5	5
1336	Q9pv01		anguilla sp	2	66	6.5	5
1337	Q9pv07		mola mola (	2	66	6.5	5
1338	Q9pv08		esox lucius	2	66	6.5	5
1339	Q9pv09		barbus tetr	2	66	6.5	5
1340	Q9pv10		chanos chan	2	66	6.5	5
1341	Q9pv11		notopterus	2	66	6.5	5
1342	Q7z4p1		osteoglossu	2	67	6.5	5
1343	Q7r5y3		homo sapien	2	67	6.5	5
1344	Q8ga62		giardia lam	2	67	6.5	5
1345	Q99ra2		escherichia	2	67	6.5	5
			staphylococ				

Right table — columns: Index | ID | ID2 | Organism | count | score | col | col

Index	ID	ID2	Organism	count	score		
1346	Q79zz2	Q79ZZ2	staphylococ	2	67	6.5	5
1347	Q7a3g9	Q7A3G9	staphylococ	2	67	6.5	5
1348	Q6g6e1	Q6G6E1	staphylococ	2	67	6.5	5
1349	Q6gdr5	Q6GDR5	staphylococ	2	67	6.5	5
1350	Q9ptz0	Q9PTZ0	polypterus	2	67	6.5	5
1351	Q9ptz3	Q9PTZ3	dicentrarch	2	67	6.5	5
1352	Q9ptz4	Q9PTZ4	chirocentru	2	67	6.5	5
1353	Q9ptz6	Q9PTZ6	amia calva	2	67	6.5	5
1354	Q9put8	Q9PUT8	salarias sp	2	67	6.5	5
1355	Q9pv02	Q9PV02	psettodes s	2	67	6.5	5
1356	Q9pv04	Q9PV04	gadus morhu	2	67	6.5	5
1357	Q9pv05	Q9PV05	harpadon sp	2	67	6.5	5
1358	Q9tp06	Q9TP06	brachydanio	2	68	6.5	5
1359	Q8cth7	Q8CTH7	staphylococ	2	68	6.5	5
1360	Q6db23	Q6DB23	erwinia car	2	68	6.5	5
1361	Q913p8	Q913P8	linum usita	2	68	6.5	5
1362	Q8l822	Q8L822	staphylococ	2	69	6.5	5
1363	Q57052	Q57052	staphylococ	2	69	6.5	5
1364	Q72wh5	Q72WH5	desulfovibr	2	69	6.5	5
1365	Q7mzj2	Q7MZJ2	photorhabdu	2	69	6.5	5
1366	Q6mcf8	Q6MCF8	parachlamyd	2	69	6.5	5
1367	Q913u7	Q913U7	foot-and-mo	2	69	6.5	5
1368	Q6b4e5	Q6B4E5	clostera an	2	69	6.5	5
1369	Q6tvf7	Q6TVF7	bovine papu	2	69	6.5	5
1370	O26195	O26195	methanobact	2	70	6.5	5
1371	P77081	P77081	escherichia	2	70	6.5	5
1372	Q8egv4	Q8EGV4	shewanella	2	70	6.5	5
1373	Q8juh7	Q8JUH7	foot-and-mo	2	70	6.5	5
1374	Q8jui6	Q8JUI6	foot-and-mo	2	70	6.5	5
1375	Q913t0	Q913T0	foot-and-mo	2	70	6.5	5
1376	Q913u6	Q913U6	foot-and-mo	2	70	6.5	5
1377	Q6tvt9	Q6TVT9	orf virus.	2	70	6.5	5
1378	Q9dj93	Q9DJ93	drosophila	2	70	6.5	5
1379	Q6iiii	Q6IIII	drosophila	2	71	6.5	5
1380	Q8d776	Q8D776	vibrio vuln	2	71	6.5	5
1381	Q9kf44	Q9KF44	bacillus ha	2	71	6.5	5
1382	Q6aqb2	Q6AQB2	desulfotale	2	71	6.5	5
1383	O09137	O09137	ratus sp.	2	71	6.5	5
1384	Q6xqf3	Q6XQF3	enterobacte	2	72	6.5	5
1385	Q8xu54	Q8XU54	ralstonia s	2	72	6.5	5
1386	Q9pc18	Q9PC18	xylella fas	2	73	6.5	5
1387	Q9lxv1	Q9LXV1	arabidopsis	2	73	6.5	5
1388	Q7uuv7	Q7UUV7	rhodopirell	2	73	6.5	5
1389	Q8van0	Q8VAN0	white spot	2	73	6.5	5
1390	Q9pmr0	YD97_CAMJE	foot-and-mo	1	74	6.5	5
1391	Q9hc47	Q9HC47	campylobact	2	74	6.5	5
1392	Q6v9d7	Q6V9D7	homo sapien	2	74	6.5	5
1393	Q83yp6	Q83YP6	penicillium	2	74	6.5	5
1394	Q746v9	Q746V9	pseudomonas	2	74	6.5	5
1395	Q82zt0	Q82ZT0	geobacter s	2	74	6.5	5
1396	Q9era4	Q9ERA4	enterococcu	2	74	6.5	5
1397	Q913p4	Q913P4	microtus ar	2	74	6.5	5
1398	Q6xm30	Q6XM30	foot-and-mo	2	74	6.5	5
1399	Q9dj22	Q9DJ22	feldmannia	2	74	6.5	5
1400	Q9dj92	Q9DJ92	foot-and-mo	2	74	6.5	5
1401	Q6ilq3	Q6ILQ3	foot-and-mo	2	75	6.5	5
1402	Q95lm4	Q95LM4	drosophila	2	75	6.5	5
1403	Q9bf34	Q9BF34	macaca fasc	2	75	6.5	5
1404	Q85fk0	Q85FK0	erinaceus c	2	75	6.5	5
1405	Q76yj9	Q76YJ9	adiantum ca	2	75	6.5	5
1406	Q8ynn7	Q8YNN7	bacteriopha	2	75	6.5	5
1407	Q9pnd7	Q9PND7	anabaena sp	2	75	6.5	5
1408	Q8jui3	Q8JUI3	campylobact	2	75	6.5	5
1409	Q6zyh5	Q6ZYH5	foot-and-mo	2	76	6.5	5
1410	Q8py85	Q8PY85	pyrobaculum	2	76	6.5	5
1411	Q8gvz5	Q8GVZ5	methanosarc	2	76	6.5	5
1412	Q83yn2	Q83YN2	oryza sativ	2	76	6.5	5
1413	Q83yp3	Q83YP3	pseudomonas	2	76	6.5	5
1414	Q83yp7	Q83YP7	pseudomonas	2	76	6.5	5
1415	Q833e6	Q833E6	enterococcu	2	76	6.5	5
1416	Q889k4	Q889K4	pseudomonas	2	76	6.5	5
1417	Q913u5	Q913U5	foot-and-mo	2	76	6.5	5
1418	Q8lec6	Q8LEC6	arabidopsis	2	77	6.5	5

1419	Q54148	shigella fl	77	2
1420	Q83YP0	pseudomonas	77	2
1421	Q9AH74	salmonella	77	2
1422	Q9AH76	escherichia	77	2
1423	Q9EZG8	streptococc	77	2
1424	Q62YB4	bacillus li	77	2
1425	Q635B7	bacillus ce	77	2
1426	Q8R9R8	thermoanaer	77	2
1427	Q8VSD1	shigella fl	77	2
1428	Q8X2Q7	escherichia	77	2
1429	Q81M63	bacillus an	77	2
1430	Q89N23	bradyrhizob	77	2
1431	Q6HDZ6	bacillus th	77	2
1432	Q913Q6	foot-and-mo	77	2
1434	V5E_HPV70	human papil	78	1
1435	P50774	treponema d	78	2
1436	Q73MI3	streptococc	78	2
1437	Q8DQ72	erwinia car	78	2
1438	Q6D620	foot-and-mo	78	2
1439	Q913S5	canine herp	78	2
1440	Q9YP99	oryza sativ	79	2
1441	Q8LH71	arabidopsis	79	2
1442	Q42006	pongine her	79	2
1443	Q8QRX9	foot-and-mo	79	2
1444	Q913T6	frog virus	79	2
1445	Q6GZN3	plutella xy	79	2
1446	Q9DW04	drosophila	80	2
1447	Q6IGM8	bactéroides	80	2
1448	Q64V26	ralstonia s	80	2
1449	Q8XVX1	bacillus ce	80	2
1450	Q734N3	shigella fl	80	2
1451	Q83JZ8	human papil	81	1
1452	V5E_HPV35	homo sapien	81	2
1453	Q68DQ1	stx2 conver	81	2
1454	Q8SC26	stx2 conver	81	2
1455	Q7Y2H0	stx1 conver	81	2
1456	Q7Y2Y3	salmonella	81	2
1457	Q8KLJ7	foot-and-mo	81	2
1458	Q91H50	rhynchospor	82	2
1459	Q02039	macaca mula	82	2
1460	Q30603	hordeum vul	82	2
1461	Q7X9R4	oryza sativ	82	2
1462	Q851F7	photorhabdu	82	2
1463	Q7N7R3	gloeobacter	82	2
1464	Q7NEN6	bacillus ha	82	2
1465	Q9K831	bacteriopha	83	2
1466	Q94ML7	bacteriopha	83	2
1467	Q6QGQ5	clostridium	83	2
1468	Q97JX0	photobacter	83	2
1469	Q6LQ25	synechococc	83	2
1470	Q7U620	bradyrhizob	83	2
1471	Q89DP8	murine hepa	83	2
1472	O72007	foot-and-mo	83	2
1473	Q8JUI2	chilo iride	83	2
1474	Q91G36	murine hepa	84	1
1475	O66193	helicobacte	84	2
1476	YA70_HELPY	acinetobact	84	2
1477	Q6J2N8	lactococcus	84	2
1478	O54681	yersinia pe	84	2
1479	Q74YN9	salmonella	84	2
1480	Q934Z3	leptospira	84	2
1481	Q72RS3	yersinia pe	84	2
1482	Q7ARA5	bacillus ce	84	2
1483	Q81N20	yersinia pe	84	2
1484	Q9ZH06	culex nigri	84	2
1485	Q919H0	cydia pomon	85	2
1486	Q91EU8	trypanosoma	85	2
1487	Q7YVK0	caenorhabdi	85	2
1488	Q9XXH2	fusobacteri	85	2
1489	Q7P2Z5	xenopus lae	85	2
1490	Q6GND4	human immun	85	2
1491	P89731	helicobacte	86	1
1492	Q92M67	bacteriopha	86	2
1493	Q9T1L1	lactobacill	86	2
1494	P94863	rickettsia	86	2
1495	Q92HX6	parachlamyd	86	2
1496	Q6MBB6	agrobacteri	87	1
1497	Q8UJG0	borrelia bu	87	2
1498	FLIQ_BORBU	euhadra bra	87	2
1499	Q75YY6	bacteriopha	87	2
1500	Q71T70	borrelia ga	87	2
	Q61IZ1	borrelia ga		
	Q8YSG8	anabaena sp		

ALIGNMENTS

RESULT 1

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Q6UWR8

ID   Q6UWR8          PRELIMINARY;     PRT;    77 AA.
AC   Q6UWR8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   GPVK512.
GN   ORFNames=UNQ512;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358675; AAQ89038.1; -.
SQ   SEQUENCE   77 AA;   8772 MW;   11OCBCF87CCC4B86 CRC64;
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  Query Match          100.0%;  Score 77;  DB 2;  Length 77;
  Best Local Similarity 100.0%;  Pred. No. 1e-71;
  Matches  77;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWHNKGLALIFCIIQSLALTWYSLSF 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWHNKGLALIFCIIQSLALTWYSLSF 60

Qy   61 IPFARDAVKKCFAVCLA 77
          |||||||||||||||||
Db   61 IPFARDAVKKCFAVCLA 77
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RESULT 2

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O95562

ID   O95562          PRELIMINARY;     PRT;    160 AA.
AC   O95562;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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RA   Rhodes S.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL035297; CAA22897.1; -.
DR   EMBL; BC068098; AAH68098.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   160 AA;   17779 MW;   F05C57532B7593BD CRC64;

```
Query Match              100.0%;   Score 77;   DB 2;   Length 160;
Best Local Similarity    100.0%;   Pred. No. 1.8e-71;
Matches   77;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1  MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    84  MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF  143

Qy    61  IPFFARDAVKKCFAVCLA  77
          ||||||||||||||||||
Db   144  IPFFARDAVKKCFAVCLA  160
```

RESULT 3
Q8VD57
ID   Q8VD57   PRELIMINARY;   PRT;   159 AA.
AC   Q8VD57;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   RIKEN cDNA 2010005O13 (Mus musculus adult male bone cDNA, RIKEN full-
DE   length enriched library, clone:9830137K19 product:hypothetical
DE   protein, full insert sequence).
GN   Name=2010005O13Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Konno H., Akiyama J., Nishi K., Nagaoka S., Sasaki N., Carninci P.,
RA   Sumi H., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa K., Izawa M., Ohara T., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Kira A., Hayashizaki Y.;
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi H., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa K., Izawa M., Ohara T., Watahiki M.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384 format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

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RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017549; AAH17549.1; -.
DR   EMBL; AK036578; BAC29488.1; -.
DR   MGD; MGI:1917362; 2010005O13Rik.
KW   Hypothetical protein.
SQ   SEQUENCE 159 AA; 17499 MW; B30B7EB5FE82A0E6 CRC64;

Query Match             28.6%;  Score 22;  DB 2;  Pred. No. 1.7e-14;
Best Local Similarity   100.0%;
Matches   22;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        38 NKGLALIFCIIQSLALTWYSLS 59
             ||||||||||||||||||||||
Db       120 NKGLALIFCIIQSLALTWYSLS 141


RESULT 4
Q7T375
ID   Q7T375      PRELIMINARY;    PRT;   161 AA.
AC   Q7T375;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein zgc:64053.
GN   ORFNames=zgc:64053;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053226; AAH53226.1; -.
DR   ZFIN; ZDB-GENE-040426-1350; zgc:64053.
KW   Hypothetical protein.
SQ   SEQUENCE 161 AA; 18025 MW; 5BACCAB7DDACDB634 CRC64;

Query Match             26.0%;  Score 20;  DB 2;  Pred. No. 2.1e-12;
Best Local Similarity   100.0%;
Matches   20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy         1 MGPVKQLKRMFEPTRLIATI 20
             ||||||||||||||||||||
Db        85 MGPVKQLKRMFEPTRLIATI 104


RESULT 5
Q86F94
ID   Q86F94      PRELIMINARY;    PRT;   113 AA.
AC   Q86F94;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Clone ZZZ409 mRNA sequence.
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RA   Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA   Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA   Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA   Xue C.L., Feng Z., Chen Z., Han Z.G.;
RT   "Evolutionary and biomedical implications of a Schistosoma japonicum
RT   complementary DNA resource.";
RL   Nat. Genet. 35:139-147(2003).
DR   EMBL; AY222969; AAP05981.1; -.
SQ   SEQUENCE 113 AA; 12524 MW; 2FF26F707A512D73 CRC64;

Query Match             11.7%;  Score 9;  DB 2;  Length 113;
Best Local Similarity   100.0%;  Pred. No. 0.39;
Matches    9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        43 LIFCIIQSL 51
             |||||||||
Db        79 LIFCIIQSL 87


RESULT 6
Q922U5
ID   Q922U5      PRELIMINARY;    PRT;   136 AA.
AC   Q922U5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   RIKEN cDNA 5630401J11 (Similar to CG5104).
GN   Name=5630401J11Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
```

RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA   Nagaraja R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006777; AAH06777.1; -.
DR   EMBL; AF466883; AAM21003.1; -.
DR   MGD; MGI:1918689; 5630401J11Rik.
DR   GO; GO:0016021; C:integral to membrane; TAS.
SQ   SEQUENCE   136 AA; 15085 MW; 3FEAF412B5E9840C CRC64;

Query Match   10.4%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPVKQLK 8
                |||||||
Db   83 MGPVKQLK 90

RESULT 7
Q8WV19
ID   Q8WV19   PRELIMINARY;   PRT;   159 AA.
AC   Q8WV19;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Chromosome 6 open reading frame 83.
GN   Name=C6orf83;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018969; AAH18969.1; -.

SQ   SEQUENCE   159 AA; 17804 MW; 0EC8A9CED7EF27E0 CRC64;

Query Match   10.4%; Score 8; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPVKQLK 8
                |||||||
Db   83 MGPVKQLK 90

RESULT 8
Q9UIC7
ID   Q9UIC7   PRELIMINARY;   PRT;   178 AA.
AC   Q9UIC7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PRGR1 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hu Y.F., Mao X.H., Zhuang M., Lu C.D.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF041429; AAF18564.1; -.
DR   Genew; HGNC:21102; C6orf83.
FT   NON_TER   1   1
SQ   SEQUENCE   178 AA; 19879 MW; 72C1E2BA35F3C6EA CRC64;

Query Match   10.4%; Score 8; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPVKQLK 8
                |||||||
Db   102 MGPVKQLK 109

RESULT 9
FUCP_ECOLI
ID   FUCP_ECOLI   STANDARD;   PRT;   438 AA.
AC   P11551;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   L-fucose permease.
GN   Name=fucP; OrderedLocusNames=b2801;
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=89315234; PubMed=2664711;
RA   Lu Z., Lin E.C.C.;
RT   "The nucleotide sequence of Escherichia coli genes for L-fucose
RT   dissimilation.";
RL   Nucleic Acids Res. 17:4883-4884(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]

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RP   SEQUENCE OF 1-31 FROM N.A.
RX   MEDLINE=90036697; PubMed=2553671;
RA   Chen Y.M., Lu Z., Lin E.C.C.;
RT   "Constitutive activation of the fucPIK operon and silencing of the
RT   divergently transcribed fucPIK operon by an IS5 element in Escherichia
RT   coli mutants selected for growth on L-1,2-propanediol.";
RL   J. Bacteriol. 171:6097-6105(1989).
RN   [4]
RP   TOPOLOGY.
RX   MEDLINE=95302988; PubMed=7783647;
RA   Gunn F.J., Tate C.G., Sansom C.E., Henderson P.J.;
RT   "Topological analyses of the L-fucose-H+ symport protein, FucP, from
RT   Escherichia coli.";
RL   Mol. Microbiol. 15:771-783(1995).
-!- FUNCTION: Transport of L-fucose into the cell.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the FHS transporter (TC 2.A.1.7) family.
--------------------------------------------------------------------------
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DR   EMBL; X15025; CAA33126.1; -.
DR   EMBL; U29581; AAB40451.1; -.
DR   EMBL; U00096; AAC75843.1; -.
DR   EMBL; M31059; AAA23822.2; -.
DR   PIR; JS0184; WQECFP.
DR   EchoBASE; EB0348; -.
DR   EcoGene; EG10352; fucP.
DR   InterPro; IPR005275; Lfuc_permease.
DR   InterPro; IPR007114; MFS.
DR   TIGRFAMs; TIGR00885; fucP; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Complete proteome; Fucose metabolism; Inner membrane; Sugar transport;
KW   Transmembrane.
FT   DOMAIN        1     24       Cytoplasmic (Probable).
FT   TRANSMEM     25     45       Probable.
FT   DOMAIN       46     55       Periplasmic (Probable).
FT   TRANSMEM     56     76       Probable.
FT   DOMAIN       77     95       Cytoplasmic (Probable).
FT   TRANSMEM     96    115       Probable.
FT   DOMAIN      116    118       Periplasmic (Probable).
FT   TRANSMEM    119    139       Probable.
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FT   TRANSMEM    167    187       Probable.
FT   DOMAIN      188    206       Periplasmic (Probable).
FT   TRANSMEM    207    227       Probable.
FT   DOMAIN      228    265       Cytoplasmic (Probable).
FT   TRANSMEM    266    286       Probable.
FT   DOMAIN      287    295       Periplasmic (Probable).
FT   TRANSMEM    296    316       Probable.
FT   DOMAIN      317    326       Cytoplasmic (Probable).
FT   TRANSMEM    327    347       Probable.
FT   DOMAIN      348    352       Periplasmic (Probable).
FT   TRANSMEM    353    373       Probable.
FT   DOMAIN      374    381       Cytoplasmic (Probable).
FT   DOMAIN      382    402       Probable.
FT   DOMAIN      403    413       Periplasmic (Probable).
FT   TRANSMEM    414    434       Probable.
FT   DOMAIN      435    438       Cytoplasmic (Probable).
SQ   SEQUENCE   438 AA;  47544 MW;  D8AA3785274A0085 CRC64;

Query Match             10.4%;  Score 8;  DB 1;  Length 438;
Best Local Similarity  100.0%;  Pred. No. 12;
  Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps  0;

Qy      27 ALTLCSAF 34
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Db     353 ALTLCSAF 360
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RESULT 10
Q8Z430
ID   Q8Z430; Q7C7H5;
AC   Q8Z430;                PRELIMINARY;      PRT;     438 AA.
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   L-fucose permease.
GN   Name=fucP; OrderedLocusNames=STY3115, t2883;
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ty2 / ATCC 700931;
RX   MEDLINE=22531367; PubMed=12644504;
RX   DOI=10.1128/JB.185.7.2330-2337.2003;
RA   Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA   Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT   "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT   and CT18.";
RL   J. Bacteriol. 185:2330-2337(2003).
DR   EMBL; AL627277; CAD02801.1; -.
DR   EMBL; AE016843; AAO70439.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   TIGRFAMs; TIGR00885; fucP; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Complete proteome.
SQ   SEQUENCE   438 AA;  47773 MW;  AFDBD4C0C344994E CRC64;

Query Match             10.4%;  Score 8;  DB 2;  Length 438;
Best Local Similarity  100.0%;  Pred. No. 12;
  Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps  0;

Qy      27 ALTLCSAF 34
           ||||||||
Db     353 ALTLCSAF 360
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RESULT 11
Q8FEE8
ID   Q8FEE8;                PRELIMINARY;      PRT;     438 AA.
AC   Q8FEE8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   L-fucose permease.
GN   Name=fucP; OrderedLocusNames=c3370;
OS   Escherichia coli O6.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=217992;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX   MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR   EMBL; AE016765; AAN81817.1; -.
DR   InterPro; IPR005275; Lfuc_permease.
DR   TIGRFAMs; TIGR00885; fucP; 1.
KW   Complete proteome.
SQ   SEQUENCE   438 AA;   47536 MW;   C919EBA3A4378CEC CRC64;

Query Match                    10.4%;  Score 8;  DB 2;  Length 438;
Best Local Similarity  100.0%;     Pred. No. 12;
Matches   8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     27 ALTLCSAF 34
          ||||||||
Db    353 ALTLCSAF 360

RESULT 12
Q83QC8
ID   Q83QC8         PRELIMINARY;         PRT;    438 AA.
AC   Q83QC8; Q7C072;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Fucose permease.
GN   Name=fucP; OrderedLocusNames=S3010, SF2815;
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=301 / Serotype 2a;
RX   MEDLINE=22727406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA   Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA   Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA   Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA   Yu J.;
RT   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT   through comparison with genomes of Escherichia coli K12 and O157.";
RL   Nucleic Acids Res. 30:4432-4441(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2457T;
RX   MEDLINE=22590274; PubMed=12704152;
RX   DOI=10.1128/IAI.71.5.2775-2786.2003;
RA   Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA   Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA   Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA   Schwartz D.C., Blattner F.R.;
RT   "Complete genome sequence and comparative genomics of Shigella
RT   flexneri serotype 2a strain 2457T.";
RL   Infect. Immun. 71:2775-2786(2003).
DR   EMBL; AE015295; AAN44303.1; -.
DR   EMBL; AE016987; AAP18128.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR005275; Lfuc_permease.
DR   InterPro; IPR007114; MFS.
DR   TIGRFAMs; TIGR00885; fucP; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Complete proteome.
SQ   SEQUENCE   438 AA;   47590 MW;   AFB09C88BE0B4C81 CRC64;

Query Match                    10.4%;  Score 8;  DB 2;  Length 438;
Best Local Similarity  100.0%;     Pred. No. 12;
Matches   8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     27 ALTLCSAF 34
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Db    353 ALTLCSAF 360

RESULT 13
Q8X6R7
ID   Q8X6R7         PRELIMINARY;         PRT;    438 AA.
AC   Q8X6R7; Q7AB68;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Fucose permease.
GN   Name=fucP; OrderedLocusNames=ECs3661, z4118;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX   MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX   MEDLINE=22156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AE005508; AAG57915.1; -.
DR   EMBL; AP002563; BAB37084.1; -.
DR   PIR; E91086; E91086.
DR   PIR; G85931; G85931.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR005275; Lfuc_permease.
DR   InterPro; IPR007114; MFS.
DR   TIGRFAMs; TIGR00885; fucP; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Complete proteome.
SQ   SEQUENCE   438 AA;   47574 MW;   C4ABF790735F41D1 CRC64;

Query Match                    10.4%;  Score 8;  DB 2;  Length 438;
Best Local Similarity  100.0%;     Pred. No. 12;
Matches   8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     27 ALTLCSAF 34
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Db    353 ALTLCSAF 360

RESULT 14
Q69WI1
ID   Q69WI1         PRELIMINARY;         PRT;    668 AA.
AC   Q69WI1;
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Search completed: April 7, 2005, 04:52:11
Job time : 262 secs

DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative aluminum-activated malate transporter.
GN   Name=P051C01.9; Synonyms=P057H07.17;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT   clone:P051C01.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT   clone:P057H07.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003763; BAD32958.1; -.
DR   EMBL; AP003619; BAD32889.1; -.
DR   InterPro; IPR006214; UPF0005.
DR   Pfam; PF01027; UPF0005; 1.
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Query Match   10.4%; Score 8; DB 2; Length 668;
Best Local Similarity   100.0%; Pred. No. 17;
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Db   90 ALTLCSAF 97

RESULT 15
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AC   Q82T85;
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DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=NE2033;
OS   Nitrosomonas europaea.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC   Nitrosomonadaceae; Nitrosomonas.
OX   NCBI_TaxID=915;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19718 / IFO 14298;
RX   MEDLINE=22586410; PubMed=12700255;
RX   DOI=10.1128/JB.185.9.2759-2773.2003;
RA   Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA   Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA   Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT   "Complete genome sequence of the ammonia-oxidizing bacterium and
RT   obligate chemolithoautotroph Nitrosomonas europaea.";
RL   J. Bacteriol. 185:2759-2773(2003).
DR   EMBL; BX321863; CAD85944.1; -.
DR   InterPro; IPR008928; Glyco_trans_6hp.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   898 AA; 103602 MW; 2CA7DCB89F5D9198 CRC64;

Query Match   10.4%; Score 8; DB 2; Length 898;
Best Local Similarity   100.0%; Pred. No. 22;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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                GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    April 7, 2005, 03:13:17 ; Search time 43 Seconds
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                           133.674 Million cell updates/sec

Title:    US-10-063-563-56
Perfect score: 410
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464064 residues

Total number of hits satisfying chosen parameters:   513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

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   5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
   6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	235	57.3	168	4	US-09-270-767-32997	Sequence 32997, A
2	235	57.3	168	4	US-09-270-767-48214	Sequence 48214, A
3	94	22.9	255	4	US-09-248-796A-20672	Sequence 20672, A
4	75	18.3	215	4	US-09-538-092-22	Sequence 2, Appl
5	66.5	16.2	404	4	US-09-489-039A-11699	Sequence 11699, A
6	66	16.1	289	4	US-09-489-039A-12390	Sequence 12390, A
7	64	15.6	416	4	US-09-252-991A-24117	Sequence 24117, A
8	64	15.6	685	4	US-08-937-067-14	Sequence 14, Appl
9	63	15.4	74	3	US-09-134-001C-3503	Sequence 3503, Ap
10	61.5	15.0	464	4	US-09-252-991A-24883	Sequence 24883, A
11	61.5	15.0	2396	1	US-08-157-005-2	Sequence 2, Appli
12	61.5	15.0	2396	3	US-08-747-863-2	Sequence 2, Appli
13	61.5	15.0	2396	4	US-09-565-864-2	Sequence 2, Appli
14	61.5	15.0	2396	4	US-10-226-065-2	Sequence 2, Appli
15	61	14.9	386	4	US-09-248-796A-17451	Sequence 17451, A
16	60.5	14.8	441	4	US-09-489-039A-10091	Sequence 10091, A
17	60	14.6	521	4	US-09-902-540-11865	Sequence 11865, A
18	60	14.6	585	4	US-08-937-067-9	Sequence 9, Appli
19	59.5	14.5	134	4	US-09-540-236-2049	Sequence 2049, Ap
20	59.5	14.5	156	4	US-09-270-767-37594	Sequence 37594, A
21	59.5	14.5	156	4	US-09-270-767-52811	Sequence 52811, A
22	59	14.4	159	4	US-09-438-185A-245	Sequence 245, Appl
23	59	14.4	244	3	US-08-772-440-2	Sequence 2, Appli
24	59	14.4	328	3	US-08-513-974B-56	Sequence 56, Appl
25	59	14.4	328	3	US-08-513-974B-380	Sequence 380, App
26	59	14.4	328	4	US-09-461-436B-56	Sequence 56, Appl
27	59	14.4	328	4	US-09-745-842-18	Sequence 18, Appl
28	59	14.4	376	4	US-09-721-870-32	Sequence 32, Appl
29	59	14.4	473	4	US-09-252-991A-22921	Sequence 22921, A
30	58.5	14.3	322	4	US-09-254-227A-11	Sequence 11, Appl
31	58.5	14.3	843	3	US-09-361-631-2	Sequence 2, Appli
32	58	14.1	153	4	US-09-270-767-32384	Sequence 32384, A
33	58	14.1	234	4	US-09-270-767-47601	Sequence 47601, A
34	58	14.1	464	2	US-09-134-000C-5084	Sequence 5084, Ap
35	58	14.1	498	4	US-08-477-451-18	Sequence 18, Appl
36	58	14.1	498	4	US-09-830-217-10	Sequence 10, Appl
37	58	14.1	565	4	US-10-278-946-10	Sequence 10, Appl
38	58	14.1	565	4	US-08-937-067-8	Sequence 8, Appli
39	58	14.1	565	4	US-08-134-000C-5782	Sequence 5782, Ap
40	58	14.1	695	6	5460961-5	Patent No. 5460961
41	58	14.1	695	6	5460961-5	Patent No. 5460961
42	58	14.1	2476	2	US-08-276-967-2	Sequence 2, Appli
43	57.5	14.0	108	4	US-09-134-000C-6807	Sequence 6807, Ap
44	57.5	14.0	1062	4	US-09-328-352-6166	Sequence 6166, Ap
45	57	13.9	185	4	US-09-538-092-759	Sequence 759, App
46	57	13.9	242	2	US-08-663-310-9	Sequence 9, Appli
47	57	13.9	242	2	US-09-006-491-9	Sequence 9, Appli
48	57	13.9	242	3	US-09-335-919-9	Sequence 9, Appli
49	57	13.9	242	3	US-08-980-832-29	Sequence 29, Appl
50	57	13.9	328	3	US-09-920-923B-29	Sequence 29, Appl
51	57	13.9	328	3	US-08-455-046-2	Sequence 2, Appli
52	57	13.9	328	4	US-09-102-710B-2	Sequence 2, Appli
53	57	13.9	693	4	US-09-252-991A-19167	Sequence 19167, A
54	57	13.9	761	4	US-09-949-016-9802	Sequence 9802, Ap
55	56.5	13.8	118	3	US-09-134-001C-5082	Sequence 5082, Ap
56	56.5	13.8	161	4	US-09-270-767-34113	Sequence 34113, A
57	56.5	13.8	161	4	US-09-270-767-49330	Sequence 49330, A
58	56.5	13.8	170	4	US-10-000-489-68	Sequence 68, Appl
59	56.5	13.8	246	4	US-09-107-532A-4119	Sequence 4119, Ap
60	56.5	13.8	408	1	US-07-951-715A-21	Sequence 21, Appl
61	56.5	13.8	408	2	US-08-459-448A-21	Sequence 21, Appl
62	56.5	13.8	408	3	US-08-459-595A-21	Sequence 21, Appl
63	56.5	13.8	408	3	US-08-459-504B-21	Sequence 21, Appl
64	56.5	13.8	408	3	US-08-459-444-21	Sequence 21, Appl
65	56.5	13.8	408	4	US-09-547-422-21	Sequence 21, Appl
66	56.5	13.8	408	4	US-09-988-462-21	Sequence 21, Appl
67	56.5	13.8	464	1	US-07-951-715A-22	Sequence 22, Appl
68	56.5	13.8	464	2	US-08-459-448A-22	Sequence 22, Appl
69	56.5	13.8	464	3	US-08-459-595A-22	Sequence 22, Appl
70	56.5	13.8	464	3	US-08-459-504B-22	Sequence 22, Appl
71	56.5	13.8	464	3	US-09-459-444-22	Sequence 22, Appl
72	56.5	13.8	464	4	US-09-547-422-22	Sequence 22, Appl
73	56.5	13.8	464	4	US-09-988-462-22	Sequence 22, Appl
74	56.5	13.8	506	4	US-09-719-919A-1	Sequence 0, Appli
75	56.5	13.8	558	4	US-09-949-016-10630	Sequence 10630, A
76	56.5	13.8	562	4	US-10-162-012-44	Sequence 44, Appl
77	56.5	13.8	1308	2	US-08-996-644-2	Sequence 2, Appli
78	56.5	13.8	1308	2	US-09-053-552-2	Sequence 2, Appli
79	56	13.7	356	4	US-09-252-991A-29888	Sequence 29888, A
80	56	13.7	2016	3	US-09-634-920-4	Sequence 4, Appli
81	56	13.7	2016	4	US-09-514-907A-2	Sequence 2, Appli
82	56	13.7	2016	4	US-09-896-994-2	Sequence 2, Appli
83	56	13.7	86	4	US-09-840-125-4	Sequence 4, Appli
84	55.5	13.5	114	4	US-09-205-258-708	Sequence 708, App
85	55.5	13.5	122	4	US-09-248-796A-20995	Sequence 20995, A
86	55.5	13.5	168	3	US-09-489-039A-9826	Sequence 9826, Ap
87	55.5	13.5	168	3	US-09-053-197A-20	Sequence 20, Appl
88	55.5	13.5	168	3	US-09-085-761A-20	Sequence 20, Appl
89	55.5	13.5	174	4	US-09-325-932A-163	Sequence 163, App
90	55.5	13.5	326	4	US-09-543-681A-6673	Sequence 6673, Ap
91	55.5	13.5	370	4	US-09-107-532A-4991	Sequence 4991, Ap
92	55.5	13.5	373	4	US-09-252-991A-19876	Sequence 19876, A
93	55.5	13.5	374	4	US-09-489-039A-8238	Sequence 8238, Ap
94	55.5	13.5	454	4	US-09-248-796A-15841	Sequence 15841, A
95	55.5	13.5	506	4	US-09-489-039A-8177	Sequence 8177, Ap
96	55.5	13.5	843	3	US-09-361-631-1	Sequence 1, Appli
97	55.5	13.5	883	4	US-09-543-681A-6947	Sequence 6947, Ap
98	55	13.4	77	4	US-09-270-767-36617	Sequence 36617, A
99	55	13.4	77	4	US-09-270-767-51834	Sequence 51834, A
100	55	13.4	207	4	US-08-811-519-23	Sequence 23, Appl

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101	55	13.4	218	4	US-09-270-767-42904	Sequence 42904, A
102	55	13.4	272	4	US-09-270-767-46084	Sequence 46084, A
103	55	13.4	289	3	US-09-134-001C-2917	Sequence 2917, Ap
104	55	13.4	327	4	US-09-107-532A-4522	Sequence 4522, Ap
105	55	13.4	354	4	US-07-759-568-2	Sequence 2, Appli
106	55	13.4	355	1	US-07-759-568-1	Sequence 1, Appli
107	55	13.4	355	1	US-08-450-393A-8	Sequence 8, Appli
108	55	13.4	355	2	US-08-390-000A-5	Sequence 5, Appli
109	55	13.4	355	3	US-08-446-669-8	Sequence 8, Appli
110	55	13.4	355	4	US-09-625-573-8	Sequence 8, Appli
111	55	13.4	355	5	PCT-US95-00476-8	Sequence 7, Appli
112	55	13.4	360	4	US-08-202-056-7	Sequence 7, Appli
113	55	13.4	360	4	US-09-409-778-4	Sequence 4, Appli
114	54.5	13.4	100	4	US-09-543-681A-4791	Sequence 4791, Ap
115	54.5	13.3	109	4	US-09-489-039A-13816	Sequence 13816, A
116	54.5	13.3	175	4	US-09-479-113B-3	Sequence 3, Appli
117	54.5	13.3	267	4	US-09-949-016-9088	Sequence 9088, Ap
118	54.5	13.3	275	4	US-09-949-016-8346	Sequence 8346, Ap
119	54.5	13.3	398	4	US-09-830-128A-5	Sequence 5, Appli
120	54.5	13.3	483	4	US-09-905-999-20	Sequence 20, Appl
121	54.5	13.3	509	4	US-09-328-352-5785	Sequence 5785, Ap
122	54.5	13.3	2763	3	US-08-496-944-2	Sequence 2, Appli
123	54.5	13.3	2818	1	US-08-510-284-1	Sequence 1, Appli
124	54.5	13.3	2818	2	US-08-411-389-2	Sequence 2, Appli
125	54.5	13.3	2818	2	US-08-449-933-2	Sequence 2, Appli
126	54.5	13.3	2818	3	US-07-966-049A-2	Sequence 2, Appli
127	54.5	13.3	2818	3	US-09-542-331-2	Sequence 2, Appli
128	54.5	13.3	2818	4	US-09-510-791-2	Sequence 2, Appli
129	54	13.2	98	4	US-09-540-236-3312	Sequence 3312, Ap
130	54	13.2	182	3	US-08-107-532A-4456	Sequence 4456, Ap
131	54	13.2	242	2	US-08-980-832-32	Sequence 32, Appl
132	54	13.2	242	4	US-09-920-923B-32	Sequence 32, Appl
133	54	13.2	279	2	US-08-326-286-7	Sequence 7, Appli
134	54	13.2	352	4	US-09-248-796A-15840	Sequence 15840, A
135	54	13.2	360	4	US-09-116-498-12	Sequence 12, Appl
136	54	13.2	360	4	US-09-852-156-12	Sequence 12, Appl
137	54	13.2	384	4	US-09-252-991A-27511	Sequence 27511, A
138	54	13.2	400	4	US-09-252-991A-22821	Sequence 22821, A
139	54	13.2	418	4	US-09-248-796A-18870	Sequence 18870, A
140	54	13.2	434	4	US-09-543-681A-7154	Sequence 7154, Ap
141	54	13.2	542	4	US-09-693-746-18	Sequence 18, Appl
142	54	13.2	543	3	US-08-937-067-13	Sequence 13, Appl
143	54	13.2	572	2	US-08-846-526-11	Sequence 11, Appl
144	54	13.2	599	3	US-09-172-339-2	Sequence 2, Appli
145	54	13.2	599	4	US-09-398-395A-22	Sequence 22, Appl
146	54	13.2	599	4	US-09-887-586A-22	Sequence 22, Appl
147	54	13.2	599	4	US-09-895-752-22	Sequence 22, Appl
148	54	13.2	599	4	US-09-903-012B-22	Sequence 22, Appl
149	54	13.2	599	4	US-09-900-797-22	Sequence 22, Appl
150	54	13.2	726	4	US-09-489-039A-7465	Sequence 7465, Ap
151	54	13.0	147	1	US-09-489-039A-13728	Sequence 13728, A
152	53.5	13.0	175	1	US-08-010-099-85	Sequence 85, Appl
153	53.5	13.0	175	4	US-08-448-716-85	Sequence 85, Appl
154	53.5	13.0	175	4	US-09-304-186-85	Sequence 85, Appl
155	53.5	13.0	175	4	US-09-754-532-85	Sequence 85, Appl
156	53.5	13.0	212	4	US-09-489-039A-7465	Sequence 7465, Ap
157	53.5	12.9	173	2	US-09-248-796A-14863	Sequence 14863, A
158	53	12.9	192	3	US-09-134-001C-3448	Sequence 3448, Ap
159	53	12.9	207	4	US-08-811-519-22	Sequence 22, Appl
160	53	12.9	248	4	US-09-248-796A-15839	Sequence 15839, A
161	53	12.9	297	4	US-09-328-352-7074	Sequence 7074, Ap
162	53	12.9	308	4	US-09-248-796A-20449	Sequence 20449, A
163	53	12.9	318	4	US-09-489-039A-10302	Sequence 10302, A
164	53	12.9	327	3	US-08-513-974B-372	Sequence 372, Appl
165	53	12.9	328	3	US-08-513-974B-371	Sequence 371, Appl
166	53	12.9	328	4	US-09-461-436B-39	Sequence 39, Appl
167	53	12.9	328	4	US-09-461-436B-39	Sequence 39, Appl
168	53	12.9	318		US-09-489-039A-10302	Sequence 10302, A
169	53	12.9	327		US-08-513-974B-372	Sequence 372, Appl
170	53	12.9	328		US-08-513-974B-371	Sequence 371, Appl
171	53	12.9	328		US-09-461-436B-39	Sequence 39, Appl
172	53	12.9	350	1	US-08-202-056-1	Sequence 1, Appli
173	53					

#					Patent	Sequence
174	53	12.9	350	1	US-08-076-093A-2	Sequence 2, Appli
175	53	12.9	350	1	US-08-450-393A-7	Sequence 7, Appli
176	53	12.9	350	1	US-08-701-265-2	Sequence 1, Appli
177	53	12.9	350	1	US-08-410-454A-1	Sequence 2, Appli
178	53	12.9	350	1	US-08-284-586-2	Sequence 1, Appli
179	53	12.9	350	2	US-08-410-456A-1	Sequence 1, Appli
180	53	12.9	350	2	US-08-805-478-2	Sequence 2, Appli
181	53	12.9	350	2	US-08-802-627A-2	Sequence 2, Appli
182	53	12.9	350	2	US-08-801-238-2	Sequence 2, Appli
183	53	12.9	350	2	US-08-801-228-2	Sequence 2, Appli
184	53	12.9	350	3	US-09-104-296-2	Sequence 2, Appli
185	53	12.9	350	3	US-08-446-669-7	Sequence 7, Appli
186	53	12.9	350	3	US-08-446-669-7	Sequence 7, Appli
187	53	12.9	350	4	US-09-625-573-7	Sequence 7, Appli
188	53	12.9	350	5	PCT-US95-00476-7	Sequence 7, Appli
189	53	12.9	375	4	US-09-540-236-3290	Sequence 3290, Ap
190	53	12.9	386	4	US-09-543-681A-8033	Sequence 8033, Ap
191	53	12.9	405	4	US-08-134-000C-5472	Sequence 5472, A
192	53	12.9	474	4	US-09-252-991A-26872	Sequence 26872, A
193	53	12.9	534	4	US-09-252-991A-30725	Sequence 30725, A
194	53	12.9	537	4	US-08-937-067-11	Sequence 11, Appl
195	53	12.9	547	4	US-09-489-039A-13843	Sequence 13843, A
196	53	12.9	555	2	US-09-328-352-5873	Sequence 5873, Ap
197	53	12.9	589	4	US-08-937-540-6	Sequence 6, Appli
198	53	12.9	590	4	US-09-398-395A-54	Sequence 54, Appl
199	53	12.9	590	4	US-09-887-586A-54	Sequence 54, Appl
200	53	12.9	590	4	US-09-895-752-54	Sequence 54, Appl
201	53	12.9	590	4	US-09-903-012B-54	Sequence 54, Appl
202	53	12.9	590	4	US-09-900-797-54	Sequence 54, Appl
203	53	12.9	768	4	US-09-489-039A-12897	Sequence 12897, A
204	53	12.9	1077	4	US-09-397-550-24	Sequence 24, Appl
205	53	12.9	1091	4	US-10-162-012-18	Sequence 18, Appl
206	53	12.9	1371	4	US-09-902-540-16024	Sequence 16024, A
207	52.5	12.8	60	4	US-09-621-976-5232	Sequence 5232, Ap
208	52.5	12.8	82	4	US-09-248-796A-22737	Sequence 22737, A
209	52.5	12.8	82	4	US-09-248-796A-25141	Sequence 25141, A
210	52.5	12.8	113	1	US-09-710-279-452	Sequence 452, App
211	52.5	12.8	113	1	US-09-710-279-1206	Sequence 1206, Ap
212	52.5	12.8	113	1	US-09-949-016-11441	Sequence 11441, A
213	52.5	12.8	175	3	US-08-010-099-83	Sequence 83, Appl
214	52.5	12.8	175	3	US-08-448-716-83	Sequence 83, Appl
215	52.5	12.8	175	3	US-08-448-716-87	Sequence 87, Appl
216	52.5	12.8	175	3	US-09-304-186-83	Sequence 87, Appl
217	52.5	12.8	175	3	US-09-304-186-87	Sequence 83, Appl
218	52.5	12.8	175	3	US-09-754-532-83	Sequence 83, Appl
219	52.5	12.8	175	3	US-09-754-532-87	Sequence 87, Appl
220	52.5	12.8	190	4	US-09-543-681A-5070	Sequence 5070, Ap
221	52.5	12.8	228	4	US-09-248-796A-20444	Sequence 20444, A
222	52.5	12.8	230	4	US-09-248-796A-14250	Sequence 14250, A
223	52.5	12.8	243	4	US-09-489-039A-13302	Sequence 13302, A
224	52.5	12.8	289	4	US-09-489-039A-10785	Sequence 10785, A
225	52.5	12.8	302	4	US-09-583-110-4512	Sequence 4512, Ap
226	52.5	12.8	302	4	US-09-107-433-4866	Sequence 4866, Ap
227	52.5	12.8	360	4	US-09-116-498-8	Sequence 8, Appli
228	52.5	12.8	360	3	US-09-517-605-10	Sequence 10, Appl
229	52.5	12.8	360	4	US-09-170-496D-28	Sequence 28, Appl
230	52.5	12.8	360	4	US-09-170-496D-180	Sequence 180, App
231	52.5	12.8	360	4	US-09-852-156-8	Sequence 8, Appli
232	52.5	12.8	423	4	US-09-489-039A-9464	Sequence 9464, Ap
233	52.5	12.8	470	2	US-08-377-440A-1	Sequence 1, Appli
234	52.5	12.8	470	3	US-09-440-530-1	Sequence 10, Appl
235	52.5	12.8	672	3	US-09-543-681A-5976	Sequence 5976, Ap
236	52.5	12.8	2787	4	US-09-245-041-15	Sequence 15, Appl
237	52.5	12.8	2787	4	US-09-358-055B-15	Sequence 15, Appl
238	52.5	12.8	2787	4	US-09-893-238-15	Sequence 15, Appl
239	52.5	12.7	2787	4	US-09-393-634-27	Sequence 27, Appl
240	52	12.7	115	4	US-09-489-039A-3932	Sequence 3932, Ap
241	52	12.7	141	4	US-09-621-976-3932	Sequence 2, Appli
242	52	12.7	212	2	US-08-663-310-2	Sequence 2, Appli
243	52	12.7	212	2	US-09-006-491-2	Sequence 2, Appli
244	52	12.7	212	4	US-09-335-919-2	Sequence 2, Appli
245	52	12.7	234	4	US-09-270-767-44557	Sequence 44557, A
246	52	12.7	262	4	US-09-270-767-45003	Sequence 45003, A

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249	51.5	12.7	52	361	4	US-09-178-637-2	Sequence 2, Appli
250	51.5	12.7	52	424	4	US-09-107-532A-5459	Sequence 5459, Ap
251	51.5	12.7	52	469	4	US-09-489-039A-10553	Sequence 10553, A
252	51.5	12.7	52	538	4	US-09-107-532A-5563	Sequence 5563, A
253	51.5	12.7	52	583	4	US-09-489-039A-13918	Sequence 13918, A
254	51.5	12.7	52	666	4	US-08-937-067-10	Sequence 10, Appl
255	51.5	12.7	52	765	4	US-09-270-767-32645	Sequence 32645, A
256	51.5	12.7	52	765	3	US-09-270-767-47862	Sequence 47862, A
257	51.5	12.7	52	1011	3	US-08-836-325-2	Sequence 2, Appli
258	51.5	12.7	52	1011	4	US-09-457-571-2	Sequence 2, Appli
259	51.5	12.7	52	1835	3	US-08-836-325-15	Sequence 15, Appl
260	51.5	12.7	52	1835	4	US-09-457-571-15	Sequence 15, Appl
261	51.5	12.7	52	1969	3	US-08-836-325-16	Sequence 16, Appl
262	51.5	12.7	52	1969	4	US-09-457-571-16	Sequence 16, Appl
263	51.5	12.7	52	1977	4	US-09-976-594-757	Sequence 757, App
264	51.5	12.7	52	1984	3	US-09-919-039-367	Sequence 367, App
265	51.5	12.7	52	1984	4	US-08-836-325-10	Sequence 10, Appl
266	51.5	12.7	52	1989	3	US-09-457-571-10	Sequence 11, Appl
267	51.5	12.7	52	1989	4	US-08-836-325-11	Sequence 11, Appl
268	51.5	12.7	52	1989	3	US-08-836-325-12	Sequence 12, Appl
269	51.5	12.7	52	1989	4	US-09-457-571-11	Sequence 12, Appl
270	51.5	12.7	52	1989	4	US-09-457-571-12	Sequence 96, Appl
271	51.5	12.6		172	4	US-09-663-600A-96	Sequence 96, Appl
272	51.5	12.6		172	4	US-09-270-767-36922	Sequence 36922, A
273	51.5	12.6		173	4	US-09-270-767-52139	Sequence 52139, A
274	51.5	12.6		173	1	US-08-354-456A-7	Sequence 7, Appli
275	51.5	12.6		174	1	US-08-010-099-82	Sequence 82, Appl
276	51.5	12.6		174	1	US-08-225-224-5	Sequence 5, Appli
277	51.5	12.6		174	2	US-08-448-716-82	Sequence 82, Appl
278	51.5	12.6		174	1	US-08-431-459A-31	Sequence 31, Appl
279	51.5	12.6		174	1	US-08-722-258-5	Sequence 5, Appli
280	51.5	12.6		174	3	US-08-833-167-49	Sequence 49, Appl
281	51.5	12.6		174	3	US-08-833-167-50	Sequence 50, Appl
282	51.5	12.6		174	3	US-08-833-167-51	Sequence 51, Appl
283	51.5	12.6		174	3	US-08-833-167-52	Sequence 52, Appl
284	51.5	12.6		174	3	US-08-833-167-53	Sequence 53, Appl
285	51.5	12.6		174	3	US-08-833-167-54	Sequence 54, Appl
286	51.5	12.6		174	3	US-08-833-167-55	Sequence 55, Appl
287	51.5	12.6		174	3	US-08-833-167-56	Sequence 56, Appl
288	51.5	12.6		174	3	US-08-833-167-96	Sequence 96, Appl
289	51.5	12.6		174	3	US-08-833-167-97	Sequence 97, Appl
290	51.5	12.6		174	3	US-08-833-167-98	Sequence 98, Appl
291	51.5	12.6		174	3	US-08-833-167-99	Sequence 99, Appl
292	51.5	12.6		174	3	US-08-833-167-100	Sequence 100, App
293	51.5	12.6		174	3	US-08-833-167-101	Sequence 101, App
294	51.5	12.6		174	3	US-08-833-167-102	Sequence 102, App
295	51.5	12.6		174	3	US-09-221-181-1	Sequence 1, Appli
296	51.5	12.6		174	3	US-09-304-186-82	Sequence 82, Appl
297	51.5	12.6		174	3	US-09-344-837A-49	Sequence 49, Appl
298	51.5	12.6		174	3	US-09-344-837A-50	Sequence 50, Appl
299	51.5	12.6		174	3	US-09-344-837A-51	Sequence 51, Appl
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301	51.5	12.6		174	3	US-09-344-837A-53	Sequence 53, Appl
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304	51.5	12.6		174	3	US-09-344-837A-56	Sequence 56, Appl
305	51.5	12.6		174	3	US-09-344-837A-96	Sequence 96, Appl
306	51.5	12.6		174	3	US-09-344-837A-97	Sequence 97, Appl
307	51.5	12.6		174	3	US-09-344-837A-98	Sequence 98, Appl
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310	51.5	12.6		174	3	US-09-344-837A-101	Sequence 101, App
311	51.5	12.6		174	3	US-09-344-837A-102	Sequence 102, App
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313	51.5	12.6		174	4	US-09-462-941-6	Sequence 6, Appli
314	51.5	12.6		174	4	US-09-479-313B-2	Sequence 2, Appli
315	51.5	12.6		174	4	US-09-754-532-82	Sequence 82, Appl
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317	51.5	12.6		174	4	US-09-950-473-2	Sequence 2, Appli
318	51.5	12.6		174	4	US-10-192-294-1	Sequence 1, Appli
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349	51.5	12.6	175	1	US-08-010-099-105	Sequence 105, App
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383	51.5	12.6	175	1	US-08-448-716-104	Sequence 104, App
384	51.5	12.6	175	1	US-08-448-716-105	Sequence 105, App
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498	51.5	12.6	177	3	US-09-344-837A-127	Sequence 127, App
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503	51.5	12.6	177	4	US-09-510-238A-304	Sequence 304, App
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823	50	12.2	262	4	US-09-489-039A-7774	Sequence 22359, A
824	50	12.2	273	3	US-09-252-991A-22359	Sequence 3016, Ap
825	50	12.2	275	4	US-09-134-001C-3016	Sequence 7149, Ap
826	50	12.2	289	4	US-09-543-681A-7149	Sequence 15052, A
827	50	12.2	301	4	US-09-248-796A-15052	Sequence 5112, Ap
830	50	12.2	301	4	US-09-583-110-5112	Sequence 5112, Ap

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831	50	12.2	301	4	US-09-107-433-2809	Sequence 2809, Appli
832	50	12.2	309	4	US-09-540-236-3022	Sequence 3022, Ap
833	50	12.2	376	4	US-09-949-016-7545	Sequence 7545, Ap
834	50	12.2	457	4	US-09-489-039A-8293	Sequence 8293, Ap
835	50	12.2	469	2	US-08-968-751-2	Sequence 2, Appli
836	50	12.2	470	3	US-09-052-089A-2	Sequence 2, Appl
837	50	12.2	504	4	US-09-949-016-11605	Sequence 11605, A
838	50	12.2	595	4	US-09-902-540-15969	Sequence 15969, A
839	50	12.2	621	4	US-09-602-787A-342	Sequence 342, Appl
840	50	12.2	1233	4	US-09-354-147C-7	Sequence 7, Appli
841	50	12.2	1243	4	US-09-354-147C-8	Sequence 8, Appli
842	50	12.2	1284	4	US-09-343-494-9	Sequence 9, Appli
843	50	12.2	1284	4	US-09-358-383C-11	Sequence 11, Appl
844	50	12.2	1284	4	US-10-160-224-9	Sequence 9, Appli
845	50	12.2	1791	4	US-09-354-147C-42	Sequence 42, Appl
846	49.5	12.1	46	3	US-08-974-549A-168	Sequence 168, App
847	49.5	12.1	46	4	US-09-402-181B-168	Sequence 168, App
848	49.5	12.1	46	4	US-09-721-456-168	Sequence 168, App
849	49.5	12.1	50	4	US-09-621-976-6194	Sequence 6194, Ap
850	49.5	12.1	101	4	US-09-540-236-2002	Sequence 2002, Ap
851	49.5	12.1	110	4	US-09-384-302A-27	Sequence 27, Appl
852	49.5	12.1	123	4	US-09-270-767-33508	Sequence 33508, A
853	49.5	12.1	123	4	US-09-270-767-48725	Sequence 48725, A
854	49.5	12.1	125	4	US-09-489-039A-7420	Sequence 7420, A
855	49.5	12.1	163	4	US-09-252-991A-29098	Sequence 29098, A
856	49.5	12.1	172	4	US-09-134-000C-5018	Sequence 5018, Ap
857	49.5	12.1	175	4	US-09-479-313B-9	Sequence 9, Appli
858	49.5	12.1	188	4	US-09-248-796A-15302	Sequence 15302, A
859	49.5	12.1	206	3	US-08-513-974B-27	Sequence 27, Appl
860	49.5	12.1	206	3	US-08-776-971-22	Sequence 22, Appl
861	49.5	12.1	206	3	US-09-461-436B-27	Sequence 27, Appl
862	49.5	12.1	206	3	US-09-576-290-22	Sequence 22, Appl
863	49.5	12.1	223	3	US-08-513-974B-315	Sequence 315, App
864	49.5	12.1	223	3	US-08-513-974B-364	Sequence 364, App
865	49.5	12.1	223	3	US-08-513-974B-368	Sequence 368, App
866	49.5	12.1	223	3	US-08-776-971-100	Sequence 100, App
867	49.5	12.1	223	3	US-08-776-971-102	Sequence 102, App
868	49.5	12.1	223	3	US-08-776-971-108	Sequence 108, App
869	49.5	12.1	223	3	US-09-576-290-100	Sequence 100, App
870	49.5	12.1	223	3	US-09-576-290-102	Sequence 102, App
871	49.5	12.1	223	3	US-09-576-290-108	Sequence 108, App
872	49.5	12.1	240	4	US-09-270-767-38489	Sequence 38489, A
873	49.5	12.1	240	4	US-09-270-767-53706	Sequence 53706, A
874	49.5	12.1	263	4	US-10-000-489-40	Sequence 40, Appl
875	49.5	12.1	289	4	US-09-134-000C-5932	Sequence 5932, Ap
876	49.5	12.1	303	4	US-09-949-016-9114	Sequence 9114, Ap
877	49.5	12.1	308	4	US-09-328-352-7093	Sequence 7093, App
878	49.5	12.1	311	4	US-09-252-991A-17395	Sequence 17395, A
879	49.5	12.1	317	4	US-09-489-039A-9602	Sequence 9602, Ap
880	49.5	12.1	338	4	US-09-270-767-46192	Sequence 46192, A
881	49.5	12.1	344	4	US-08-681-192-2	Sequence 2, Appli
882	49.5	12.1	348	4	US-09-360-376-13	Sequence 13, Appl
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893	49.5	12.1	560	4	US-09-134-000C-5889	Sequence 5889, Appli
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895	49.5	12.1	560	3	US-08-854-050-6	Sequence 6, Appli
896	49.5	12.1	560	4	US-09-430-323-6	Sequence 6, Appli
897	49.5	12.1	603	3	US-09-766-253-6	Sequence 6, Appli
898	49.5	12.1	603	3	US-09-149-727-6	Sequence 6, Appli
899	49.5	12.1	603	4	US-09-270-957-17	Sequence 17, Appl
900	49.5	12.1	604	4	US-09-270-957-23	Sequence 23, Appl
901	49.5	12.1	659	4	US-09-893-525-37	Sequence 37, Appl
902	49.5	12.1	745	4	US-09-489-039A-10904	Sequence 10904, A
903	49.5	12.1	832	3	US-08-630-820-7	Sequence 7, Appli

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906	49.5	12.1	937	3	US-09-005-180A-4	Sequence 4, Appli
907	49.5	12.1	940	4	US-09-328-352-8165	Sequence 8165, Ap
908	49.5	12.1	944	4	US-09-538-092-452	Sequence 452, App
909	49.5	12.1	1010	4	US-09-118-276-12	Sequence 12, Appl
910	49	12.0	1131	4	US-09-252-991A-31247	Sequence 31247, A
911	49	12.0	74	4	US-09-270-767-39467	Sequence 39467, A
912	49	12.0	74	4	US-09-270-767-54684	Sequence 54684, A
913	49	12.0	148	4	US-09-270-767-45573	Sequence 45573, A
914	49	12.0	150	4	US-09-107-433-3841	Sequence 3841, Ap
915	49	12.0	192	4	US-09-540-236-3328	Sequence 3328, Ap
916	49	12.0	204	4	US-09-252-991A-21145	Sequence 21145, A
917	49	12.0	229	4	US-09-328-352-6458	Sequence 6458, Ap
918	49	12.0	256	4	US-09-328-352-7827	Sequence 7827, Ap
919	49	12.0	268	4	US-09-248-796A-17195	Sequence 17195, A
920	49	12.0	285	4	US-09-248-796A-14977	Sequence 14977, A
921	49	12.0	286	4	US-09-710-279-402	Sequence 402, App
922	49	12.0	342	4	US-09-248-796A-27396	Sequence 27396, A
923	49	12.0	357	4	US-09-723-806A-9	Sequence 9, Appli
924	49	12.0	380	4	US-09-902-540-14637	Sequence 14637, A
925	49	12.0	385	4	US-09-252-991A-24469	Sequence 24469, A
926	49	12.0	408	4	US-09-248-796A-16068	Sequence 16068, A
927	49	12.0	453	4	US-09-710-279-1516	Sequence 1516, Ap
928	49	12.0	454	3	US-09-134-001C-3501	Sequence 3501, Ap
929	49	12.0	456	4	US-09-543-681A-6063	Sequence 6063, Ap
930	49	12.0	487	4	US-09-489-039A-12980	Sequence 12980, A
931	49	12.0	535	4	US-09-252-991A-21652	Sequence 21652, A
932	49	12.0	565	4	US-03-489-039A-8414	Sequence 8414, Ap
933	49	12.0	706	2	US-08-987-289-2	Sequence 2, Appli
934	49	12.0	727	4	US-09-543-681A-7968	Sequence 7968, Ap
935	49	12.0	1019	4	US-09-397-550-10	Sequence 10, Appl
936	49	12.0	1038	4	US-09-621-976-6408	Sequence 6408, Ap
937	49	12.0	1065	4	US-09-397-550-11	Sequence 11, Appl
938	49	12.0	1085	4	US-09-397-550-12	Sequence 12, Appl
939	49	12.0	1091	4	US-09-397-550-22	Sequence 22, Appl
940	49	12.0	1765	4	US-10-162-012-15	Sequence 15, Appl
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942	48.5	11.8	56	4	US-09-792-024-98	Sequence 98, Appl
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945	48.5	11.8	100	4	US-09-270-767-48616	Sequence 48616, A
946	48.5	11.8	109	4	US-09-328-352-6204	Sequence 6204, Ap
947	48.5	11.8	109	4	US-09-328-352-7123	Sequence 7123, Ap
948	48.5	11.8	125	4	US-09-489-039A-11686	Sequence 11686, A
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951	48.5	11.8	153	4	US-09-270-767-50713	Sequence 50713, A
952	48.5	11.8	154	4	US-09-489-847-233	Sequence 233, App
953	48.5	11.8	166	4	US-08-311-731A-299	Sequence 299, App
954	48.5	11.8	171	4	US-09-489-847-152	Sequence 152, App
955	48.5	11.8	175	4	US-09-479-313B-4	Sequence 4, Appli
956	48.5	11.8	175	4	US-09-479-313B-6	Sequence 6, Appli
957	48.5	11.8	207	4	US-09-489-847-312	Sequence 312, App
958	48.5	11.8	254	4	US-09-107-532A-4025	Sequence 4025, Ap
959	48.5	11.8	292	4	US-09-543-681A-7272	Sequence 7272, Ap
960	48.5	11.8	295	4	US-09-710-279-654	Sequence 654, App
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962	48.5	11.8	307	4	US-09-193-510-3	Sequence 3, Appli
963	48.5	11.8	307	3	US-09-368-402-3	Sequence 3, Appli
964	48.5	11.8	308	4	US-09-248-796A-15413	Sequence 15413, A
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966	48.5	11.8	330	4	US-09-543-681A-4735	Sequence 4735, Ap
967	48.5	11.8	334	3	US-09-134-001C-3851	Sequence 3851, Ap
968	48.5	11.8	338	4	US-09-489-039A-7801	Sequence 7801, Ap
969	48.5	11.8	353	4	US-09-902-540-14186	Sequence 14186, A
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971	48.5	11.8	360	1	US-08-746-682A-11	Sequence 11, Appl
972	48.5	11.8	361	4	US-09-252-991A-25005	Sequence 25005, A
973	48.5	11.8	434	2	US-08-529-600D-2	Sequence 2, Appli
974	48.5	11.8	434	3	US-08-973-275-4	Sequence 4, Appli
975	48.5	11.8	434	3	US-09-122-632-2	Sequence 2, Appli
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981	48.5	11.8	529	4	US-09-784-859-6	Sequence 6, Appli
982	48.5	11.8	529	4	US-10-414-186-85	Sequence 85, Appl
983	48.5	11.8	529	4	US-09-825-561A-12	Sequence 12, Appl
984	48.5	11.8	529	4	US-10-243-072-85	Sequence 85, Appl
985	48.5	11.8	544	4	US-09-540-236-2905	Sequence 2905, Ap
986	48.5	11.8	557	4	US-09-252-991A-21787	Sequence 21787, A
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988	48.5	11.8	703	4	US-09-134-000C-5072	Sequence 5072, Ap
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992	48.5	11.8	886	4	US-09-631-603-14	Sequence 14, Appl
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994	48.5	11.8	2386	4	US-09-029-047C-4	Sequence 4, Appli
995	48	11.7	71	4	US-09-621-976-5656	Sequence 5656, Ap
996	48	11.7	73	4	US-09-149-476-579	Sequence 579, App
997	48	11.7	101	4	US-09-270-767-40263	Sequence 40263, A
998	48	11.7	101	4	US-09-270-767-55479	Sequence 55479, A
999	48	11.7	117	4	US-09-270-767-34845	Sequence 34845, A
1000	48	11.7	117	4	US-09-270-767-50062	Sequence 50062, A
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1012	48	11.7	169	4	US-09-540-236-2163	Sequence 2163, Ap
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1014	48	11.7	174	4	US-09-149-476-424	Sequence 424, App
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1077	48	11.7	550	3	US-09-361-718-28	Sequence 28, Appl
1078	48	11.7	550	4	US-09-398-395A-28	Sequence 28, Appl
1079	48	11.7	550	4	US-09-887-586A-28	Sequence 28, Appl
1080	48	11.7	550	4	US-09-895-752-28	Sequence 28, Appl
1081	48	11.7	550	4	US-09-903-012B-28	Sequence 28, Appl
1082	48	11.7	562	4	US-09-900-797-28	Sequence 28, Appl
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1084	48	11.7	573	4	US-09-270-767-38339	Sequence 38339, A
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ALIGNMENTS

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; Sequence 32997, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32997
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-32997

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;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48214
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-48214

  Query Match             57.3%;  Score 235;  DB 4;  Length 168;
  Best Local Similarity   62.2%;  Pred. No. 5e-22;
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RESULT 5
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; Sequence 11699, Application US/09489039A
; Patent No. 6610836
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;   APPLICANT: Gary Breton et. al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;   TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 2709.2004001
;   CURRENT APPLICATION NUMBER: US/09/489,039A
;   CURRENT FILING DATE: 2000-01-27
;   PRIOR APPLICATION NUMBER: US 60/117,747
;   PRIOR FILING DATE: 1999-01-29
;   NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11699
;   LENGTH: 404
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11699

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; Sequence 12390, Application US/09489039A
; Patent No. 6610836
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;   APPLICANT: Gary Breton et. al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;   TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 2709.2004001
;   CURRENT APPLICATION NUMBER: US/09/489,039A
;   CURRENT FILING DATE: 2000-01-27
;   PRIOR APPLICATION NUMBER: US 60/117,747
;   PRIOR FILING DATE: 1999-01-29
;   NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12390
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12390

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RESULT 7
US-09-252-991A-24117
; Sequence 24117, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
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; Sequence 20672, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;   APPLICANT: Keith Weinstock et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;   TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.132
;   CURRENT APPLICATION NUMBER: US/09/248,796A
;   CURRENT FILING DATE: 1999-02-12
;   PRIOR APPLICATION NUMBER: US 60/074,725
;   PRIOR FILING DATE: 1998-02-13
;   PRIOR APPLICATION NUMBER: US 60/096,409
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20672
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-20672

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RESULT 4
US-09-538-092-22
; Sequence 22, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;   APPLICANT: Giot, Loic
;   APPLICANT: Mansfield, Traci A.
;   TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;   FILE REFERENCE: 15966-542
;   CURRENT APPLICATION NUMBER: US/09/538,092
;   CURRENT FILING DATE: 2000-03-29
;   PRIOR APPLICATION NUMBER: US 60/127,352
;   PRIOR FILING DATE: 1999-04-01
;   PRIOR APPLICATION NUMBER: US 60/178,965
;   PRIOR FILING DATE: 2000-02-01
;   NUMBER OF SEQ ID NOS: 1387
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;   LENGTH: 215
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;   ORGANISM: Saccharomyces cerevisiae
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;     NAME/KEY: misc_feature
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;     OTHER INFORMATION: Polypeptide Accession Number YBL102W
US-09-538-092-22

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RESULT 9
US-09-134-001C-3503
; Sequence 3503, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;   TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC-007
;   CURRENT APPLICATION NUMBER: US/09/134,001C
;   CURRENT FILING DATE: 1998-08-13
;   PRIOR APPLICATION NUMBER: US 60/064,964
;   PRIOR APPLICATION FILING DATE: 1997-11-08
;   PRIOR APPLICATION NUMBER: US 60/055,779
;   PRIOR APPLICATION FILING DATE: 1997-08-14
;   NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3503
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3503

Query Match   15.4%; Score 63; DB 3; Length 74;
Best Local Similarity   36.5%; Pred. No. 1.1;
Matches   19; Conservative   6; Mismatches   15; Indels   12; Gaps   3;

Qy   8 KRMFEPTRLIATIMVLLCFALTLC---SAFW-------WHNKGLALIFCILQ 49
            | |:| :|| |::|| | || |||:|||||||
Db   12 KSMFQVFYNVKTVWNF--WALTECISIDKAIWLSTIKGWHNEGIMNICLILQ 61

RESULT 10
US-09-252-991A-24883
; Sequence 24883, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24883
;   LENGTH: 464
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24883

Query Match   15.0%; Score 61.5; DB 4; Length 464;
Best Local Similarity   25.4%; Pred. No. 13;
Matches   17; Conservative   8; Mismatches   23; Indels   19; Gaps   3;

Qy   9 RMFEPTRLIATIMVLLCFALTLCSAFWH-----------------------NKGLALIFCILQSLAL 53
            ||: |::: || |||| :| : |||| :||
Db   48 KMF---RMLVLFMVFFCCSSASADAFWWQVNGIDSLRDKSFASPGEGCSAVLAYFQSQG- 103

Qy   54 TWYSLSF 60
            | |:|||
Db   104 SGYSFSF 110

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24117
LENGTH: 416
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24117

Query Match   15.6%; Score 64; DB 4; Length 416;
Best Local Similarity   38.2%; Pred. No. 5.7;
Matches   13; Conservative   6; Mismatches   15; Indels   0; Gaps   0;

Qy   34 FWWHNKGLALIFCILQSLALTWYSLSFIPFARDA 67
            |||: ||| | :|:||||| |: |
Db   46 FWYFFGSLALLVLVNQILTGIWLTMSFTPSAEEA 79

RESULT 8
US-08-937-067-14
; Sequence 14, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
;   APPLICANT: Unansky, Samuil
;   APPLICANT: Melkonyan, Hovsep
;   TITLE OF INVENTION: A FAMILY OF GENES ENCODING
;   TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/937,067
;   FILING DATE:
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/937,067
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lehnhardt, Susan K.
;   REGISTRATION NUMBER: 33,943
;   REFERENCE/DOCKET NUMBER: 23647-20018.00
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 813-5600
;   TELEFAX: (650) 494-0792
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 685 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-937-067-14

Query Match   15.6%; Score 64; DB 4; Length 685;
Best Local Similarity   22.1%; Pred. No. 10;
Matches   15; Conservative   15; Mismatches   15; Indels   26; Gaps   1;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60

RESULT 11
US-08-157-005-2
; Sequence 2, Application US/08157005
; Patent No. 5620691
; GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
; APPLICANT: Terpstra, Catharinus
; APPLICANT: Pol, Johannes M
; APPLICANT: Moorman, Robertus J
; APPLICANT: Meulenberg, Johanna J
; TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper & Dunham
;   STREET: 30 Rockefeller Plaza
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10112
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/157,005
;   FILING DATE: 26-NOV-1993
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 91201398.4
;   FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 92200781.0
;   FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/NL92/00096
;   FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Moran, Thomas F
;   REGISTRATION NUMBER: 16,579
;   REFERENCE/DOCKET NUMBER: 44819
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 977-9550
;   TELEFAX: (212) 315-1931
;   TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2396 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-157-005-2

Query Match   15.0%; Score 61.5; DB 1; Length 2396;
Best Local Similarity   30.1%; Pred. No. 85;
Matches   22; Conservative   14; Mismatches   26; Indels   11; Gaps   5;

Qy   8 KRMFEPTR-LIATIMVLLCFALTLC---SAFWWHNKGLALIFCILQSLALTWYSLSFIPF 63
              :::||||.| :|||||||||||||| :.|| | ||||| .|:| |||:
Db   1220 RQLWEPVRGLVVGPSGLLCVILGKLLGGSRYLWH---VLLRLCMLADLAL---SLVYV-V 1272

Qy   64 ARDAVKKCFAVCL 76
              :: |||.:|:
Db   1273 SQGRCHKCWGKCI 1285

RESULT 12
US-08-747-863-2
; Sequence 2, Application US/08747863
; Patent No. 6197310
; GENERAL INFORMATION:

; APPLICANT: Wensvoort, Gert
; APPLICANT: Terpstra, Catharinus
; APPLICANT: Pol, Johannes M
; APPLICANT: Moorman, Robertus J
; APPLICANT: Meulenberg, Johanna J
; TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Trask, Britt & Rossa
;   STREET: 525 South 300 East
;   CITY: Salt Lake City
;   STATE: Utah
;   COUNTRY: USA
;   ZIP: 84111
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: WINDOWS95
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/747,863
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/157,005
;   FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 91201398.4
;   FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 92200781.0
;   FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/NL92/00096
;   FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Turner, Allen C.
;   REGISTRATION NUMBER: 33041
;   REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (801) 532-1922
;   TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2396 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-747-863-2

Query Match   15.0%; Score 61.5; DB 3; Length 2396;
Best Local Similarity   30.1%; Pred. No. 85;
Matches   22; Conservative   14; Mismatches   26; Indels   11; Gaps   5;

Qy   8 KRMFEPTR-LIATIMVLLCFALTLC---SAFWWHNKGLALIFCILQSLALTWYSLSFIPF 63
              :::||||.| :|||||||||||||| :.|| | ||||| .|:| |||:
Db   1220 RQLWEPVRGLVVGPSGLLCVILGKLLGGSRYLWH---VLLRLCMLADLAL---SLVYV-V 1272

Qy   64 ARDAVKKCFAVCL 76
              :: |||.:|:
Db   1273 SQGRCHKCWGKCI 1285

RESULT 13
US-09-565-864-2
; Sequence 2, Application US/09565864
; Patent No. 6455245
; GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
;   Terpstra, Catharinus
;   Pol, Johannes M
;   Moorman, Robertus J

```
                Meulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
                    VACCINE COMPOSITIONS AND DIAGNOSTIC KITS

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper & Dunham
    STREET: 30 Rockefeller Plaza
    CITY: New York
    STATE: New York
    COUNTRY: USA
    ZIP: 10112
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/565,864
    FILING DATE: 05-May-2000
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/157,005
    FILING DATE: <Unknown>
    APPLICATION NUMBER: EP 91201398.4
    FILING DATE: 06-JUN-1991
    APPLICATION NUMBER: EP 92200781.0
    FILING DATE: 18-MAR-1992
    APPLICATION NUMBER: PCT/NL92/00096
    FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
    NAME: Moran, Thomas F
    REGISTRATION NUMBER: 16,579
    REFERENCE/DOCKET NUMBER: 44819
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 977-9550
    TELEFAX: (212) 315-1931
    TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2396 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-565-864-2

Query Match            15.0%;   Score 61.5;   DB 4;   Length 2396;
Best Local Similarity  30.1%;   Pred. No. 85;
Matches  22;  Conservative  14;  Mismatches  26;  Indels  11;  Gaps 5;

Qy      8 KRMFEPTR-LIATIMVLLCFALTLC---SAFWWHNKGLALIFCILQSLALTWYSLSFPF 63
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Db   1220 RQLWEPVRGLVVGPSGLLCVILGKLLGGSRYLWH---VLLRLCMLADLAL---SLVYV-V 1272

Qy     64 ARDAVKKCFAVCL 76
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Db   1273 SQGRCHKCWGKCI 1285


RESULT 14
US-10-226-065-2
; Sequence 2, Application US/10226065
; Patent No. 6806086
; GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
;            Terpstra, Catharinus
;            Pol, Johannes M
;            Moorman, Robertus J
;            Meulenberg, Johanna J
; TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
;                     VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
```

```
;   ADDRESSEE: Cooper & Dunham
;   STREET: 30 Rockefeller Plaza
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10112
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/226,065
;   FILING DATE: 21-Aug-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/565,864
;   FILING DATE: 05-May-2000
;   APPLICATION NUMBER: 08/157,005
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: EP 91201398.4
;   FILING DATE: 06-JUN-1991
;   APPLICATION NUMBER: EP 92200781.0
;   FILING DATE: 18-MAR-1992
;   APPLICATION NUMBER: PCT/NL92/00096
;   FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Moran, Thomas F
;   REGISTRATION NUMBER: 16,579
;   REFERENCE/DOCKET NUMBER: 44819
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 977-9550
;   TELEFAX: (212) 315-1931
;   TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 2396 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-226-065-2

Query Match            15.0%;   Score 61.5;   DB 4;   Length 2396;
Best Local Similarity  30.1%;   Pred. No. 85;
Matches  22;  Conservative  14;  Mismatches  26;  Indels  11;  Gaps 5;

Qy      8 KRMFEPTR-LIATIMVLLCFALTLC---SAFWWHNKGLALIFCILQSLALTWYSLSFPF 63
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Db   1220 RQLWEPVRGLVVGPSGLLCVILGKLLGGSRYLWH---VLLRLCMLADLAL---SLVYV-V 1272

Qy     64 ARDAVKKCFAVCL 76
          ||:|
Db   1273 SQGRCHKCWGKCI 1285


RESULT 15
US-09-248-796A-17451
; Sequence 17451, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17451
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;  LENGTH: 386
;  TYPE: PRT
;  ORGANISM: Candida albicans
US-09-248-796A-17451

Query Match            14.9%;  Score 61;  DB 4;  Length 386;
Best Local Similarity  31.3%;  Pred. No. 13;
Matches   26;  Conservative    7;  Mismatches   18;  Indels   32;  Gaps    6;

Qy    11 FEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCI----------LQSLALTWY-SLS 59
            || |||||||  |::  ||:        ||       ||      |||| | | |:|
Db   310 FGPTGLIGTFMVVFLFAM------WF----VLSVCILVVMEGTSAMLHSLRLHWVESMS 358

Qy    60 -------FIPFA-RDAVKKCF 72
                  | ::| |:||
Db   359 KYFEGGGSAFETFTFKGLLKQCF 381

Search completed: April 7, 2005, 03:29:18
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OM protein - protein search, using sw model

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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.
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                                        (without alignments)
                           181.303 Million cell updates/sec

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Sequence: 1 MGPVKQLKRMFEPTRLIATI..........LSFIPFARDAVKKCFAVCLA 77

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               Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   Published Applications AA:*
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          2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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         13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
         14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
         15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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         18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

### SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 27 | 410 | 100.0 | 77 | 10 | US-09-997-428-283 | Sequence 283, App |
| 562 | 410 | 100.0 | 77 | 14 | US-10-174-587-214 | Sequence 214, App |
| 626 | 410 | 100.0 | 77 | 14 | US-10-063-742-56 | Sequence 56, Appl |
| 741 | 410 | 100.0 | 77 | 17 | US-10-972-317-56 | Sequence 56, Appl |
| 742 | 410 | 100.0 | 160 | 9 | US-09-799-777-22 | Sequence 22, Appl |
| 743 | 410 | 98.5 | 170 | 15 | US-10-276-774-2357 | Sequence 2357, Ap |
| 744 | 404 | 74.6 | 160 | 11 | US-09-978-360A-561 | Sequence 561, App |
| 745 | 306 | 74.6 | 124 | 15 | US-10-264-237-2023 | Sequence 2023, Ap |
| 746 | 306 | 74.6 | 159 | 9 | US-09-731-872-419 | Sequence 419, App |
| 747 | 306 | 72.7 | 159 | 10 | US-09-876-997-419 | Sequence 419, App |
| 748 | 298 | 42.4 | 178 | 16 | US-10-755-889-34 | Sequence 34, Appl |
| 749 | 174 | 38.8 | 166 | 16 | US-10-767-701-36649 | Sequence 36649, A |
| 750 | 159 | 38.0 | 133 | 15 | US-10-424-599-203780 | Sequence 203780, |
| 751 | 156 | 38.0 | 178 | 15 | US-10-424-599-212115 | Sequence 212115, |
| 752 | 144 | 35.1 | 171 | 16 | US-10-437-963-190904 | Sequence 190904, |
| 753 | 143 | 34.9 | 160 | 16 | US-10-767-701-52394 | Sequence 52394, A |
| 754 | 136 | 33.2 | 207 | 15 | US-10-425-114-36635 | Sequence 72979, A |
| 755 | 136 | 33.2 | 219 | 15 | US-10-425-114-36635 | Sequence 36635, A |
| 756 | 95 | 23.2 | 144 | 16 | US-10-437-963-148937 | Sequence 148937, |
| 757 | 88.5 | 21.6 | 220 | 15 | US-10-424-599-232471 | Sequence 232471, |
| 758 | 88.5 | 21.6 | 268 | 15 | US-10-425-114-44499 | Sequence 44499, A |
| 759 | 84.5 | 20.6 | 231 | 16 | US-10-437-963-139616 | Sequence 139616, |
| 760 | 84.5 | 20.6 | 248 | 15 | US-10-425-114-64833 | Sequence 64833, A |
| 761 | 81 | 19.8 | 1158 | 15 | US-10-282-122A-56861 | Sequence 56861, A |
| 762 | 76.5 | 18.7 | 1721 | 16 | US-10-437-963-122039 | Sequence 122039, |
| 763 | 70.5 | 17.2 | 277 | 16 | US-10-437-963-185752 | Sequence 185752, |
| 764 | 69.5 | 17.0 | 319 | 17 | US-10-774-355A-1379 | Sequence 1379, Ap |
| 765 | 67 | 16.3 | 309 | 17 | US-10-774-355A-1766 | Sequence 1766, Ap |
| 766 | 66 | 16.1 | 263 | 15 | US-10-282-122A-59487 | Sequence 59487, A |
| 767 | 65 | 15.9 | 118 | 16 | US-10-437-963-140199 | Sequence 140199, |
| 768 | 65 | 15.9 | 484 | 15 | US-10-282-122A-46885 | Sequence 46885, A |
| 769 | 64.5 | 15.7 | 1149 | 16 | US-10-437-963-169904 | Sequence 169904, |
| 770 | 64 | 15.6 | 82 | 16 | US-10-767-701-45254 | Sequence 45254, A |
| 771 | 64 | 15.6 | 109 | 15 | US-10-424-599-214181 | Sequence 214181, |
| 772 | 64 | 15.6 | 129 | 15 | US-10-335-977-8985 | Sequence 8985, Ap |
| 773 | 64 | 15.6 | 278 | 14 | US-10-029-386-32852 | Sequence 32852, A |
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| 778 | 64 | 15.6 | 685 | 14 | US-10-146-474-14 | Sequence 14, Appl |
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| 782 | 64 | 15.6 | 694 | 14 | US-10-285-976-53 | Sequence 53, Appl |
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| 1014 | 313 | 13.5 | 55.5 | 14 | US-10-017-161-944 | Sequence 944, App |
| 1015 | 313 | 13.5 | 55.5 | 15 | US-10-424-599-818 | Sequence 818, App |
| 1016 | 322 | 13.5 | 55.5 | 16 | US-10-437-963-11790 | Sequence 11790, A |
| 1017 | 322 | 13.5 | 55.5 | 9 | US-09-815-242-11790 | Sequence 11790, A |
| 1018 | 345 | 13.5 | 55.5 | 9 | US-09-738-626-4062 | Sequence 4062, Ap |
| 1019 | 349 | 13.5 | 55.5 | 15 | US-10-282-122A-69893 | Sequence 69893, A |
| 1020 | 355 | 13.5 | 55.5 | 14 | US-10-237-563-32 | Sequence 32, Appl |
| 1021 | 365 | 13.5 | 55.5 | 14 | US-10-43-650A-122 | Sequence 122, App |
| 1022 | 384 | 13.5 | 55.5 | 9 | US-09-886-055-87 | Sequence 87, Appl |
| 1023 | 384 | 13.5 | 55.5 | 10 | US-09-804-291-87 | Sequence 87, Appl |
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| 1025 | 526 | 13.5 | 55.5 | 15 | US-10-25-114-53321 | Sequence 53321, A |
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| 1027 | 702 | 13.5 | 55.5 | 15 | US-10-369-493-9311 | Sequence 9311, Ap |
| 1028 | 720 | 13.5 | 55.5 | 15 | US-10-369-493-17737 | Sequence 17737, A |
| 1029 | 843 | 13.5 | 55.5 | 10 | US-09-927-315-7 | Sequence 7, Appli |
| 1030 | 843 | 13.5 | 55.5 | 13 | US-10-124-598-1 | Sequence 1, Appli |
| 1031 | 843 | 13.5 | 55.5 | 14 | US-10-096-144-1 | Sequence 1, Appli |
| 1032 | 843 | 13.5 | 55.5 | 14 | US-10-246-785-6 | Sequence 7, Appli |
| 1033 | 843 | 13.5 | 55.5 | 14 | US-10-190-417-7 | Sequence 7, Appli |
| 1034 | 843 | 13.5 | 55.5 | 15 | US-10-179-373-17 | Sequence 17, Appl |
| 1035 | 843 | 13.5 | 55.5 | 15 | US-10-436-715-38 | Sequence 38, Appl |
| 1036 | 843 | 13.5 | 55.5 | 15 | US-10-436-715-70 | Sequence 70, Appl |
| 1037 | 843 | 13.5 | 55.5 | 16 | US-10-725-103-17 | Sequence 17, Appl |
| 1038 | 843 | 13.5 | 55.5 | 16 | US-10-725-489-17 | Sequence 17, Appl |
| 1039 | 843 | 13.5 | 55.5 | 16 | US-10-725-080A-17 | Sequence 17, Appl |
| 1040 | 843 | 13.5 | 55.5 | 16 | US-10-725-472A-17 | Sequence 17, Appl |
| 1041 | 930 | 13.5 | 55.5 | 15 | US-10-282-122A-69755 | Sequence 69755, A |
| 1042 | 65 | 13.4 | 55 | 15 | US-10-24-599-156694 | Sequence 156694, |
| 1043 | 78 | 13.4 | 55 | 16 | US-10-767-701-35011 | Sequence 35011, A |

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| 1049 | 55 | 13.4 | 137 | 16 | US-10-725-472A-12 | Sequence 12, Appl |
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| 1057 | 55 | 13.4 | 355 | 14 | US-10-237-563-27 | Sequence 27, Appl |
| 1058 | 55 | 13.4 | 355 | 14 | US-10-237-563-28 | Sequence 28, Appl |
| 1059 | 55 | 13.4 | 355 | 14 | US-10-237-563-29 | Sequence 29, Appl |
| 1060 | 55 | 13.4 | 355 | 14 | US-10-237-563-30 | Sequence 30, Appl |
| 1061 | 55 | 13.4 | 355 | 14 | US-10-237-563-31 | Sequence 31, Appl |
| 1062 | 55 | 13.4 | 355 | 14 | US-10-237-563-33 | Sequence 33, Appl |
| 1063 | 55 | 13.4 | 360 | 13 | US-10-087-192-882 | Sequence 882, App |
| 1064 | 55 | 13.4 | 360 | 14 | US-10-099-007A-16 | Sequence 16, Appl |
| 1065 | 55 | 13.4 | 360 | 14 | US-10-225-567A-386 | Sequence 386, App |
| 1066 | 55 | 13.4 | 360 | 14 | US-10-239-423-77 | Sequence 77, Appli |
| 1067 | 55 | 13.4 | 360 | 14 | US-10-101-148-4 | Sequence 4, Appli |
| 1068 | 55 | 13.4 | 360 | 17 | US-10-690-880-25 | Sequence 25, Appli |
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| 1070 | 55 | 13.4 | 399 | 15 | US-10-276-774-2394 | Sequence 2394, Ap |
| 1071 | 55 | 13.4 | 402 | 17 | US-10-869-630-58 | Sequence 58, Appl |
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| 1075 | 55 | 13.4 | 439 | 15 | US-10-282-122A-56446 | Sequence 56446, A |
| 1076 | 55 | 13.4 | 443 | 15 | US-10-282-122A-56240 | Sequence 56240, A |
| 1077 | 55 | 13.4 | 482 | 15 | US-10-424-599-183275 | Sequence 183275, |
| 1078 | 55 | 13.4 | 550 | 15 | US-10-424-599-284384 | Sequence 284384, |
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| 1082 | 54.5 | 13.4 | 1139 | 15 | US-10-282-122A-78117 | Sequence 78117, A |
| 1083 | 54.5 | 13.4 | 1507 | 16 | US-10-437-963-192321 | Sequence 192321, |
| 1084 | 54.5 | 13.3 | 67 | 15 | US-10-424-599-260939 | Sequence 260939, |
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| 1234 | 54.5 | 13.3 | 245 | 14 | US-10-042-211A-89 | Sequence 89, Appl |
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| 1267 | 54.5 | 13.3 | 245 | 14 | US-10-331-496A-36 | Sequence 36, Appl |
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| 1272 | 54.5 | 13.3 | 245 | 15 | US-10-913-553-90 | Sequence 90, Appl |
| 1273 | 54.5 | 13.3 | 245 | 16 | US-10-696-639-63 | Sequence 63, Appl |
| 1275 | 54.5 | 13.3 | 279 | 14 | US-10-017-161-2286 | Sequence 2286, Ap |
| 1276 | 54.5 | 13.3 | 279 | 15 | US-10-292-798-1932 | Sequence 1932, Ap |
| 1277 | 54.5 | 13.3 | 284 | 14 | US-10-106-698-6305 | Sequence 6305, Ap |
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| 1279 | 54.5 | 13.3 | 293 | 14 | US-10-023-601-44 | Sequence 44, Appl |
| 1280 | 54.5 | 13.3 | 314 | 14 | US-10-017-161-950 | Sequence 950, App |
| 1281 | 54.5 | 13.3 | 318 | 14 | US-10-023-597-12 | Sequence 12, Appl |
| 1282 | 54.5 | 13.3 | 318 | 15 | US-10-292-798-824 | Sequence 824, App |
| 1283 | 54.5 | 13.3 | 318 | 15 | US-10-343-650A-124 | Sequence 124, App |
| 1284 | 54.5 | 13.3 | 318 | 16 | US-10-473-518-73 | Sequence 73, Appl |
| 1285 | 54.5 | 13.3 | 362 | 15 | US-10-282-122A-76533 | Sequence 76533, A |
| 1286 | 54.5 | 13.3 | 368 | 15 | US-10-282-122A-47483 | Sequence 47483, A |
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| 1288 | 54.5 | 13.3 | 374 | US-10-447-328-16 | Sequence 16, Appl |
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| 1291 | 54.5 | 13.3 | 398 | US-09-796-338A-17 | Sequence 17, Appl |
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| 1295 | 54.5 | 13.3 | 398 | US-10-225-567A-477 | Sequence 477, App |
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| 1297 | 54.5 | 13.3 | 398 | US-10-241-220-104 | Sequence 104, App |
| 1298 | 54.5 | 13.3 | 398 | US-10-407-079-93 | Sequence 93, Appl |
| 1299 | 54.5 | 13.3 | 398 | US-10-295-027-748 | Sequence 748, App |
| 1300 | 54.5 | 13.3 | 398 | US-10-295-027-823 | Sequence 823, App |
| 1301 | 54.5 | 13.3 | 398 | US-10-771-417-5 | Sequence 5, Appli |
| 1302 | 54.5 | 13.3 | 398 | US-10-757-262-32 | Sequence 32, Appl |
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| 1304 | 54.5 | 13.3 | 403 | US-10-826-508-30 | Sequence 30, Appl |
| 1305 | 54.5 | 13.3 | 403 | US-09-895-686-5 | Sequence 5, Appli |
| 1306 | 54.5 | 13.3 | 403 | US-10-097-340-121 | Sequence 121, App |
| 1307 | 54.5 | 13.3 | 403 | US-10-225-567A-599 | Sequence 599, App |
| 1308 | 54.5 | 13.3 | 403 | US-10-016-656-2 | Sequence 2, Appli |
| 1309 | 54.5 | 13.3 | 403 | US-10-600-816-6 | Sequence 6, Appli |
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| 1311 | 54.5 | 13.3 | 413 | US-10-282-122A-58631 | Sequence 58631, A |
| 1312 | 54.5 | 13.3 | 427 | US-09-826-50-32 | Sequence 32, Appl |
| 1313 | 54.5 | 13.3 | 438 | US-10-282-122A-43328 | Sequence 43328, A |
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| 1315 | 54.5 | 13.3 | 483 | US-10-267-502-356 | Sequence 356, App |
| 1316 | 54.5 | 13.3 | 499 | US-10-322-281-763 | Sequence 763, App |
| 1317 | 54.5 | 13.3 | 673 | US-10-437-963-132040 | Sequence 132040, |
| 1318 | 54.5 | 13.3 | 700 | US-10-437-963-138967 | Sequence 138967, |
| 1319 | 54.5 | 13.3 | 778 | US-10-437-963-141491 | Sequence 141491, |
| 1320 | 54.5 | 13.3 | 931 | US-10-436-715-61 | Sequence 61, Appl |
| 1321 | 54.5 | 13.3 | 1012 | US-10-437-963-128073 | Sequence 128073, |
| 1322 | 54 | 13.2 | 88 | US-10-424-599-157980 | Sequence 157980, |
| 1323 | 54 | 13.2 | 95 | US-10-767-701-52925 | Sequence 52925, A |
| 1324 | 54 | 13.2 | 118 | US-10-437-963-169713 | Sequence 169713, |
| 1325 | 54 | 13.2 | 165 | US-10-424-599-149217 | Sequence 149217, |
| 1326 | 54 | 13.2 | 188 | US-10-094-749-3153 | Sequence 3153, Ap |
| 1327 | 54 | 13.2 | 242 | US-09-920-923-32 | Sequence 32, Appl |
| 1328 | 54 | 13.2 | 242 | US-10-166-225A-181 | Sequence 181, App |
| 1329 | 54 | 13.2 | 242 | US-10-695-980-32 | Sequence 32, Appl |
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| 1333 | 54 | 13.2 | 310 | US-10-774-355A-1603 | Sequence 1603, Ap |
| 1334 | 54 | 13.2 | 318 | US-10-774-355A-2203 | Sequence 2203, Ap |
| 1335 | 54 | 13.2 | 331 | US-10-421-654-102 | Sequence 102, App |
| 1336 | 54 | 13.2 | 347 | US-10-282-122A-66553 | Sequence 66553, A |
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| 1339 | 54 | 13.2 | 396 | US-10-425-114-73110 | Sequence 73110, A |
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| 1341 | 54 | 13.2 | 412 | US-10-292-798-1872 | Sequence 1872, Ap |
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| 1343 | 54 | 13.2 | 529 | US-10-847-102A-41 | Sequence 41, Appl |
| 1344 | 54 | 13.2 | 540 | US-09-804-551B-2 | Sequence 2, Appli |
| 1345 | 54 | 13.2 | 540 | US-10-270-333-120 | Sequence 120, App |
| 1346 | 54 | 13.2 | 542 | US-10-283-423-18 | Sequence 18, Appl |
| 1347 | 54 | 13.2 | 542 | US-10-213-821-18 | Sequence 18, Appl |
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| 1349 | 54 | 13.2 | 543 | US-09-938-956-7 | Sequence 7, Appli |
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| 1355 | 54 | 13.2 | 574 | US-09-847-102A-54 | Sequence 54, Appl |
| 1356 | 54 | 13.2 | 574 | US-10-285-976-51 | Sequence 51, Appl |
| 1357 | 54 | 13.2 | 599 | US-09-895-752-22 | Sequence 22, Appl |
| 1358 | 54 | 13.2 | 599 | US-09-887-586A-22 | Sequence 22, Appl |
| 1359 | 54 | 13.2 | 599 | US-09-903-012-22 | Sequence 22, Appl |
| 1360 | 54 | 13.2 | 599 | US-09-900-797-22 | Sequence 22, Appl |

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| 1361 | 54 | 13.2 | 599 | 11 | US-09-893-820-22 | Sequence 22, Appl |
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| 1367 | 53.5 | 13.0 | 42 | 14 | US-10-231-417-305 | Sequence 305, App |
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| 1389 | 53.5 | 13.0 | 310 | 17 | US-10-774-355A-1924 | Sequence 1924, Ap |
| 1390 | 53.5 | 13.0 | 319 | 14 | US-10-156-761-12615 | Sequence 12615, A |
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| 1413 | 53 | 12.9 | 234 | 15 | US-10-335-977-5578 | Sequence 5578, Ap |
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| 1425 | 53 | 12.9 | 305 | 17 | US-10-957-135-63 | Sequence 63, Appl |
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| 1427 | 53 | 12.9 | 319 | 15 | US-10-425-114-38015 | Sequence 38015, A |
| 1428 | 53 | 12.9 | 328 | 14 | US-10-278-087A-39 | Sequence 39, Appl |
| 1429 | 53 | 12.9 | 350 | 9 | US-09-782-980-83 | Sequence 83, Appl |
| 1430 | 53 | 12.9 | 350 | 9 | US-09-884-430-7 | Sequence 7, Appli |
| 1431 | 53 | 12.9 | 350 | 9 | US-09-104-063-2 | Sequence 2, Appli |
| 1432 | 53 | 12.9 | 350 | 10 | US-09-893-512-9 | Sequence 9, Appli |
| 1433 | 53 | 12.9 | 350 | 14 | US-10-099-007A-15 | Sequence 15, Appl |

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| 1434 | 53 | 12.9 | 350 | 14 | US-10-225-567A-463 | Sequence 463, App |
| 1435 | 53 | 12.9 | 350 | 14 | US-10-336-489-7 | Sequence 7, Appli |
| 1436 | 53 | 12.9 | 350 | 14 | US-10-239-423-76 | Sequence 76, Appl |
| 1437 | 53 | 12.9 | 350 | 15 | US-10-666-689-2 | Sequence 2, Appli |
| 1438 | 53 | 12.9 | 350 | 15 | US-10-436-549-546 | Sequence 546, App |
| 1439 | 53 | 12.9 | 350 | 15 | US-10-423-543-94 | Sequence 94, Appl |
| 1440 | 53 | 12.9 | 350 | 16 | US-10-741-601-290 | Sequence 290, App |
| 1441 | 53 | 12.9 | 350 | 16 | US-10-806-018-83 | Sequence 83, Appl |
| 1442 | 53 | 12.9 | 350 | 16 | US-10-712-425-546 | Sequence 546, App |
| 1443 | 53 | 12.9 | 350 | 17 | US-10-741-600-835 | Sequence 835, App |
| 1444 | 53 | 12.9 | 350 | 17 | US-10-773-032-546 | Sequence 546, App |
| 1445 | 53 | 12.9 | 351 | 15 | US-10-424-599-185019 | Sequence 185019, |
| 1446 | 53 | 12.9 | 353 | 15 | US-10-424-599-202258 | Sequence 202258, |
| 1447 | 53 | 12.9 | 354 | 16 | US-10-437-963-182825 | Sequence 182825, |
| 1448 | 53 | 12.9 | 357 | 16 | US-10-600-816-17 | Sequence 17, Appl |
| 1449 | 53 | 12.9 | 360 | 14 | US-10-225-567A-86 | Sequence 86, Appl |
| 1450 | 53 | 12.9 | 360 | 14 | US-10-290-078-3 | Sequence 3, Appli |
| 1451 | 53 | 12.9 | 368 | 15 | US-10-282-122A-50018 | Sequence 50018, A |
| 1452 | 53 | 12.9 | 382 | 15 | US-10-282-122A-68649 | Sequence 68649, A |
| 1453 | 53 | 12.9 | 412 | 15 | US-10-425-114-73098 | Sequence 73098, A |
| 1454 | 53 | 12.9 | 429 | 15 | US-10-335-977-5579 | Sequence 5579, Ap |
| 1455 | 53 | 12.9 | 448 | 15 | US-10-369-493-21148 | Sequence 21148, A |
| 1456 | 53 | 12.9 | 467 | 16 | US-10-437-963-127783 | Sequence 127783, |
| 1457 | 53 | 12.9 | 468 | 15 | US-10-276-774-2430 | Sequence 2430, Ap |
| 1458 | 53 | 12.9 | 476 | 15 | US-10-461-194-90 | Sequence 90, Appl |
| 1459 | 53 | 12.9 | 483 | 15 | US-10-108-260A-3990 | Sequence 3990, Ap |
| 1460 | 53 | 12.9 | 500 | 10 | US-09-847-102A-36 | Sequence 36, Appl |
| 1461 | 53 | 12.9 | 501 | 15 | US-10-369-493-6412 | Sequence 6412, Ap |
| 1462 | 53 | 12.9 | 528 | 14 | US-10-260-046-14 | Sequence 14, Appl |
| 1463 | 53 | 12.9 | 528 | 14 | US-10-260-046-16 | Sequence 16, Appl |
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| 1465 | 53 | 12.9 | 537 | 10 | US-09-847-102A-50 | Sequence 50, Appl |
| 1466 | 53 | 12.9 | 537 | 14 | US-10-146-474-11 | Sequence 11, Appl |
| 1467 | 53 | 12.9 | 537 | 14 | US-10-285-976-45 | Sequence 45, Appl |
| 1468 | 53 | 12.9 | 537 | 15 | US-10-301-764-11 | Sequence 11, Appli |
| 1469 | 53 | 12.9 | 537 | 15 | US-10-251-769-4 | Sequence 4, Appli |
| 1470 | 53 | 12.9 | 538 | 14 | US-10-152-548-8 | Sequence 8, Appli |
| 1471 | 53 | 12.9 | 540 | 9 | US-09-780-557-2 | Sequence 2, Appli |
| 1472 | 53 | 12.9 | 543 | 15 | US-10-282-122A-44937 | Sequence 44937, A |
| 1473 | 53 | 12.9 | 555 | 15 | US-10-369-493-1689 | Sequence 1689, Ap |
| 1474 | 53 | 12.9 | 558 | 15 | US-10-275-026A-2 | Sequence 2, Appli |
| 1475 | 53 | 12.9 | 563 | 15 | US-10-369-493-3157 | Sequence 3157, Ap |
| 1476 | 53 | 12.9 | 588 | 14 | US-10-259-165-148 | Sequence 148, App |
| 1477 | 53 | 12.9 | 590 | 9 | US-09-895-752-54 | Sequence 54, Appl |
| 1478 | 53 | 12.9 | 590 | 9 | US-09-887-586A-54 | Sequence 54, Appl |
| 1479 | 53 | 12.9 | 590 | 9 | US-09-903-012-54 | Sequence 54, Appl |
| 1480 | 53 | 12.9 | 590 | 10 | US-09-900-797-54 | Sequence 54, Appl |
| 1481 | 53 | 12.9 | 590 | 11 | US-09-893-820-54 | Sequence 54, Appl |
| 1482 | 53 | 12.9 | 590 | 15 | US-10-469-993-6 | Sequence 6, Appli |
| 1483 | 53 | 12.9 | 619 | 15 | US-10-425-114-59691 | Sequence 59691, A |
| 1484 | 53 | 12.9 | 654 | 16 | US-10-437-963-138976 | Sequence 138976, |
| 1485 | 53 | 12.9 | 666 | 10 | US-09-847-102A-47 | Sequence 47, Appl |
| 1486 | 53 | 12.9 | 666 | 14 | US-10-285-976-43 | Sequence 43, Appl |
| 1487 | 53 | 12.9 | 675 | 15 | US-10-425-114-69229 | Sequence 69229, A |
| 1488 | 53 | 12.9 | 683 | 16 | US-10-437-963-132584 | Sequence 132584, |
| 1489 | 53 | 12.9 | 688 | 15 | US-10-425-114-62844 | Sequence 62844, A |
| 1490 | 53 | 12.9 | 688 | 15 | US-10-425-114-70844 | Sequence 70844, A |
| 1491 | 53 | 12.9 | 703 | 15 | US-10-225-066A-208 | Sequence 208, App |
| 1492 | 53 | 12.9 | 703 | 15 | US-10-374-780A-2364 | Sequence 2364, Ap |
| 1493 | 53 | 12.9 | 717 | 15 | US-10-282-122A-76101 | Sequence 76101, A |
| 1494 | 53 | 12.9 | 731 | 15 | US-10-282-122A-60220 | Sequence 60220, A |
| 1495 | 53 | 12.9 | 782 | 14 | US-10-066-543-1424 | Sequence 1424, Ap |
| 1496 | 53 | 12.9 | 1077 | 17 | US-10-902-531-24 | Sequence 24, Appl |
| 1497 | 53 | 12.9 | 1091 | 9 | US-09-875-423-5 | Sequence 5, Appli |
| 1498 | 53 | 12.9 | 1091 | 14 | US-10-162-012-18 | Sequence 18, Appl |
| 1499 | 53 | 12.9 | 1091 | 15 | US-10-162-102-18 | Sequence 18, Appl |
| 1500 | 53 | 12.9 | 1134 | 16 | US-10-437-963-105184 | Sequence 105184, |

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Job time : 161 secs

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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:     April 7, 2005, 03:16:28 ; Search time 44 Seconds
                                       (without alignments)
                         168.379 Million cell updates/sec

Title:          US-10-063-563-56
Perfect score:  410
Sequence:       1 MGPVKQLKRMFEPTRLIATI.........LSFIPFARDAVKKCFAVCLA 77

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 9621763 residues

Total number of hits satisfying chosen parameters:  283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :  PIR 79:*
         1: Pir1:*
         2: Pir2:*
         3: Pir3:*
         4: Pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	106	25.9	235	2	T19408	hypothetical prote
2	79	19.3	385	2	T05049	hypothetical prote
3	75	18.3	215	2	S45393	probable membrane
4	66.5	16.2	466	2	T02324	hypothetical prote
5	65	15.9	272	2	F58930	cytochrome-c oxida
6	64.5	15.7	379	2	AI0825	probable 3-phenylp
7	64	15.6	96	2	A69826	hypothetical prote
8	64	15.6	342	2	A38908	spa40 protein - Sh
9	64	15.6	351	2	T26918	hypothetical prote
10	64	15.6	403	2	F83092	probable cytochrom
11	64	15.6	681	2	F95885	probable iron ABC
12	63	15.4	258	2	S73803	MG256 homolog H91
13	63	15.4	387	2	S74522	hypothetical prote
14	63	15.4	1022	2	T16599	hypothetical prote
15	62.5	15.2	255	2	S49295	hypothetical prote
16	62.5	15.2	347	2	D71690	hypothetical prote
17	62.5	15.2	379	1	G65030	Probable 3-phenylp
18	62.5	15.2	379	2	E85898	MFS transporter [i
19	62.5	15.2	379	2	B91054	probable 3-phenylp
20	62.5	15.2	438	2	AI0862	L-fucose permease
21	61.5	15.0	93	2	T30672	hypothetical prote
22	61.5	15.0	340	2	T21472	hypothetical prote
23	61.5	15.0	420	2	D86708	cell division prot
24	61.5	15.0	2396	2	B36861	orf 1a protein - L
25	61.5	15.0	230	1	S22406	hydrogenase (EC 1.
26	61	14.9	373	2	A98094	type III secretion
27	61	14.9	373	2	E85939	hypothetical prote
28	61	14.9	392	2	T33014	hypothetical prote
29	60.5	14.8	59	2	T29595	hypothetical prote
30	60.5	14.8	180	2	E97355	hypothetical prote
31	60.5	14.8	339	2	E99878	hypothetical prote
32	60.5	14.8	385	2	AH0353	probable transport
33	60.5	14.8	401	2	T44831	probable emulsan r
34	60	14.6	313	2	E64896	probable membrane
35	60	14.6	424	2	T20542	hypothetical prote
36	59.5	14.5	221	2	C82010	probable integral
37	59.5	14.5	221	2	C81238	hypothetical prote
38	59.5	14.5	244	2	S25988	hypothetical prote
39	59.5	14.5	654	2	S11049	potassium channel
40	59.5	14.5	998	2	S77225	sensory transducti
41	59.5	14.5	1031	2	T43458	hypothetical prote
42	59	14.4	141	2	C86521	hypothetical prote
43	59	14.4	141	2	G72100	hypothetical prote
44	59	14.4	233	2	T22977	hypothetical prote
45	59	14.4	260	2	T11122	cytochrome-c oxida
46	59	14.4	265	2	AI3428	O-antigen export s
47	59	14.4	299	2	T11070	NADH2 dehydrogenas
48	59	14.4	328	2	JC4800	P2Y6 receptor - hu
49	59	14.4	359	2	A48921	interleukin-8 rece
50	59	14.4	386	2	AD0218	flagellar biosynth
51	59	14.4	399	2	T16277	hypothetical prote
52	59	14.4	471	2	E83173	hypothetical prote
53	59	14.4	626	2	D88601	protein Y49B10.11
54	59	14.4	780	2	D90753	hypothetical prote
55	59	14.4	780	2	B85617	hypothetical prote
56	59	14.4	795	2	T01059	hypothetical prote
57	58.5	14.3	358	2	B64616	flagellar biosynth
58	58.5	14.3	476	2	S21144	potassium channel
59	58.5	14.3	499	2	I77466	potassium channel
60	58.5	14.3	519	2	S31133	hypothetical prote
61	58.5	14.3	718	2	T26646	hypothetical prote
62	58.5	14.3	1170	2	A81368	probable 2-acylgly
63	58	14.1	169	2	A81445	probable integral
64	58	14.1	232	1	B71145	probable cobalamin
65	58	14.1	230	2	H75189	cobalamin (5'-phos
66	58	14.1	315	2	AG3535	dipeptide transpor
67	58	14.1	334	2	B81406	interleukin-8 rece
68	58	14.1	356	2	S42096	interleukin-8 rece
69	58	14.1	370	2	T36352	hypothetical prote
70	58	14.1	383	2	S54213	flagellar biosynth
71	58	14.1	479	2	E91195	probable permease
72	58	14.1	479	2	F86042	probable permease
73	58	14.1	479	2	C65167	hypothetical 51.0
74	58	14.1	565	2	JE0338	Frizzled-2 protein
75	58	14.1	641	2	A45054	probable intercell
76	58	14.1	647	2	JE0337	Frizzled-1 protein
77	58	14.1	696	2	AB1566	hypothetical prote
78	58	14.1	743	2	AB3145	hypothetical prote
79	58	14.1	747	2	F98142	iron(III) ABC tran
80	58	14.1	2476	2	T34022	zonadhesin - pig
81	57.5	14.0	136	2	E36790	hypothetical prote
82	57.5	14.0	167	2	S11411	hypothetical prote
83	57.5	14.0	250	2	AD1197	ABC transporter tr
84	57.5	14.0	328	2	A70145	prolipoprotein dia
85	57.5	14.0	336	2	T32721	hypothetical prote
86	57.5	14.0	372	2	S52054	ubiquinol-cytochro
87	57.5	14.0	387	2	T04908	hypothetical prote
88	57.5	14.0	533	1	QRBCM2	methyl-accepting c
89	57.5	14.0	533	2	C90953	methyl-accepting c
90	57.5	14.0	533	2	G85801	methyl-accepting c
91	57.5	14.0	729	2	A91038	hypothetical prote
92	57.5	14.0	742	2	D85882	hypothetical prote
93	57.5	14.0	768	2	H65013	yfeA protein - Esc
94	57.5	14.0	837	2	T19074	hypothetical prote
95	57.5	14.0	1002	2	B54145	sodium-chloride tr
96	57.5	14.0	1057	2	E87545	AcrB/AcrF fam
97	57.5	14.0	1607	2	T13250	hypothetical prote
98	57	13.9	157	1	W5WLR1	E5 protein - rhesu
99	57	13.9	185	2	S67238	probable membrane
100	57	13.9	305	2	AB1332	heme O oxygenase h
101	57	13.9	305	2	AB1703	heme O oxygenase h
102	57	13.9	367	2	AD1786	cell division prot

No.			Length	Accession	N	Description
103	57	13.9	674	B82954	2	conserved hypothet
104	57	13.9	712	AG0175	2	probable membrane
105	57	13.9	745	OPHUM	1	myeloperoxidase (E
106	57	13.9	780	H64830	2	probable membrane
107	57	13.9	825	C28894	2	myeloperoxidase (E
108	57	13.9	830	B28894	2	myeloperoxidase (E
109	57	13.9	952	B84534	2	hypothetical prote
110	57	13.9	3473	A46112	1	genome polyprotein
111	57	13.9	3473	S27927	2	polyprotein - rice
112	56.5	13.8	89	S51911	2	cryptogene protein
113	56.5	13.8	229	E70838	2	hypothetical prote
114	56.5	13.8	250	AB1555	2	ABC transporter tr
115	56.5	13.8	338	S22623	2	undecaprenyl-phosp
116	56.5	13.8	402	B69843	2	conserved hypothet
117	56.5	13.8	437	A69172	2	conserved hypothet
118	56.5	13.8	465	T03024	2	calcium-dependent
119	56.5	13.8	475	AI2439	2	hypothetical prote
120	56.5	13.8	514	T35371	2	probable Na+/H+ an
121	56.5	13.8	533	T38644	2	conserved hypothet
122	56.5	13.8	607	T11032	2	NADH2 dehydrogenas
123	56.5	13.8	653	A39922	2	hypothetical prote
124	56.5	13.8	658	T16040	2	potassium channel
125	56.5	13.8	1202	T37867	2	hypothetical prote
126	56	13.7	193	A53697	2	insulin-like growt
127	56	13.7	269	H64146	2	hypothetical prote
128	56	13.7	321	T24572	2	hypothetical prote
129	56	13.7	324	T17978	2	probable ribonucle
130	56	13.7	351	T15112	2	hypothetical prote
131	56	13.7	380	T11299	2	ubiquinol-cytochro
132	56	13.7	393	E82283	2	conserved hypothet
133	56	13.7	429	G64649	2	hypothetical prote
134	56	13.7	527	S75063	1	Na+/H+-exchanging
135	56	13.7	558	E83905	2	hypothetical prote
136	56	13.7	645	T27186	2	hypothetical prote
137	56	13.7	684	T33785	2	hypothetical prote
138	56	13.7	694	S71786	2	wingless receptor
139	56	13.7	1682	A45380	2	sodium channel pro
140	56	13.7	2016	A38195	2	sodium channel pro
141	56	13.7	2019	A33996	2	sodium channel pro
142	55.5	13.5	100	C97798	2	hypothetical prote
143	55.5	13.5	198	PC1134	1	hypothetical prote
144	55.5	13.5	210	A49872	1	cytochrome-c oxida
145	55.5	13.5	268	C64234	2	proline iminopepti
146	55.5	13.5	298	S15433	2	hypothetical prote
147	55.5	13.5	321	S39586	2	peptide transport
148	55.5	13.5	322	B83579	2	hypothetical prote
149	55.5	13.5	355	AC2926	2	exopolysaccharide
150	55.5	13.5	355	D98356	2	exopolysaccharide
151	55.5	13.5	359	S55653	2	hypothetical prote
152	55.5	13.5	476	S15314	2	undecaprenyl-phosp
153	55.5	13.5	539	T22041	2	hypothetical prote
154	55.5	13.5	552	T23755	2	hypothetical prote
155	55.5	13.5	720	E82561	2	toxin secretion AB
156	55.5	13.5	734	T24908	2	hypothetical prote
157	55.5	13.5	1063	A33830	2	cation efflux syst
158	55.5	13.5	1063	JC4700	2	cadmium, zinc, cob
159	55.5	13.5	1275	AD0332	2	probable membrane
160	55.5	13.5	1321	A60165	2	sodium channel pro
161	55	13.4	98	T11083	2	NADH2 dehydrogenas
162	55	13.4	118	F34792	2	Ig heavy chain pre
163	55	13.4	128	E88449	2	protein F54D8.2 [i
164	55	13.4	176	B90343	2	hypothetical prote
165	55	13.4	321	AD3367	2	sodium/bile acid c
166	55	13.4	340	AB2183	2	hypothetical prote
167	55	13.4	347	S70364	2	cannabinoid recept
168	55	13.4	354	A23669	2	interleukin-8 rece
169	55	13.4	355	JQ1231	2	interleukin-8 rece
170	55	13.4	360	A53611	2	interleukin-8 rece
171	55	13.4	375	C75201	2	na+/h+ antiporter
172	55	13.4	439	A64769	2	branched-chain ami
173	55	13.4	439	C90685	2	branched-chain ami
174	55	13.4	439	G85535	2	branched-chain ami
175	55	13.4	449	H69862	2	Na+-transporting A

No.	Description	Accession	N	Length		
176	DNA-damage-inducib	G86097	2	459	13.4	55
177	DNA-damage-inducib	C91257	2	459	13.4	55
178	hypothetical prote	B86285	2	481	13.4	55
179	hypothetical prote	T19071	2	503	13.4	55
180	frizzled protein h	T13484	2	526	13.4	55
181	hypothetical prote	T19598	2	693	13.4	55
182	cellulase (EC 3.2.	CZCLEM	1	814	13.4	55
183	hypothetical prote	F75134	2	1010	13.4	55
184	Na+/K+-exchanging	A37227	2	1017	13.4	55
185	probable potassium	AI0379	2	1139	13.4	55
186	hypothetical prote	C36807	2	169	13.3	54.5
187	amastigote surface	B54853	2	174	13.3	54.5
188	probable membrane	B96975	2	234	13.3	54.5
189	tetrapan TSPAN-6	A59258	2	245	13.3	54.5
190	phosphatidate cyti	A82729	2	284	13.3	54.5
191	B. subtilis SpoIII	AE1431	2	287	13.3	54.5
192	B. subtilis SpoIII	AC1805	2	287	13.3	54.5
193	protein C18B10.2 [	G89103	2	300	13.3	54.5
194	probable integral	AE0010	2	300	13.3	54.5
195	protein kinase STY	I49068	2	306	13.3	54.5
196	NADH2 dehydrogenas	QXMS1M	1	315	13.3	54.5
197	NADH2 dehydrogenas	T12591	2	315	13.3	54.5
198	probable phosphata	C71311	2	348	13.3	54.5
199	flagella-associate	G83954	2	362	13.3	54.5
200	hypothetical prote	T34372	2	363	13.3	54.5
201	serine transport p	B64536	2	378	13.3	54.5
202	hypothetical prote	AB2189	2	413	13.3	54.5
203	L-fucose permease	WQBCFP	1	421	13.3	54.5
204	fucose permease [i	B91086	2	438	13.3	54.5
205	fucose permease [i	G85931	2	438	13.3	54.5
206	depressed growth-r	S14145	2	442	13.3	54.5
207	hexosephosphate tr	G64206	2	461	13.3	54.5
208	protein kinase STY	A39676	2	483	13.3	54.5
209	hypothetical prote	T33197	2	488	13.3	54.5
210	NADH2 dehydrogenas	E58931	2	492	13.3	54.5
211	delayed rectifier	A48672	2	499	13.3	54.5
212	potassium channel	I84204	2	499	13.3	54.5
213	potassium channel	A33814	2	499	13.3	54.5
214	GumJ protein XF236	F82566	2	510	13.3	54.5
215	phosphorylase kina	S51600	2	560	13.3	54.5
216	hypothetical prote	T32479	2	563	13.3	54.5
217	NADH2 dehydrogenas	S47880	2	602	13.2	54
218	probable membrane	S64156	2	616	13.2	54
219	potassium channel	S24125	2	660	13.2	54
220	Trg protein - frui	A55160	1	720	13.2	54
221	neurofibromatosis I -	B55282	2	2818	13.2	54
222	neurofibromin I -	JC5196	2	2820	13.2	54
223	neurofibromin - mo	I54352	2	2825	13.2	54
224	probable membrane	S52831	2	167	13.2	54
225	hypothetical prote	T11234	2	193	13.2	54
226	cytochrome-c oxida	S58988	2	259	13.2	54
227	phosphonate ABC tr	AE2010	2	264	13.2	54
228	conserved hypothet	H81155	2	265	13.2	54
229	phosphate transpor	E64426	2	315	13.2	54
230	hypothetical prote	T33297	2	325	13.2	54
231	uncharacterized co	B97271	2	337	13.2	54
232	cytochrome P450 ho	T04734	2	338	13.2	54
233	hypothetical prote	G83171	2	347	13.2	54
234	hypothetical prote	T21627	2	348	13.2	54
235	interleukin-8 rece	A53752	2	358	13.2	54
236	hypothetical prote	AF2115	2	387	13.2	54
237	potassium uptake p	B65190	2	432	13.2	54
238	hypothetical prote	B99946	2	498	13.2	54
239	apolipoprotein N-a	G97761	2	499	13.2	54
240	iron(III)-transpor	AE3580	2	558	13.2	54
241	hemagglutinin prec	HMIVT1	1	566	13.2	54
242	frizzled-7 protein	JE0339	2	574	13.2	54
243	limonene cyclase -	A48863	2	599	13.2	54
244	regulator of patho	G82721	2	662	13.2	54
245	probable glucosyl	A84639	2	690	13.2	54
246	probable potassium	T01493	2	764	13.2	54
247	probable membrane	S45135	2	894	13.2	54
248	hypothetical prote	C96637	2	1272	13.2	54

#						Description
249	53.5	13.0	139	PC4217	2	hypothetical 139 p
250	53.5	13.0	184	S76935	2	hypothetical prote
251	53.5	13.0	226	JQ1574	1	major surface anti
252	53.5	13.0	226	JQ1576	1	major surface anti
253	53.5	13.0	226	JQ2101	2	surface antigen -
254	53.5	13.0	226	JQ2106	2	surface antigen -
255	53.5	13.0	263	AB0555	2	probable membrane
256	53.5	13.0	265	T46952	2	probable membrane
257	53.5	13.0	298	AB3892	2	hypothetical prote
258	53.5	13.0	299	B95149	2	heat shock protein
259	53.5	13.0	313	E45774	2	odorant receptor 8
260	53.5	13.0	350	C56118	2	vetispiradiene syn
261	53.5	13.0	354	B88650	2	protein C09G12.4 [
262	53.5	13.0	355	AB0426	2	two-component syst
263	53.5	13.0	362	E71637	2	hypothetical prote
264	53.5	13.0	362	G97849	2	hypothetical prote
265	53.5	13.0	379	PC4180	2	thiazide-sensitive
266	53.5	13.0	400	I39792	2	multidrug-efflux t
267	53.5	13.0	429	T28950	2	hypothetical prote
268	53.5	13.0	429	G64844	2	probable membrane
269	53.5	13.0	452	AF0765	2	undecaprenyl-phosp
270	53.5	13.0	523	T11916	2	NADH2 dehydrogenas
271	53.5	13.0	578	G82950	2	conserved hypothet
272	53.5	13.0	603	T11843	2	NADH2 dehydrogenas
273	53.5	13.0	627	S37954	2	RNA polymerase I t
274	53.5	13.0	706	D81236	2	nitrogen regulatio
275	53.5	13.0	706	B82009	2	probable two-compo
276	53.5	13.0	770	S76883	2	nitric-oxide reduc
277	53.5	13.0	927	A48085	2	transcription fact
278	53.5	13.0	1021	G01202	2	NaCl electroneutra
279	53.5	13.0	1083	H86921	2	probable arabinosy
280	53.5	13.0	1488	T02856	2	probable membrane
281	53	12.9	119	B90198	2	hypothetical prote
282	53	12.9	174	A54853	2	amastigote surface
283	53	12.9	174	C54853	2	amastigote surface
284	53	12.9	228	D90513	2	hypothetical prote
285	53	12.9	229	A05198	2	hypothetical prote
286	53	12.9	255	AC3368	2	diguanylate cyclas
287	53	12.9	288	A83040	2	hypothetical prote
288	53	12.9	297	AG0143	2	probable LysR-fami
289	53	12.9	301	H70505	2	hypothetical prote
290	53	12.9	330	S55595	2	G protein-coupled
291	53	12.9	337	AE3216	2	ABC transporter, m
292	53	12.9	338	T21161	2	hypothetical prote
293	53	12.9	343	T27798	2	hypothetical prote
294	53	12.9	350	A39445	2	interleukin-8 rece
295	53	12.9	353	B96767	2	unknown protein F2
296	53	12.9	360	S36750	2	cannabinoid recept
297	53	12.9	361	T39784	2	hypothetical prote
298	53	12.9	415	B81373	2	transmembrane tran
299	53	12.9	429	S41527	2	citrate (si)-synth
300	53	12.9	429	G71937	2	hypothetical prote
301	53	12.9	431	T11911	2	hypothetical prote
302	53	12.9	440	C82410	2	conserved hypothet
303	53	12.9	458	D97799	2	NADH2 dehydrogenas
304	53	12.9	469	S73404	2	MG061 homolog R02_
305	53	12.9	490	G69282	1	hypothetical prote
306	53	12.9	501	B89135	2	protein F25G6.7 [i
307	53	12.9	509	D86146	2	F22L4.11 protein -
308	53	12.9	512	B83060	2	iron (III)-transpo
309	53	12.9	520	T26201	2	hypothetical prote
310	53	12.9	537	JC7127	2	frizzled protein 4
311	53	12.9	553	C81024	2	hypothetical prote
312	53	12.9	555	S69671	2	hypothetical prote
313	53	12.9	555	B70409	2	carbon starvation
314	53	12.9	558	F81967	2	probable inner mem
315	53	12.9	590	S34960	1	NADH2 dehydrogenas
316	53	12.9	611	C58893	2	NADH2 dehydrogenas
317	53	12.9	655	A86153	2	hypothetical prote
318	53	12.9	666	JC7312	2	frizzled-3 protein
319	53	12.9	692	T05111	2	hypothetical prote
320	53	12.9	717	AD0627	2	probable membrane
321	53	12.9	746	AD1622	2	probable integral

#						Description
322	53	12.9	849	D88368	2	protein F19H8.4 [i
323	53	12.9	1091	T30256	2	calcium channel al
324	52.5	12.8	83	F84510	2	hypothetical prote
325	52.5	12.8	90	S34798	2	nodulin (clone GmN
326	52.5	12.8	111	AI2312	2	hypothetical prote
327	52.5	12.8	133	B97400	2	hypothetical prote
328	52.5	12.8	133	AC2618	2	conserved hypothet
329	52.5	12.8	137	H90546	2	hypothetical prote
330	52.5	12.8	148	AH0175	2	probable membrane
331	52.5	12.8	183	QQBPGL	1	git protein - phag
332	52.5	12.8	195	E71000	2	hypothetical prote
333	52.5	12.8	261	T11306	2	cytochrome-c oxida
334	52.5	12.8	263	T22536	2	hypothetical prote
335	52.5	12.8	268	AI1175	2	spermidine/putresc
336	52.5	12.8	268	AG1532	2	spermidine/putresc
337	52.5	12.8	278	D83080	2	hypothetical prote
338	52.5	12.8	285	B97144	2	probable permease
339	52.5	12.8	289	F88939	2	protein C05E4.5 [i
340	52.5	12.8	299	S59144	2	NADH2 dehydrogenas
341	52.5	12.8	321	TO2236	2	NBS-LRR type resis
342	52.5	12.8	356	S37356	2	spaS protein - Sal
343	52.5	12.8	360	G02064	2	G protein-coupled
344	52.5	12.8	364	S67855	2	GumF protein - Xan
345	52.5	12.8	374	T10349	2	very-late factor 1
346	52.5	12.8	395	E90896	2	probable transport
347	52.5	12.8	395	B85721	2	probable transport
348	52.5	12.8	395	A64908	2	membrane protein y
349	52.5	12.8	436	T36320	2	hypothetical prote
350	52.5	12.8	441	G75306	2	drug transport pro
351	52.5	12.8	452	G85647	2	hypothetical prote
352	52.5	12.8	452	G90787	2	hypothetical prote
353	52.5	12.8	487	G90496	2	transporter (impor
354	52.5	12.8	489	I51532	2	potassium channel
355	52.5	12.8	513	C69809	2	spore germination
356	52.5	12.8	597	AE2780	2	conserved hypothet
357	52.5	12.8	646	G97559	2	probable cyclic be
358	52.5	12.8	691	H71405	2	hypothetical prote
359	52.5	12.8	717	S31034	2	retrovirus-related
360	52.5	12.8	717	S31035	2	retrovirus-related
361	52.5	12.8	735	AD0341	2	probable membrane
362	52.5	12.8	836	C82726	2	DNA uptake protein
363	52.5	12.8	848	TO2053	1	s-receptor kinase
364	52.5	12.8	902	S49931	2	SYG1 protein - yea
365	52.5	12.8	1082	T45096	2	probable arabinosy
366	52.5	12.7	184	F82270	2	probable type IV p
367	52	12.7	208	T24065	2	hypothetical prote
368	52	12.7	213	AI3280	2	hypothetical prote
369	52	12.7	252	F87575	2	ABC transporter, p
370	52	12.7	260	G81290	2	probable capsule p
371	52	12.7	261	T11460	2	cytochrome-c oxida
372	52	12.7	282	D72771	2	probable bacterioc
373	52	12.7	301	B97972	2	conserved hypothet
374	52	12.7	311	F95374	2	probable ABC trans
375	52	12.7	313	F90884	2	probable transport
376	52	12.7	313	A85734	2	probable transport
377	52	12.7	329	C75122	2	hypothetical prote
378	52	12.7	340	C72851	2	AcOrf-11 protein -
379	52	12.7	345	T34998	2	probable transmemb
380	52	12.7	352	T27298	2	hypothetical prote
381	52	12.7	377	T27316	2	hypothetical prote
382	52	12.7	398	T20901	2	hypothetical prote
383	52	12.7	404	T32998	2	hypothetical prote
384	52	12.7	447	G89917	2	branched-chain ami
385	52	12.7	477	E95158	2	hypothetical prote
386	52	12.7	477	E98024	2	hypothetical prote
387	52	12.7	502	T25263	2	hypothetical prote
388	52	12.7	545	E90460	2	probable inner mem
389	52	12.7	574	S46178	2	NADH2 dehydrogenas
390	52	12.7	590	QQTCS5	1	phosphate-repressi
391	52	12.7	763	AD0170	2	NADH2 dehydrogenas
392	52	12.7	866	I79267	2	probable membrane
393	52	12.7	990	TO1896	2	traB protein - Bsc
394	52	12.7	1450	A84780	2	probable ABC trans

SeqNo	Score1	Score2	Accession	N	Len	Description
395	52	12.7	T31418	2	1505	synaptonemal compl
396	52	12.7	S54771	2	1977	sodium channel alp
397	52	12.7	A46269	2	2005	sodium channel alp
398	51.5	12.6	T03344	2	309	conserved hypothet
399	51.5	12.6	T28322	2	93	gene e23 protein -
400	51.5	12.6	A32995	2	113	ORF MSV161 probabl
401	51.5	12.6	B83892	2	137	t complex sterilit
402	51.5	12.6	A36886	2	203	protein-disulfide
403	51.5	12.6	FQHUGL	1	204	surface protein PA
404	51.5	12.6	OBUTMB	1	209	gramlocyte colony
405	51.5	12.6	F85019	2	252	cytochrome-c oxida
406	51.5	12.6	S75891	2	262	hypothetical prote
407	51.5	12.6	T11590	2	271	hypothetical prote
408	51.5	12.6	S60477	2	281	1-acylglycerol-3-p
409	51.5	12.6	T32720	2	293	hypothetical prote
410	51.5	12.6	S76512	2	296	hypothetical prote
411	51.5	12.6	A99017	2	302	heat shock protein
412	51.5	12.6	T47551	2	317	nuclear envelope m
413	51.5	12.6	H95143	2	317	conserved hypothet
414	51.5	12.6	F98011	2	317	conserved hypothet
415	51.5	12.6	T21589	2	318	hypothetical prote
416	51.5	12.6	A86439	2	320	protein T19E23.9 [
417	51.5	12.6	AC0658	2	321	peptide transport
418	51.5	12.6	T08572	2	375	hypothetical prote
419	51.5	12.6	F72859	2	379	very late expressi
420	51.5	12.6	F82871	2	383	conserved hypothet
421	51.5	12.6	T38194	2	383	hypothetical prote
422	51.5	12.6	S64082	2	387	probable membrane
423	51.5	12.6	AD0678	2	395	probable membrane
424	51.5	12.6	PC2168	2	411	phosphoenolpyruvat
425	51.5	12.6	A64763	2	418	probable transport
426	51.5	12.6	D85530	2	418	probable transport
427	51.5	12.6	H90679	2	418	probable transport
428	51.5	12.6	T28827	2	420	hypothetical prote
429	51.5	12.6	G86645	2	446	damage-inducible p
430	51.5	12.6	H64636	2	461	proline/betaine tr
431	51.5	12.6	T10025	2	467	hypothetical prote
432	51.5	12.6	B83368	2	469	hypothetical prote
433	51.5	12.6	S75464	2	474	hypothetical prote
434	51.5	12.6	S61891	2	477	undecaprenyl-phosp
435	51.5	12.6	AD2993	2	492	succinoglycan bios
436	51.5	12.6	F98290	2	493	exoT protein (impo
437	51.5	12.6	JH0313	2	499	potassium channel
438	51.5	12.6	ODUTMB	1	549	cytochrome-c oxida
439	51.5	12.6	T03714	2	550	5-epi-aristolochen
440	51.5	12.6	T08174	2	559	sesquiterpene cycl
441	51.5	12.6	H71562	2	605	probable flagellar
442	51.5	12.6	T11830	2	612	NADH2 dehydrogenas
443	51.5	12.6	AE3091	2	612	conserved hypothet
444	51.5	12.6	B98195	2	648	hypothetical 91.8K
445	51.5	12.6	T05149	2	683	protein kinase hom
446	51.5	12.6	B87265	2	696	Kup system potassi
447	51.5	12.6	T48464	2	705	hypothetical prote
448	51.5	12.6	LEEBBV	1	707	hemolysin secretio
449	51.5	12.6	H70374	2	787	NADH2 dehydrogenas
450	51.5	12.6	A86783	2	824	glycosyl transfera
451	51.5	12.6	FOMSIA	1	827	retrovirus-related
452	51.5	12.6	A47296	2	1023	thiazide-sensitive
453	51.5	12.6	T05646	2	1111	hypothetical prote
454	51.5	12.6	T20968	2	2610	hypothetical prote
455	51	12.4	AH1492	2	56	probable secreted
456	51	12.4	W5WL35	2	81	E5 protein - human
457	51	12.4	S60434	2	101	probable membrane
458	51	12.4	T33239	2	109	synaptobrevin SNB-
459	51	12.4	H82385	2	143	conserved hypothet
460	51	12.4	B69066	2	208	conserved hypothet
461	51	12.4	S73641	2	225	hypothetical prote
462	51	12.4	JQ1571	1	226	major surface anti
463	51	12.4	JQ1572	1	226	major surface anti
464	51	12.4	E70114	2	233	hemolysin III (ypl
465	51	12.4	H95122	2	266	ABC-2 transporter,
466	51	12.4	G83934	2	285	hypothetical prote
467	51	12.4	AH1503	2	301	probable membrane

SeqNo	Score1	Score2	Accession	N	Len	Description
468	51	12.4	D90198	2	312	transposase ISC123
469	51	12.4	T05993	2	314	probable peroxidas
470	51	12.4	D90342	2	319	transposase ISC123
471	51	12.4	C90370	2	321	conserved hypothet
472	51	12.4	G81312	2	323	protein-export mem
473	51	12.4	I55450	2	328	G protein-coupled
474	51	12.4	T23902	2	336	hypothetical prote
475	51	12.4	T11390	2	346	NADH2 dehydrogenas
476	51	12.4	T12290	2	348	NADH2 dehydrogenas
477	51	12.4	A39008	2	359	histamine H2 recep
478	51	12.4	T14084	2	360	hypothetical prote
479	51	12.4	A83458	2	380	hypothetical prote
480	51	12.4	G72569	2	385	hypothetical prote
481	51	12.4	E96516	2	389	F16N3.13 [imported
482	51	12.4	AG0184	2	393	probable multidrug
483	51	12.4	AH0020	2	394	conserved integral
484	51	12.4	AB3479	2	407	sensory transducti
485	51	12.4	S38125	2	418	hypothetical prote
486	51	12.4	C82305	2	421	ubiquinol-cytochro
487	51	12.4	E70968	2	433	hypothetical prote
488	51	12.4	A84824	2	435	probable nematode-
489	51	12.4	H96542	2	443	unknown protein [i
490	51	12.4	F70302	2	446	transporter (Pho87
491	51	12.4	T07883	2	505	cellulase (EC 3.2.
492	51	12.4	T21887	2	513	hypothetical prote
493	51	12.4	T43919	2	528	yfuB protein [impo
494	51	12.4	AI2321	2	528	hypothetical prote
495	51	12.4	S48932	2	546	hypothetical prote
496	51	12.4	G86440	2	546	hypothetical prote
497	51	12.4	HMIVT2	1	566	hemagglutinin prec
498	51	12.4	T15324	2	597	hypothetical prote
499	51	12.4	S36736	2	600	nisT protein - Lac
500	51	12.4	E48951	2	606	nisin transport pr
501	51	12.4	T11334	2	606	NADH2 dehydrogenas
502	51	12.4	F81277	2	628	hypothetical prote
503	51	12.4	T32324	2	634	hypothetical prote
504	51	12.4	T28868	2	646	hypothetical prote
505	51	12.4	H83141	2	766	probable two-compo
506	51	12.4	T33217	2	840	hypothetical prote
507	51	12.4	T25338	2	870	hypothetical prote
508	51	12.4	JH0440	2	898	RAD54 protein - ye
509	51	12.4	G96637	2	967	hypothetical prote
510	51	12.4	T04740	2	1013	hypothetical prote
511	51	12.4	S67794	2	1125	probable membrane
512	51	12.4	T18355	2	1187	hypothetical prote
513	51	12.4	T09224	2	1216	spindle assembly c
514	51	12.4	B40025	2	1293	maleless protein,
515	51	12.4	T37308	2	1528	ATPase homolog - C
516	51	12.4	S64540	2	2039	probable calcium c
517	51	12.4	S28600	2	4085	hypothetical prote
518	50.5	12.3	S49642	2	102	probable membrane
519	50.5	12.3	AC3033	2	114	hypothetical prote
520	50.5	12.3	H90513	2	119	hypothetical prote
521	50.5	12.3	A99253	2	140	hypothetical prote
522	50.5	12.3	G85799	2	141	NADH2 dehydrogenas
523	50.5	12.3	C90951	2	141	hypothetical prote
524	50.5	12.3	E64949	2	171	hypothetical prote
525	50.5	12.3	T25696	2	176	hypothetical prote
526	50.5	12.3	H82141	2	179	probable membrane
527	50.5	12.3	S58618	2	184	hypothetical prote
528	50.5	12.3	D90361	2	203	disulfide bond for
529	50.5	12.3	S10125	2	222	NADH2 dehydrogenas
530	50.5	12.3	AF1995	2	224	hypothetical prote
531	50.5	12.3	JC7697	2	261	alpha-2u-globulin
532	50.5	12.3	AD0743	2	270	hypothetical prote
533	50.5	12.3	S55010	2	277	beta-casein-like p
534	50.5	12.3	S62760	2	278	probable membrane
535	50.5	12.3	C82128	2	280	cytochrome-c oxida
536	50.5	12.3	T31089	2	283	cytochrome-c oxida
537	50.5	12.3	S64317	2	285	4-amino-4-deoxycho
538	50.5	12.3	T19362	2		probable ABC trans
539	50.5	12.3	T18678	2		probable membrane
540	50.5	12.3	H69369	2		branched-chain ami

No.			Length	Accession	N	Description
541	50.5	12.3	286	I46855	2	voltage-gated pota
542	50.5	12.3	286	C81147	2	sulfate ABC transp
543	50.5	12.3	286	G81875	2	sulfate ABC transp
544	50.5	12.3	298	E90172	2	hypothetical prote
545	50.5	12.3	306	H86695	2	ABC transporter pe
546	50.5	12.3	309	AB0343	2	probable phosphati
547	50.5	12.3	310	S40808	2	polynucleotide ade
548	50.5	12.3	310	G86073	2	probable endonucle
549	50.5	12.3	310	A91227	2	probable endonucle
550	50.5	12.3	317	T33861	2	hypothetical prote
551	50.5	12.3	335	AC1343	2	hypothetical prote
552	50.5	12.3	335	AG1713	2	hypothetical prote
553	50.5	12.3	345	T16498	2	hypothetical prote
554	50.5	12.3	346	T11194	2	NADH2 dehydrogenas
555	50.5	12.3	353	S28787	2	neuropeptide Y/pep
556	50.5	12.3	368	S01651	2	probable RNA-direc
557	50.5	12.3	383	C71683	2	rod shape-determin
558	50.5	12.3	401	AD0969	2	glutamate permease
559	50.5	12.3	401	D91082	2	probable transport
560	50.5	12.3	401	B85927	2	partial probable t
561	50.5	12.3	402	G96642	2	hypothetical prote
562	50.5	12.3	403	A90925	2	probable transport
563	50.5	12.3	403	B85773	2	probable transport
564	50.5	12.3	417	AB0682	2	probable membrane
565	50.5	12.3	417	F90916	2	probable transport
566	50.5	12.3	417	F64915	2	membrane protein y
567	50.5	12.3	417	C85765	2	probable transport
568	50.5	12.3	418	S56369	2	hypothetical 44.8K
569	50.5	12.3	418	H86109	2	probable transport
570	50.5	12.3	418	B98269	2	probable transport
571	50.5	12.3	446	S22614	2	hypothetical prote
572	50.5	12.3	449	T50555	2	delta-8 sphingolip
573	50.5	12.3	459	P81914	2	probable transmemb
574	50.5	12.3	470	AE1930	2	ammonium transport
575	50.5	12.3	471	B64099	2	undecaprenyl-phosp
576	50.5	12.3	473	T04218	2	hypothetical prote
577	50.5	12.3	483	A81352	2	integral membrane
578	50.5	12.3	483	S69894	2	major DNA-binding
579	50.5	12.3	564	AC2893	2	adenylate cyclase
580	50.5	12.3	564	F97668	2	probable electron
581	50.5	12.3	572	S46051	2	probable resistanc
582	50.5	12.3	575	B83586	2	probable permease
583	50.5	12.3	603	H90061	2	hypothetical prote
584	50.5	12.3	604	C90619	2	NADH dehydrogenase
585	50.5	12.3	604	T38017	2	hypothetical prote
586	50.5	12.3	608	T35755	2	probable branched
587	50.5	12.3	634	E96927	2	probable permease
588	50.5	12.3	677	A71406	2	hypothetical prote
589	50.5	12.3	719	T45845	2	conserved hypothet
590	50.5	12.3	721	D82496	2	leucocyte antigen
591	50.5	12.3	742	I37225	2	hypothetical prote
592	50.5	12.3	771	H84845	2	hypothetical prote
593	50.5	12.3	772	T26313	2	hypothetical prote
594	50.5	12.3	779	T49717	2	related to BCS1 pr
595	50.5	12.3	788	I64045	2	recombination prot
596	50.5	12.3	792	T00487	2	probable potassium
597	50.5	12.3	830	T01058	2	hypothetical prote
598	50.5	12.3	847	G85666	2	conserved hypothet
599	50.5	12.3	847	AH0636	2	periplasmic glucan
600	50.5	12.3	847	F64847	2	glucan biosynthesi
601	50.5	12.3	857	C90807	2	membrane glycosylt
602	50.5	12.3	974	PXLNPD	1	H+-exporting ATPas
603	50.5	12.3	1098	G70697	2	probable arabinosy
604	50.5	12.3	1099	T16283	2	hypothetical prote
605	50.5	12.3	1143	I84547	4	hypothetical mdl f
606	50.5	12.3	4568	T08030	4	dynein beta heavy
607	50	12.2	83	S22207	2	photosystem I 8K p
608	50	12.2	87	T26867	2	hypothetical prote
609	50	12.2	98	T17091	2	NADH2 dehydrogenas
610	50	12.2	115	T17082	2	NADH2 dehydrogenas
611	50	12.2	121	AH2497	2	hypothetical prote
612	50	12.2	133	S61662	2	dolichyl-diphospho
613	50	12.2	133	B70027	2	hypothetical prote

No.			Length	Accession	N	Description
614	50	12.2	175	AB0185	2	probable membrane
615	50	12.2	274	T05509	2	hypothetical prote
616	50	12.2	286	H89003	2	protein T24A6.5 [i
617	50	12.2	287	B82546	2	pre-pilin leader p
618	50	12.2	291	B72284	2	oligopeptide ABC t
619	50	12.2	301	E95104	1	conserved hypothet
620	50	12.2	306	QREBOB	2	oligopeptide trans
621	50	12.2	306	AH0650	2	probable endonucle
622	50	12.2	308	T20043	2	hypothetical prote
623	50	12.2	325	B87234	2	conserved membrane
624	50	12.2	328	T44931	1	mocR protein [impo
625	50	12.2	338	S44207	2	hypothetical prote
626	50	12.2	340	T24615	2	hypothetical prote
627	50	12.2	342	S51891	2	probable membrane
628	50	12.2	349	A75612	2	phosphate ABC tran
629	50	12.2	349	I55601	2	Na/taurocholate co
630	50	12.2	357	A45619	2	ubiquinol-cytochro
631	50	12.2	380	T41016	2	DNA mismatch repai
632	50	12.2	381	T02589	2	hypothetical prote
633	50	12.2	388	C40605	2	hmc 3'-region hypo
634	50	12.2	396	E64143	1	chloramphenicol re
635	50	12.2	419	T19260	2	hypothetical prote
636	50	12.2	427	G70936	2	hypothetical prote
637	50	12.2	436	G70058	2	hypothetical prote
638	50	12.2	440	D87076	2	probable conserved
639	50	12.2	443	BVECTC	1	threonine-serine p
640	50	12.2	443	C85973	2	threonine-serine p
641	50	12.2	443	D91128	2	threonine-serine p
642	50	12.2	443	F89426	2	protein M162.5 [im
643	50	12.2	451	A95379	2	HYPOTHETICAL 50.8
644	50	12.2	467	AB2493	2	hypothetical prote
645	50	12.2	483	T20895	2	hypothetical prote
646	50	12.2	487	T23776	2	hypothetical prote
647	50	12.2	494	AE1372	2	proteins involved
648	50	12.2	495	T20885	2	hypothetical prote
649	50	12.2	496	G71693	2	apolipoprotein n-a
650	50	12.2	504	T29338	2	hypothetical prote
651	50	12.2	507	F97765	2	hypothetical prote
652	50	12.2	528	AI0359	2	iron(III)-transpor
653	50	12.2	529	B84813	2	hypothetical prote
654	50	12.2	547	AE1022	2	probable membrane
655	50	12.2	553	T40438	2	hypothetical prote
656	50	12.2	555	S56946	2	probable membrane
657	50	12.2	575	H69450	2	proly1-tRNA synthe
658	50	12.2	575	F71360	2	probable K+ transp
659	50	12.2	607	AH0381	2	probable ATP trans
660	50	12.2	611	S68138	2	NADH2 dehydrogenas
661	50	12.2	616	T19873	2	hypothetical prote
662	50	12.2	720	G64836	2	probable membrane
663	50	12.2	720	D90759	1	hypothetical prote
664	50	12.2	720	B85623	2	hypothetical prote
665	50	12.2	729	G70539	2	hypothetical prote
666	50	12.2	752	B82146	2	hypothetical prote
667	50	12.2	820	C81252	2	probable NADH2 deh
668	50	12.2	952	H84583	2	hypothetical prote
669	50	12.2	1020	A34474	2	Na+/K+-exchanging
670	50	12.2	1020	B24639	2	Na+/K+-exchanging
671	50	12.2	1023	JC4013	2	major acidic nucle
672	50	12.2	1029	D81379	2	probable membrane
673	50	12.2	1040	S56229	2	transmembrane effl
674	50	12.2	1130	T20288	2	hypothetical prote
675	50	12.2	1284	T13168	2	probable potassium
676	50	12.2	1302	S30327	2	multidrug resistan
677	50	12.2	1400	I38185	1	protein-tyrosine k
678	50	12.2	1835	I54323	2	sodium channel alp
679	50	12.2	1836	I64893	2	sodium channel alp
680	50	12.2	1836	JS0648	2	sodium channel alp
681	50	12.2	1840	CHRTM1	1	sodium channel pro
682	49.5	12.1	84	W5WL51	1	B5 protein - human
683	49.5	12.1	107	AC3315	2	hypothetical membr
684	49.5	12.1	110	F90830	2	integral membrane
685	49.5	12.1	110	C85688	2	hypothetical prote
686	49.5	12.1	110	JN0329	2	ethidium efflux pr

#			Accession	Len	Description
687	49.5	12.1	AD0744	131	probable membrane
688	49.5	12.1	D70387	154	hypothetical prote
689	49.5	12.1	AB1185	160	B. subtilis YdbS p
690	49.5	12.1	S40721	214	hypothetical prote
691	49.5	12.1	A75628	219	response regulator
692	49.5	12.1	S42069	236	TEGT protein - rat
693	49.5	12.1	DEECSI	238	succinate dehydrog
694	49.5	12.1	B90722	238	succinate dehydrog
695	49.5	12.1	D85573	239	succinate dehydrog
696	49.5	12.1	AC0591	242	hypothetical prote
697	49.5	12.1	T14791	261	cytochrome-c oxida
698	49.5	12.1	T11770	265	hypothetical prote
699	49.5	12.1	B84468	266	cytochrome-c oxida
700	49.5	12.1	C45164	276	probable permease
701	49.5	12.1	H83568	281	middle surface pro
702	49.5	12.1	JQ2226	292	hypothetical prote
703	49.5	12.1	A60547	302	probable phosphati
704	49.5	12.1	B84421	310	probable phosphati
705	49.5	12.1	H82138	311	cytochrome aa3 con
706	49.5	12.1	T44610	313	hypothetical prote
707	49.5	12.1	T24994	318	NADH2 dehydrogena
708	49.5	12.1	QQRT1M	328	hypothetical prote
709	49.5	12.1	T32210	339	hypothetical prote
710	49.5	12.1	T21473	343	hypothetical prote
711	49.5	12.1	B84129	344	chemokine receptor
712	49.5	12.1	JC5942	362	flagellar biosynth
713	49.5	12.1	C81453	366	probable membrane
714	49.5	12.1	S53898	368	partial beta-D-glu
715	49.5	12.1	A85768	370	beta-D-glucuronida
716	49.5	12.1	D90919	394	cell division cont
717	49.5	12.1	S48522	400	large surface prot
718	49.5	12.1	JQ2230	423	cell division prot
719	49.5	12.1	C82763	428	hypothetical prote
720	49.5	12.1	T00731	431	probable O-antigen
721	49.5	12.1	B97277	435	probable sugar tra
722	49.5	12.1	AC0104	452	proline/betaine tr
723	49.5	12.1	A71877	452	hypothetical prote
724	49.5	12.1	C72295	459	NADH2 dehydrogenas
725	49.5	12.1	S10196	488	hypothetical prote
726	49.5	12.1	C86183	494	branched chain ami
727	49.5	12.1	AC1742	506	protein involved i
728	49.5	12.1	D64048	521	iron (III) ABC tra
729	49.5	12.1	A85088	542	hypothetical prote
730	49.5	12.1	B81662	565	apolipoprotein N-a
731	49.5	12.1	HMIVGM	575	hemagglutinin prec
732	49.5	12.1	AI1996	579	hypothetical prote
733	49.5	12.1	AI1789	592	ABC transporter (A
734	49.5	12.1	D64044	603	hypothetical prote
735	49.5	12.1	GBECGC	603	beta-glucuronidase
736	49.5	12.1	T11284	604	NADH2 dehydrogenas
737	49.5	12.1	I36917	615	glycoprotein lib -
738	49.5	12.1	AH2248	645	proteinase [import
739	49.5	12.1	AI2963	645	cellulose synthase
740	49.5	12.1	D98319	647	hypothetical prote
741	49.5	12.1	A83908	669	bo-type ubiquinol
742	49.5	12.1	S64795	669	suppressor protein
743	49.5	12.1	E71127	724	hypothetical prote
744	49.5	12.1	AE2538	765	cation transportin
745	49.5	12.1	T46178	791	hypothetical prote
746	49.5	12.1	A99514	808	conserved hypothet
747	49.5	12.1	T04459	834	hypothetical prote
748	49.5	12.1	A97178	944	probable permease
749	49.5	12.1	S56936	1051	vacuolar protein-s
750	49.5	12.1	B83330		RND divalent metal
751	49	12.0	H81337	62	probable periplasm
752	49	12.0	S14206	98	NADH2 dehydrogenas
753	49	12.0	A26696	101	NADH2 dehydrogenas
754	49	12.0	S60405	104	hypothetical prote
755	49	12.0	AG0137	110	conserved hypothet
756	49	12.0	T11513	114	NADH2 dehydrogenas
757	49	12.0	AD2309	136	hypothetical prote
758	49	12.0	E71051	151	hypothetical prote
759	49	12.0	S59155	155	NADH2 dehydrogenas

Description	#			Len	Accession	
probable membrane	760	49	12.0	157	H95891	2
hypothetical prote	761	49	12.0	158	S39770	2
B. subtilis YdbS p	762	49	12.0	178	A71730	2
hypothetical prote	763	49	12.0	179	JC1151	2
response regulator	764	49	12.0	185	H83296	2
TEGT protein - rat	765	49	12.0	202	AF0604	2
succinate dehydrog	766	49	12.0	222	T18587	2
succinate dehydrog	767	49	12.0	229	F64398	2
succinate dehydrog	768	49	12.0	235	C89949	2
hypothetical prote	769	49	12.0	246	A69013	2
cytochrome-c oxida	770	49	12.0	259	S50337	2
hypothetical prote	771	49	12.0	261	T11540	2
cytochrome-c oxida	772	49	12.0	263	A95865	2
probable permease	773	49	12.0	267	G75377	2
probable phosphati	774	49	12.0	294	T11379	2
probable phosphati	775	49	12.0	300	F81799	2
cytochrome aa3 con	776	49	12.0	301	AH1144	2
NADH2 dehydrogenas	777	49	12.0	302	B81696	2
hypothetical prote	778	49	12.0	302	G86920	2
hypothetical prote	779	49	12.0	320	T26259	2
hypothetical prote	780	49	12.0	332	T19649	2
chemokine receptor	781	49	12.0	332	S03871	2
flagellar biosynth	782	49	12.0	348	T12281	2
probable membrane	783	49	12.0	356	S13221	2
partial beta-D-glu	784	49	12.0	357	T25499	2
beta-D-glucuronida	785	49	12.0	368	AF1992	2
cell division cont	786	49	12.0	378	C83465	2
large surface prot	787	49	12.0	381	T29927	2
cell division prot	788	49	12.0	386	AD2649	2
hypothetical prote	789	49	12.0	386	C97431	2
probable O-antigen	790	49	12.0	391	AC0326	2
probable sugar tra	791	49	12.0	398	T44331	2
proline/betaine tr	792	49	12.0	399	A87392	2
hypothetical prote	793	49	12.0	403	C83825	2
NADH2 dehydrogenas	794	49	12.0	405	T21188	2
hypothetical prote	795	49	12.0	408	T34467	2
protein involved i	796	49	12.0	408	D81387	2
iron (III) ABC tra	797	49	12.0	414	T22760	2
hypothetical prote	798	49	12.0	415	F96499	2
apolipoprotein N-a	799	49	12.0	439	AF0551	2
hemagglutinin prec	800	49	12.0	439	JQ0007	2
hypothetical prote	801	49	12.0	443	E96956	2
ABC transporter (A	802	49	12.0	459	C65212	2
hypothetical prote	803	49	12.0	460	AH0968	2
beta-glucuronidase	804	49	12.0	462	T11136	2
NADH2 dehydrogenas	805	49	12.0	463	E83242	2
glycoprotein lib -	806	49	12.0	478	T11318	2
proteinase [import	807	49	12.0	480	G86285	2
cellulose synthase	808	49	12.0	516	H70935	2
hypothetical prote	809	49	12.0	520	C89980	2
bo-type ubiquinol	810	49	12.0	521	T41621	2
suppressor protein	811	49	12.0	523	AI1970	2
hypothetical prote	812	49	12.0	541	AC2392	2
cation transportin	813	49	12.0	546	G71348	2
hypothetical prote	814	49	12.0	547	A40656	2
conserved hypothet	815	49	12.0	553	B83714	2
hypothetical prote	816	49	12.0	559	G71327	2
probable permease	817	49	12.0	569	S74053	2
vacuolar protein-s	818	49	12.0	569	T18831	2
probable periplasm	819	49	12.0	599	G86288	2
NADH2 dehydrogenas	820	49	12.0	618	E96834	2
NADH2 dehydrogenas	821	49	12.0	624		2
hypothetical prote	822	49	12.0	662	T47649	2
conserved hypothet	823	49	12.0	693	H86214	2
NADH2 dehydrogenas	824	49	12.0	706	JE0164	2
hypothetical prote	825	49	12.0	772	G02860	2
hypothetical prote	826	49	12.0	772	S65532	2
NADH2 dehydrogenas	827	49	12.0	780	T29580	2
conserved hypothet	828	49	12.0	787	G86436	2
glycoprotein H pre	829	49	12.0	842	S18462	2
ferrichrome-iron r	830	49	12.0	853	AC2079	2
hypothetical prote	831	49	12.0	854	T23155	2
metabotropic gluta	832	49	12.0	871	A46742	2
CTF4 protein - yea				927	A45039	2

#			accession	#	2	description
833	48.5	12.0	A57487	939	2	inositol-polyphosp
834	49	12.0	C71248	976	2	hypothetical prote
835	49	12.0	S53602	1502	2	carbamoyl-phosphat
836	49	12.0	T52081	1515	2	MRP-like ABC trans
837	48.5	11.8	JC6573	113	1	outer-arm dynein 1
838	48.5	11.8	B64248	118	2	hypothetical prote
839	48.5	11.8	AC2739	137	2	conserved hypothet
840	48.5	11.8	AD0368	138	2	probable membrane
841	48.5	11.8	A87036	139	2	probable conserved
842	48.5	11.8	H70531	148	2	hypothetical prote
843	48.5	11.8	A97520	152	2	hypothetical prote
844	48.5	11.8	F71319	162	2	hypothetical prote
845	48.5	11.8	B96510	169	2	hypothetical prote
846	48.5	11.8	B30020	174	2	NADH2 dehydrogenas
847	48.5	11.8	S70898	179	2	intracellular sept
848	48.5	11.8	H84165	206	2	hypothetical prote
849	48.5	11.8	S76279	206	2	hypothetical prote
850	48.5	11.8	JQ1579	226	1	major surface anti
851	48.5	11.8	JQ1580	226	2	major surface anti
852	48.5	11.8	JQ2119	226	2	surface antigen -
853	48.5	11.8	JQ2225	226	2	small surface prot
854	48.5	11.8	S05118	230	2	hypothetical prote
855	48.5	11.8	S58563	230	2	cemA protein - mai
856	48.5	11.8	I38334	237	2	TEGT (testis enhan
857	48.5	11.8	T41063	238	2	hypothetical prote
858	48.5	11.8	T30127	245	2	hypothetical prote
859	48.5	11.8	B84147	249	2	ABC transporter (p
860	48.5	11.8	AH1482	252	2	hypothetical prote
861	48.5	11.8	H97708	259	2	hypothetical prote
862	48.5	11.8	A90175	260	2	conserved hypothet
863	48.5	11.8	T50011	264	2	hypothetical prote
864	48.5	11.8	S07747	265	2	hypothetical prote
865	48.5	11.8	B81431	267	2	ABC transporter in
866	48.5	11.8	D82001	269	2	probable integral
867	48.5	11.8	G81230	269	2	conserved hypothet
868	48.5	11.8	AH1924	275	2	hypothetical prote
869	48.5	11.8	AD0099	280	2	prepilin peptidase
870	48.5	11.8	S19420	283	2	hypothetical prote
871	48.5	11.8	G90386	299	2	conserved hypothet
872	48.5	11.8	E71534	300	2	probable pbp2b met
873	48.5	11.8	H64153	308	2	hypothetical prote
874	48.5	11.8	T11402	318	2	NADH2 dehydrogenas
875	48.5	11.8	AD3134	322	2	hypothetical prote
876	48.5	11.8	H71884	326	2	iron (III) dicitra
877	48.5	11.8	A64631	326	2	iron(III) dicitrat
878	48.5	11.8	B83636	327	2	hypothetical prote
879	48.5	11.8	H98153	332	2	peptide ABC transp
880	48.5	11.8	T34124	334	2	hypothetical prote
881	48.5	11.8	A97643	334	2	exopolysaccharide
882	48.5	11.8	AD2866	338	2	acetyltransferase
883	48.5	11.8	A83389	338	2	probable permease
884	48.5	11.8	B69544	340	2	hypothetical prote
885	48.5	11.8	D75274	350	2	hypothetical prote
886	48.5	11.8	T21855	351	2	probable ABC transp
887	48.5	11.8	B81402	361	2	probable integral
888	48.5	11.8	A82567	363	2	GumF protein XF236
889	48.5	11.8	S33573	382	1	ubiquinol-cytochro
890	48.5	11.8	B96522	389	2	hypothetical prote
891	48.5	11.8	H69048	389	2	conserved hypothet
892	48.5	11.8	B96780	393	2	nitrate transporte
893	48.5	11.8	C83422	403	2	hypothetical prote
894	48.5	11.8	T20453	404	2	hypothetical prote
895	48.5	11.8	C71971	413	2	serine transport p
896	48.5	11.8	A81394	418	2	probable sugar tra
897	48.5	11.8	F97133	419	2	phage-related, hea
898	48.5	11.8	T32470	439	2	hypothetical prote
899	48.5	11.8	AH3587	444	2	glycerol-3-phospha
900	48.5	11.8	B82219	446	2	PTS system, cellob
901	48.5	11.8	G81187	459	2	Na+/H+ antiporter
902	48.5	11.8	H85087	461	2	hypothetical prote
903	48.5	11.8	B88613	462	2	protein T27B9.5 [i
904	48.5	11.8	B82943	470	2	probable ABC subst
905	48.5	11.8	T31717	473	2	hypothetical prote
906	48.5	11.8	480	A83487	2	probable MFS trans
907	48.5	11.8	481	C95920	2	hypothetical membr
908	48.5	11.8	507	T44785	2	hypothetical prote
909	48.5	11.8	512	B90050	2	hypothetical prote
910	48.5	11.8	529	S71774	1	calcium-dependent
911	48.5	11.8	544	B75541	2	probable multidrug
912	48.5	11.8	576	T25375	2	hypothetical prote
913	48.5	11.8	582	H82393	2	probable L-lactate
914	48.5	11.8	588	G82118	2	succinate dehydrog
915	48.5	11.8	588	T48766	2	probable sugar tra
916	48.5	11.8	592	D84431	2	probable endosomal
917	48.5	11.8	606	S41830	2	NADH2 dehydrogenas
918	48.5	11.8	644	A25684	2	hypothetical prote
919	48.5	11.8	685	S65974	2	conserved hypothet
920	48.5	11.8	692	H71494	2	probable thiol-dis
921	48.5	11.8	711	C49219	2	toxin apxIII secre
922	48.5	11.8	748	T47250	2	complex I intermed
923	48.5	11.8	792	G84830	2	probable potassium
924	48.5	11.8	809	IJBODD	1	desmocollin 2b pre
925	48.5	11.8	863	IJBODC	1	desmocollin 2a pre
926	48.5	11.8	886	A57172	2	probable hormone r
927	48.5	11.8	1065	B69795	2	acriflavin resista
928	48.5	11.8	1333	S65812	2	RNA-directed DNA p
929	48.5	11.8	2098	T13166	2	rough deal protein
930	48.5	11.8	2386	T39911	2	rad3 checkpoint pr
931	48.5	11.8	3149	QQBE8	1	BPLF1 protein - hu
932	48	11.7	82	T10148	2	sugar transport pr
933	48	11.7	115	T11057	2	NADH2 dehydrogenas
934	48	11.7	115	T17173	2	NADH2 dehydrogenas
935	48	11.7	115	S60397	2	hypothetical prote
936	48	11.7	115	AI0332	2	probable membrane
937	48	11.7	118	G1YC	1	gene 1 protein - S
938	48	11.7	126	B83265	2	hypothetical prote
939	48	11.7	129	T04230	2	hypothetical prote
940	48	11.7	139	S72641	2	probable ABC-type
941	48	11.7	145	F81338	2	probable periplasm
942	48	11.7	171	S72489	2	hypothetical prote
943	48	11.7	180	B97242	2	hypothetical prote
944	48	11.7	197	I39723	2	ORF13 - Agrobacter
945	48	11.7	198	JT0356	2	Cop protein - Clos
946	48	11.7	200	F70900	2	hypothetical prote
947	48	11.7	200	B90933	2	NADH2 dehydrogenas
948	48	11.7	200	F85781	2	hypothetical prote
949	48	11.7	211	H64931	2	probable membrane
950	48	11.7	230	D69529	2	conserved hypothet
951	48	11.7	230	E71315	2	conserved hypothet
952	48	11.7	251	AH0732	2	probable bacteriop
953	48	11.7	261	S47876	2	cytochrome-c oxida
954	48	11.7	261	T11293	2	cytochrome-c oxida
955	48	11.7	264	E95410	2	probable ABC trans
956	48	11.7	266	G82386	2	amino acid ABC tra
957	48	11.7	277	T29611	2	hypothetical prote
958	48	11.7	293	AD3438	2	CDPdiacylglycerol-
959	48	11.7	294	E97671	2	thuf protein (AF17
960	48	11.7	294	AB2896	2	hypothetical prote
961	48	11.7	296	E69025	2	conserved hypothet
962	48	11.7	300	G81069	2	conserved hypothet
963	48	11.7	302	H82045	2	conserved hypothet
964	48	11.7	303	JQ1382	2	hypothetical 34K p
965	48	11.7	306	J23686	2	hypothetical prote
966	48	11.7	309	S51356	2	olfactory receptor
967	48	11.7	317	C82411	2	hypothetical prote
968	48	11.7	319	S73290	1	cytochrome c-type
969	48	11.7	321	T06932	2	plastoquinol-plast
970	48	11.7	321	D90353	2	conserved hypothet
971	48	11.7	327	T34720	2	probable lipoprote
972	48	11.7	333	C82888	2	phenylalanine-tRNA
973	48	11.7	340	T41757	2	AcMNPV orf11 - Bom
974	48	11.7	341	AF1319	2	ferrichrome ABC tr
975	48	11.7	341	AF1691	2	ferrichrome ABC tr
976	48	11.7	345	T25561	2	hypothetical prote
977	48	11.7	348	T12287	2	NADH2 dehydrogenas
978	48	11.7	348	T12285	2	NADH2 dehydrogenas

#			ID		Accession	Description
979	48	11.7	348	2	B83869	hypothetical prote
980	48	11.7	349	2	T09858	NADH2 dehydrogenas
981	48	11.7	349	2	T09948	NADH2 dehydrogenas
982	48	11.7	354	1	RGXLOA	GTP-binding regula
983	48	11.7	357	2	B71708	hypothetical prote
984	48	11.7	363	1	CBUTB	ubiquinol-cytochro
985	48	11.7	363	1	S01431	nodulation protein
986	48	11.7	367	2	T23273	hypothetical prote
987	48	11.7	369	2	AE2345	phospho-N-acetylmu
988	48	11.7	369	2	H88208	protein K02A2.1 [i
989	48	11.7	371	2	F81357	probable membrane-
990	48	11.7	374	2	B58889	ubiquinol-cytochro
991	48	11.7	379	2	T24814	hypothetical prote
992	48	11.7	383	2	F70752	hypothetical prote
993	48	11.7	387	2	I69202	G protein-coupled
994	48	11.7	388	2	S59860	hypothetical prote
995	48	11.7	389	2	S71336	mesotocin receptor
996	48	11.7	391	2	S07743	ubiquinol-cytochro
997	48	11.7	392	2	G85076	probable reverse t
998	48	11.7	408	2	B82507	sodium/glutamate s
999	48	11.7	418	2	S67138	probable membrane
1000	48	11.7	419	2	D72357	hypothetical prote
1001	48	11.7	428	2	S38461	ubiquinol-cytochro
1002	48	11.7	428	2	PC4163	toxin-co-regulated
1003	48	11.7	428	2	JC4601	hypothetical 48.2k
1004	48	11.7	429	2	G97528	citrate synthase [
1005	48	11.7	429	2	AH2747	protein C27A12.8 [
1006	48	11.7	436	2	H87793	branched-chain ami
1007	48	11.7	439	2	AB0389	proton-glutamate s
1008	48	11.7	447	2	F82619	glycerol-3-phospha
1009	48	11.7	452	1	JNECGT	sn-glycerol-3-phos
1010	48	11.7	452	2	E91019	sn-glycerol-3-phos
1011	48	11.7	452	2	G85863	efflux protein [lim
1012	48	11.7	452	2	AC3184	probable membrane-
1013	48	11.7	454	1	T25203	NADH2 dehydrogenas
1014	48	11.7	458	2	H71657	NADH2 dehydrogenas
1015	48	11.7	462	2	D81251	amino acid transpo
1016	48	11.7	465	2	B69825	D-serine/D-alanine
1017	48	11.7	474	2	AH0226	hypothetical prote
1018	48	11.7	488	2	F96724	hypothetical prote
1019	48	11.7	493	2	A71875	protein C27A12.7 [
1020	48	11.7	497	2	G87793	hypothetical prote
1021	48	11.7	500	2	AD1047	probable amino aci
1022	48	11.7	509	2	F71526	hypothetical prote
1023	48	11.7	523	2	JQ1926	polyprotein - hepa
1024	48	11.7	528	2	D85048	hypothetical prote
1025	48	11.7	532	2	S46831	probable membrane
1026	48	11.7	535	2	T41384	probable turgor pr
1027	48	11.7	537	2	AE2454	two-component sens
1028	48	11.7	557	2	T27130	hypothetical prote
1029	48	11.7	564	2	AH2321	hypothetical prote
1030	48	11.7	581	2	JC7086	FZD10 protein - hu
1031	48	11.7	586	2	S64779	probable membrane
1032	48	11.7	615	2	G82658	periplasmic glucan
1033	48	11.7	627	2	D90452	hypothetical prote
1034	48	11.7	644	2	T37692	probable transport
1035	48	11.7	705	2	T19595	hypothetical prote
1036	48	11.7	727	2	S27043	neurotransmitter t
1037	48	11.7	744	2	T34116	voltage-gated pota
1038	48	11.7	790	2	A82200	cation transport A
1039	48	11.7	840	2	T02164	hypothetical prote
1040	48	11.7	848	2	T34823	probable turgor pr
1041	48	11.7	881	2	T25786	hypothetical prote
1042	48	11.7	908	2	AH0055	probable cation-tr
1043	48	11.7	921	2	T51804	respiratory burst
1044	48	11.7	928	2	T01191	RNA-directed DNA p
1045	48	11.7	1149	2	T18515	adenosinetriphosph
1046	48	11.7	1206	2	B86445	hypothetical prote
1047	48	11.7	1245	1	VHWV82	structural polypro
1048	48	11.7	1337	2	T38949	hypothetical prote
1049	48	11.7	1355	2	T22552	hypothetical prote
1050	48	11.7	1687	2	T30176	EGF repeat transme
1051	48	11.7	1765	2	T42388	sodium channel alp

#	Length				Accession	Description
1052	2005	11.7	48	2	B25019	sodium channel pro
1053	2163	11.7	48	1	S50675	pre-mRNA splicing
1054	3014	11.7	48	1	JC5620	genome polyprotein
1055	50	11.6	47.5	2	H90537	hypothetical prote
1056	132	11.6	47.5	2	T18122	hypothetical prote
1057	83	11.6	47.5	2	F82246	conserved hypothet
1058	138	11.6	47.5	2	F81355	probable integral
1059	140	11.6	47.5	2	B86283	hypothetical prote
1060	146	11.6	47.5	2	C84113	acetobutylicum pho
1061	148	11.6	47.5	2	C84113	hypothetical prote
1062	151	11.6	47.5	2	T33937	hypothetical prote
1063	151	11.6	47.5	2	H65017	hypothetical prote
1064	151	11.6	47.5	2	C85886	hypothetical prote
1065	163	11.6	47.5	2	H91041	hypothetical prote
1066	168	11.6	47.5	2	D64025	conserved hypothet
1067	168	11.6	47.5	2	AF2802	hypothetical prote
1068	171	11.6	47.5	2	G97581	phosphatidylglycer
1069	174	11.6	47.5	2	AD0554	NADH2 dehydrogenas
1070	179	11.6	47.5	2	S01189	hypothetical prote
1071	195	11.6	47.5	2	T22143	hypothetical prote
1072	196	11.6	47.5	2	B90202	tumor related prot
1073	201	11.6	47.5	2	T01982	hypothetical prote
1074	204	11.6	47.5	2	A86636	serine O-acetyltra
1075	220	11.6	47.5	2	AG1466	hypothetical wtf p
1076	243	11.6	47.5	2	T41562	hypothetical prote
1077	247	11.6	47.5	2	AD1983	hypothetical prote
1078	247	11.6	47.5	2	T16061	conserved hypothet
1079	249	11.6	47.5	2	E89994	phosphatidate cyti
1080	249	11.6	47.5	1	SYECDG	CDP-diglyceride sy
1081	249	11.6	47.5	2	A99651	CDP-diglyceride sy
1082	261	11.6	47.5	2	A85502	H+-transporting tw
1083	261	11.6	47.5	2	JQ1513	H+-transporting tw
1084	265	11.6	47.5	2	B34167	hypothetical prote
1085	272	11.6	47.5	2	T14645	cysZ protein - Hae
1086	275	11.6	47.5	2	E64182	conserved hypothet
1087	275	11.6	47.5	1	E75548	hypothetical prote
1088	278	11.6	47.5	2	F69777	hypothetical prote
1089	280	11.6	47.5	2	T28869	hypothetical prote
1090	284	11.6	47.5	2	AI2517	probable dimethyl
1091	305	11.6	47.5	2	T25829	hypothetical prote
1092	311	11.6	47.5	2	AH0680	conserved hypothet
1093	313	11.6	47.5	2	B84187	NADH2 dehydrogenas
1094	313	11.6	47.5	2	H82541	hypothetical prote
1095	317	11.6	47.5	2	T11160	NADH2 dehydrogenas
1096	319	11.6	47.5	2	D96793	conserved hypothet
1097	323	11.6	47.5	1	T11337	NADH2 dehydrogenas
1098	325	11.6	47.5	2	A58892	hypothetical prote
1099	326	11.6	47.5	2	T32174	hypothetical prote
1100	326	11.6	47.5	2	AC2953	hypothetical prote
1101	329	11.6	47.5	2	B98330	hypothetical prote
1102	329	11.6	47.5	2	AG2951	probable oligopept
1103	332	11.6	47.5	2	F98331	alpha-2,3-sialyltr
1104	333	11.6	47.5	2	A49879	G protein-coupled
1105	346	11.6	47.5	2	I65989	NADH2 dehydrogenas
1106	346	11.6	47.5	2	T14133	hypothetical prote
1107	354	11.6	47.5	2	T33309	conserved hypothet
1108	358	11.6	47.5	2	T32319	hypothetical prote
1109	366	11.6	47.5	2	F71897	flagellar biosynth
1110	367	11.6	47.5	2	T33462	hypothetical prote
1111	370	11.6	47.5	2	T28892	conserved hypothet
1112	372	11.6	47.5	2	A80602	NADH2 dehydrogenas
1113	379	11.6	47.5	2	B64819	hypothetical prote
1114	387	11.6	47.5	2	H86364	hypothetical prote
1115	394	11.6	47.5	2	F82692	hypothetical prote
1116	403	11.6	47.5	2	AB0713	probable membrane
1117	404	11.6	47.5	2	F64923	probable membrane
1118	404	11.6	47.5	2	AD0005	hypothetical prote
1119	418	11.6	47.5	2	H81699	conserved hypothet
1120	423	11.6	47.5	2	AB2308	probable membrane
1121	423	11.6	47.5	2	AH1407	sodium/glutamate s
1122	425	11.6	47.5	2	AH1783	conserved hypothet
1123	427	11.6	47.5	2	B86737	hypothetical prote
1124	443	11.6	47.5	2	S42658	PTS system galacti

No.	Score	Value	Length	N	Accession	Description
1125	47.5	11.6	449	2	S76839	hypothetical prote
1126	47.5	11.6	457	2	D83867	hypothetical prote
1127	47.5	11.6	463	2	G69829	probable integral
1128	47.5	11.6	465	2	AE3192	hypothetical prote
1129	47.5	11.6	474	2	D83396	two component sens
1130	47.5	11.6	480	2	G70008	conserved hypothet
1131	47.5	11.6	482	2	T01762	NADH dehydrogenase
1132	47.5	11.6	483	2	P75360	hypothetical prote
1133	47.5	11.6	485	2	G82037	potassium uptake p
1134	47.5	11.6	486	2	H84805	hypothetical prote
1135	47.5	11.6	488	2	T11230	NADH2 dehydrogenas
1136	47.5	11.6	492	2	AC0768	probable transmemb
1137	47.5	11.6	497	2	G86878	arginine/ornitine
1138	47.5	11.6	515	2	D95924	probable phosphogl
1139	47.5	11.6	516	2	G86243	hypothetical prote
1140	47.5	11.6	520	2	A56118	vetispiradiene syn
1141	47.5	11.6	529	2	AC2619	virulence factor M
1142	47.5	11.6	546	2	A69890	hypothetical prote
1143	47.5	11.6	557	2	C97401	virulence factor m
1144	47.5	11.6	557	2	E86106	yidB protein [simi
1145	47.5	11.6	557	2	S56342	yidB protein - Esc
1146	47.5	11.6	559	2	H91265	hypothetical prote
1147	47.5	11.6	559	2	S62503	inorganic phosphat
1148	47.5	11.6	575	2	T08964	hypothetical prote
1149	47.5	11.6	594	2	T45842	calcium dependent
1150	47.5	11.6	595	2	JC8012	G;protein-coupled
1151	47.5	11.6	598	2	B90589	sugar ABC transpor
1152	47.5	11.6	603	2	C90621	NADH dehydrogenase
1153	47.5	11.6	606	2	T11909	NADH2 dehydrogenas
1154	47.5	11.6	620	2	A96668	probable endo-beta
1155	47.5	11.6	623	2	T16167	hypothetical prote
1156	47.5	11.6	626	2	E90079	hypothetical prote
1157	47.5	11.6	643	2	B69373	conserved hypothet
1158	47.5	11.6	657	2	E83041	probable chemotaxi
1159	47.5	11.6	708	2	C30169	leukotoxin express
1160	47.5	11.6	715	2	A34408	peroxidase (EC 1.1
1161	47.5	11.6	737	2	AE0819	probable membrane
1162	47.5	11.6	749	2	A69861	conserved hypothet
1163	47.5	11.6	778	2	T16111	hypothetical prote
1164	47.5	11.6	782	2	T39696	methionyl tRNA syn
1165	47.5	11.6	802	2	T05596	probable potassium
1166	47.5	11.6	832	2	S76815	hypothetical prote
1167	47.5	11.6	857	2	JC7716	hypothetical prote
1168	47.5	11.6	858	2	T08881	prominin - rat
1169	47.5	11.6	919	2	T21663	prominin - mouse
1170	47.5	11.6	932	2	H86325	hypothetical prote
1171	47.5	11.6	958	2	AC0204	hypothetical prote
1172	47.5	11.6	1094	2	T05472	probable integral
1173	47.5	11.6	1165	2	T15279	hypothetical prote
1174	47.5	11.6	1174	2	A40853	potassium channel
1175	47.5	11.6	1493	2	H71445	hypothetical prote
1176	47.5	11.6	1876	2	S50235	1,3-beta-glucan sy
1177	47.5	11.6	2055	2	T31617	hypothetical prote
1178	47.5	11.6	2223	2	A47447	calcium channel pr
1179	47.5	11.6	2242	2	A57541	pyrimidine synthes
1180	47	11.5	61	2	S78741	protein YPR170w-a
1181	47	11.5	82	1	H84046	hypothetical prote
1182	47	11.5	84	1	W5WL31	E5 protein - human
1183	47	11.5	92	2	E81100	conserved hypothet
1184	47	11.5	92	2	JN0095	conserved hypothet
1185	47	11.5	105	2	E71132	hypothetical prote
1186	47	11.5	116	2	G82398	hypothetical 10.6K
1187	47	11.5	121	2	A24272	Ig heavy chain pre
1188	47	11.5	122	2	C82926	hypothetical prote
1189	47	11.5	125	2	D85595	probable membrane
1190	47	11.5	125	2	H90744	probable membrane
1191	47	11.5	125	2	H64822	probable membrane
1192	47	11.5	131	2	S65197	hypothetical prote
1193	47	11.5	137	1	B64239	ubiquinol-cytochro
1194	47	11.5	149	2	T11066	NADH2 dehydrogenas
1195	47	11.5	162	2	G98046	conserved hypothet
1196	47	11.5	167	2	B71518	probable signal pe
1197	47	11.5	167	2	B64904	fimbrial protein p
1198	47	11.5	187	2	T49684	hypothetical prote
1199	47	11.5	192	2	G71920	hypothetical prote
1200	47	11.5	200	2	F84708	probable integral
1201	47	11.5	203	2	B83606	hypothetical prote
1202	47	11.5	206	2	S56059	probable membrane
1203	47	11.5	212	2	AF1644	hypothetical prote
1204	47	11.5	219	2	T47881	hypothetical prote
1205	47	11.5	223	2	B96927	response regulator
1206	47	11.5	224	2	T21101	hypothetical prote
1207	47	11.5	234	2	T35312	probable integral
1208	47	11.5	235	1	QQBY1M	mRNA maturase-rela
1209	47	11.5	235	2	G81138	probable succinate
1210	47	11.5	254	2	B83286	hypothetical prote
1211	47	11.5	260	1	OTXL3	cytochrome-c oxida
1212	47	11.5	260	2	S22850	ERS1 protein - yea
1213	47	11.5	262	2	H71390	cytochrome-c oxida
1214	47	11.5	264	2	H81720	conserved hypothet
1215	47	11.5	272	2	H87075	probable conserved
1216	47	11.5	272	2	D86482	protein F5J5.3 [im
1217	47	11.5	286	2	B70614	probable mmaAl pro
1218	47	11.5	297	2	T36786	probable integral
1219	47	11.5	300	1	A32566	ubiquinol-cytochro
1220	47	11.5	300	2	S40858	hypothetical 32.9K
1221	47	11.5	300	2	H91233	probable transport
1222	47	11.5	300	2	H86080	probable transport
1223	47	11.5	301	2	S50737	probable membrane
1224	47	11.5	306	2	G85704	oligopeptide trans
1225	47	11.5	306	2	H90846	oligopeptide trans
1226	47	11.5	306	2	B36263	oligopeptide trans
1227	47	11.5	306	2	D70409	hypothetical prote
1228	47	11.5	308	2	AC1053	probable membrane
1229	47	11.5	313	2	D69336	conserved hypothet
1230	47	11.5	319	2	D90344	transposase ISC123
1231	47	11.5	319	2	B90466	transposase ISC123
1232	47	11.5	319	2	H90321	transposase ISC123
1233	47	11.5	319	2	T51280	hypothetical prote
1234	47	11.5	321	2	P90862	peptide transport
1235	47	11.5	321	2	C85756	peptide transport
1236	47	11.5	321	2	H64877	peptide transport
1237	47	11.5	322	2	S68128	NADH2 dehydrogenas
1238	47	11.5	325	2	F82558	lipopolysaccharide
1239	47	11.5	328	2	T20582	hypothetical prote
1240	47	11.5	330	2	E64826	ybjX protein - Esc
1241	47	11.5	330	2	C71009	hypothetical prote
1242	47	11.5	336	2	T19498	hypothetical prote
1243	47	11.5	340	2	T25677	hypothetical prote
1244	47	11.5	344	2	T25567	hypothetical prote
1245	47	11.5	345	2	T24533	hypothetical prote
1246	47	11.5	348	2	T11301	NADH2 dehydrogenas
1247	47	11.5	348	2	T12291	NADH2 dehydrogenas
1248	47	11.5	352	2	AF3073	hypothetical prote
1249	47	11.5	356	2	C40656	regulatory protein
1250	47	11.5	357	2	AB1176	spermidine/putresc
1251	47	11.5	357	2	AH1532	spermidine/putresc
1252	47	11.5	358	2	T11165	ubiquinol-cytochro
1253	47	11.5	358	2	H83554	hypothetical prote
1254	47	11.5	359	2	JC4120	histamine H2 recep
1255	47	11.5	360	2	AE0068	phospho-N-acetylmu
1256	47	11.5	365	2	F95857	probable sugar ABC
1257	47	11.5	371	2	C98213	sugar ABC transpor
1258	47	11.5	378	2	S51591	chitinase (EC 3.2.
1259	47	11.5	380	2	D84295	hypothetical prote
1260	47	11.5	390	2	T12421	NADH2 dehydrogenas
1261	47	11.5	390	2	S66497	isotocin receptor
1262	47	11.5	394	2	C64185	ubiquinol-cytochro
1263	47	11.5	394	2	D65167	hypothetical prote
1264	47	11.5	395	2	S76793	probable membrane
1265	47	11.5	396	2	S54999	hypothetical prote
1266	47	11.5	401	2	D83873	ubiquinol-cytochro
1267	47	11.5	411	2	H72084	cbs domain protein
1268	47	11.5	419	2	T25565	hypothetical prote
1269	47	11.5	431	2	D86433	hypothetical prote
1270	47	11.5	433	2	T30807	TRAF interacting p

Seq	Accession	N	Len			Description
1271	H64713	2	438	11.5	47	Na+/H+-exchanging
1272	B29413	1	440	11.5	47	ubiquinol-cytochro
1273	JL0144	2	440	11.5	47	interleukin-6 rece
1274	JC5520	2	440	11.5	47	serotonin receptor
1275	H90253	2	443	11.5	47	NADH-Ubiquinone/pl
1276	F95243	2	443	11.5	47	sensor histidine k
1277	C98108	2	443	11.5	47	histidine kinase (
1278	B81367	2	446	11.5	47	probable transmemb
1279	B83033	2	446	11.5	47	prpbable MFS trans
1280	I49480	2	458	11.5	47	alpha-2 adrenergic
1281	A37869	2	458	11.5	47	alpha-2B-adrenergi
1282	A40392	2	458	11.5	47	alpha-2-adrenergic
1283	T11202	2	459	11.5	47	NADH2 dehydrogenas
1284	AF1079	2	461	11.5	47	amino acid transpo
1285	G96655	2	465	11.5	47	unknown protein, 2
1286	P96806	2	470	11.5	47	probable AUX1-like
1287	T23728	2	476	11.5	47	hypothetical prote
1288	T15657	2	481	11.5	47	hypothetical prote
1289	G83142	2	482	11.5	47	probable transport
1290	T16443	2	483	11.5	47	hypothetical prote
1291	D86285	2	487	11.5	47	hypothetical prote
1292	T16402	2	488	11.5	47	hypothetical prote
1293	AG0557	2	491	11.5	47	AmpG protein [impo
1294	S67314	2	494	11.5	47	regulatory protein
1295	T46923	2	499	11.5	47	hypothetical prote
1296	AI0963	2	500	11.5	47	two-component syst
1297	B41853	2	500	11.5	47	hexose phosphate t
1298	AI1913	2	500	11.5	47	apolipoprotein N-a
1299	DELVN2	1	501	11.5	47	NADH2 dehydrogenas
1300	E87021	2	505	11.5	47	probable integral-
1301	T22398	2	529	11.5	47	hypothetical prote
1302	A35343	2	531	11.5	47	glucuronosyltransf
1303	T27235	2	532	11.5	47	hypothetical prote
1304	B72542	2	548	11.5	47	probable cytochrom
1305	F88392	2	559	11.5	47	protein MO1G5.5 [i
1306	T33425	2	559	11.5	47	hypothetical prote
1307	A70755	2	582	11.5	47	hypothetical prote
1308	S73366	2	600	11.5	47	carnitine O-palmit
1309	E96742	2	609	11.5	47	probable ABC trans
1310	T07420	2	631	11.5	47	ATP/ADP-transporte
1311	S78171	2	637	11.5	47	heme lyase yejR -
1312	H85043	2	637	11.5	47	hypothetical prote
1313	T52460	2	657	11.5	47	hypothetical prote
1314	JW0107	1	689	11.5	47	very-long-chain ac
1315	A42163	2	718	11.5	47	Na+/myo-inositol c
1316	T47648	2	720	11.5	47	ABC transporter-li
1317	H81088	2	742	11.5	47	ABC transporter fa
1318	H81855	2	742	11.5	47	prbable cytolysin
1319	B64656	2	858	11.5	47	cell division prot
1320	H88085	2	888	11.5	47	protein T11F1.8 [i
1321	A54809	2	909	11.5	47	disease resistance
1322	S13913	1	924	11.5	47	hexokinase (EC 2.7
1323	T32381	2	980	11.5	47	hypothetical prote
1324	A87063	2	983	11.5	47	conserved large me
1325	T38074	2	1004	11.5	47	hypothetical prote
1326	S72698	2	1008	11.5	47	transport protein
1327	T33372	2	1010	11.5	47	hypothetical prote
1328	B24862	2	1021	11.5	47	Na+/K+-exchanging
1329	A53491	2	1191	11.5	47	bumetanide-sensiti
1330	D96723	2	1198	11.5	47	hypothetical prote
1331	S48375	2	1375	11.5	47	hypothetical prote
1332	T14603	2	1718	11.5	47	hypothetical prote
1333	I51964	2	1836	11.5	47	sodium channel alp
1334	A37361	2	1938	11.5	47	probable integral
1335	S68176	2	1972	11.5	47	TOG protein - huma
1336	T30890	2	2262	11.5	46.5	calcium channel al
1337	52	2	52	11.3	46.5	light-harvesting p
1338	S23285	2	102	11.3	46.5	hypothetical prote
1339	S12809	2	115	11.3	46.5	NADH2 dehydrogenas
1340	T17176	2	121	11.3	46.5	transporter, mfs s
1341	S69859	2	132	11.3	46.5	hypothetical prote
1342	H86846	2	141	11.3	46.5	NADH2 dehydrogenas
1343	D81508	2	144	11.3	46.5	Conserved hypothet
1344	A86593	2	148	11.3	46.5	CT568 hypothetical
1345	H72032	2	148	11.3	46.5	ct568 hypothetical
1346	AI1542	2	160	11.3	46.5	B. subtilis YdbS p
1347	C35216	2	164	11.3	46.5	FP18 protein - fow
1348	T22102	2	164	11.3	46.5	hypothetical prote
1349	D86761	2	165	11.3	46.5	NADH2 dehydrogenas
1350	DERZN6	1	176	11.3	46.5	hypothetical prote
1351	T31499	2	177	11.3	46.5	probable intracell
1352	AG0267	2	180	11.3	46.5	hypothetical prote
1353	E72459	2	183	11.3	46.5	lipoprotein signal
1354	G71698	2	194	11.3	46.5	NADH2 dehydrogenas
1355	JQ2137	1	199	11.3	46.5	conserved hypothet
1356	B64169	2	220	11.3	46.5	probable amino aci
1357	G83371	2	225	11.3	46.5	surface antigen -
1358	JQ2120	2	226	11.3	46.5	succinate dehydrog
1359	F83448	2	235	11.3	46.5	B. subtilis YhfI p
1360	AB1191	2	243	11.3	46.5	OccM protein - Agr
1361	B42600	2	245	11.3	46.5	octopine permease
1362	B41044	2	246	11.3	46.5	hypothetical prote
1363	E64040	2	247	11.3	46.5	hypothetical prote
1364	F83578	2	276	11.3	46.5	hypothetical prote
1365	T16014	2	279	11.3	46.5	probable permease
1366	C83356	2	288	11.3	46.5	sn-glycerol-3-phos
1367	A80462	2	295	11.3	46.5	sugar permease hom
1368	D70018	2	300	11.3	46.5	hypothetical prote
1369	B70888	2	302	11.3	46.5	hypothetical prote
1370	AB1536	2	303	11.3	46.5	hypothetical prote
1371	B82468	2	311	11.3	46.5	probable membrane
1372	AB0677	2	315	11.3	46.5	NADH2 dehydrogenas
1373	T11833	2	318	11.3	46.5	NADH2 dehydrogenas
1374	T11389	2	318	11.3	46.5	J319 protein - Afr
1375	D43680	2	319	11.3	46.5	cobalamin biosynth
1376	D83848	2	319	11.3	46.5	prolipoprotein dia
1377	H90600	2	322	11.3	46.5	probable membrane
1378	AE0324	2	323	11.3	46.5	maltose ABC transp
1379	G90487	2	323	11.3	46.5	hypothetical prote
1380	T26350	2	325	11.3	46.5	protein C36C5.10 [
1381	A88990	2	330	11.3	46.5	hypothetical prote
1382	T31826	2	341	11.3	46.5	ferric anguibactin
1383	G82880	2	341	11.3	46.5	hypothetical prote
1384	T28772	2	342	11.3	46.5	probable permease
1385	D83282	2	343	11.3	46.5	hypothetical prote
1386	T32051	2	343	11.3	46.5	hypothetical prote
1387	T29003	2	346	11.3	46.5	hypothetical prote
1388	G71983	2	351	11.3	46.5	hypothetical prote
1389	C96643	2	352	11.3	46.5	secretory protein
1390	AC0851	2	356	11.3	46.5	protein F37B4.9 [i
1391	D88979	2	356	11.3	46.5	hypothetical prote
1392	B59105	2	359	11.3	46.5	ubiquinol-cytochro
1393	H22848	1	371	11.3	46.5	probable membrane
1394	AB0276	2	372	11.3	46.5	probable periplasm
1395	AI0163	2	378	11.3	46.5	VLF-1 orf77 - Bomb
1396	T41820	2	379	11.3	46.5	large surface anti
1397	T13474	2	382	11.3	46.5	hypothetical prote
1398	B83205	2	383	11.3	46.5	hypothetical prote
1399	H70821	2	386	11.3	46.5	probable integral
1400	F81343	2	395	11.3	46.5	hypothetical prote
1401	T01201	2	396	11.3	46.5	hypothetical prote
1402	C83470	2	397	11.3	46.5	sodium-glutamate s
1403	YOECNQ	1	401	11.3	46.5	glutamate transpor
1404	A98195	2	401	11.3	46.5	glutamate transpor
1405	B86042	2	401	11.3	46.5	m33-B isoform - mo
1406	152590	2	403	11.3	46.5	alpha(1,3)-fucosyl
1407	B36340	2	405	11.3	46.5	conserved hypothet
1408	AI3148	2	405	11.3	46.5	hypothetical prote
1409	T19176	2	407	11.3	46.5	hypothetical prote
1410	T19326	2	409	11.3	46.5	transporter, mfs s
1411	AD3417	2	418	11.3	46.5	hypothetical prote
1412	F72213	2	421	11.3	46.5	bme3 protein (AF07
1413	B98139	2	425	11.3	46.5	probable manganese
1414	E87171	2	426	11.3	46.5	probable D-ribulos
1415	S78599	2	427	11.3	46.5	hypothetical prote
1416	T48284	2	428	11.3	46.5	hypothetical prote

No.					Accession		Description
1417	46.5	11.3	445	2	B65221		probable amino aci
1418	46.5	11.3	445	2	A91266		probable amino aci
1419	46.5	11.3	445	2	F86106		probable amino aci
1420	46.5	11.3	448	2	S50622		hypothetical prote
1421	46.5	11.3	454	2	A38643		protein kinase (EC
1422	46.5	11.3	458	2	T11528		NADH2 dehydrogenase
1423	46.5	11.3	458	2	B99613		NADH dehydrogenase
1424	46.5	11.3	459	2	T11333		NADH2 dehydrogenas
1425	46.5	11.3	459	1	BDBC		melibiose carrier
1426	46.5	11.3	469	2	C86107		melibiose permease
1427	46.5	11.3	469	2	F91266		melibiose permease
1428	46.5	11.3	474	2	AE1075		probable two-compo
1429	46.5	11.3	484	2	S53641		protein kinase clk
1430	46.5	11.3	489	2	A96837		hypothetical prote
1431	46.5	11.3	489	2	T27445		hypothetical prote
1432	46.5	11.3	491	2	T11894		NADH2 dehydrogenas
1433	46.5	11.3	492	2	C90985		probable export pr
1434	46.5	11.3	492	2	F85830		probable export pr
1435	46.5	11.3	493	1	D64806		probable proton/ol
1436	46.5	11.3	493	2	F90720		probable transport
1437	46.5	11.3	493	2	D85571		probable transport
1438	46.5	11.3	496	2	S75790		hypothetical prote
1439	46.5	11.3	508	2	A89817		hypothetical prote
1440	46.5	11.3	511	2	H75097		polysaccharide bio
1441	46.5	11.3	519	2	H96661		unknown protein, 5
1442	46.5	11.3	526	2	T01089		hypothetical prote
1443	46.5	11.3	530	1	B48529		ubiquinol-cytochro
1444	46.5	11.3	546	2	T46718		probable farnesyl
1445	46.5	11.3	548	2	T06266		germacrene C synth
1446	46.5	11.3	548	2	T06265		germacrene C synth
1447	46.5	11.3	548	2	H82432		sucrose-6-phosphat
1448	46.5	11.3	553	2	T01535		probable cytochrom
1449	46.5	11.3	554	2	T11267		NADH2 dehydrogenas
1450	46.5	11.3	557	2	F82481		decarboxylase, gro
1451	46.5	11.3	588	1	DEECSF		succinate dehydrog
1452	46.5	11.3	588	2	C85573		succinate dehydrog
1453	46.5	11.3	588	2	AB0591		succinate dehydrog
1454	46.5	11.3	588	2	D90722		hypothetical prote
1455	46.5	11.3	598	2	T48980		hypothetical prote
1456	46.5	11.3	607	2	S01939		hypothetical prote
1457	46.5	11.3	647	2	AG2114		hydroxamate-depend
1458	46.5	11.3	654	2	A96235		hypothetical prote
1459	46.5	11.3	654	2	AC3051		hypothetical prote
1460	46.5	11.3	659	2	D84633		probable multispan
1461	46.5	11.3	677	2	T11231		NADH2 dehydrogenas
1462	46.5	11.3	716	2	AC2449		ABC transporter AT
1463	46.5	11.3	721	2	C84677		probable membrane
1464	46.5	11.3	732	2	S47688		cd2+-exporting ATP
1465	46.5	11.3	781	2	T51433		probable cation tr
1466	46.5	11.3	792	2	S72831		hypothetical prote
1467	46.5	11.3	800	2	G89831		hypothetical prote
1468	46.5	11.3	827	2	A95877		hypothetical prote
1469	46.5	11.3	881	2	S46633		probable membrane
1470	46.5	11.3	890	2	S44150		coat protein - str
1471	46.5	11.3	926	1	OPPGIT		iodide peroxidase
1472	46.5	11.3	963	2	A55926		DNA binding protei
1473	46.5	11.3	971	2	I39166		cellular apoptosis
1474	46.5	11.3	978	2	E96787		protein T4O12.5 [i
1475	46.5	11.3	979	2	A35913		regulatory factor
1476	46.5	11.3	1036	2	D84741		probable cellulose
1477	46.5	11.3	1079	2	I59362		calcium/polyvalent
1478	46.5	11.3	1140	2	B97820		hypothetical prote
1479	46.5	11.3	1215	2	S50428		probable Ca2+-tran
1480	46.5	11.3	1237	2	H81660		DNA polymerase III
1481	46.5	11.3	1344	2	H84557		hypothetical prote
1482	46.5	11.3	1365	2	T00833		RNA-directed DNA p
1483	46.5	11.3	1411	2	S48442		PDR11 protein - ye
1484	46.5	11.3	1681	2	A55138		sodium channel mNa
1485	46.5	11.3	1695	2	JB0084		voltage-gated sodi
1486	46.5	11.3	2052	2	T37711		probable n-end-rec
1487	46.5	11.3	2150	2	T32497		hypothetical prote
1488	46	11.2	69	2	B83300		hypothetical prote
1489	46	11.2	78	2	T19053		hypothetical prote
1490	46	11.2	96	2	S55012		NADH2 dehydrogenas
1491	46	11.2	102	2	F81879		probable membrane
1492	46	11.2	108	2	C87494		conserved hypothet
1493	46	11.2	110	2	S58811		ubiquinol-cytochro
1494	46	11.2	110	2	S58805		ubiquinol-cytochro
1495	46	11.2	110	2	S58808		ubiquinol-cytochro
1496	46	11.2	113	2	S37091		tcpI protein - Vib
1497	46	11.2	115	1	DNHUN3		NADH2 dehydrogenas
1498	46	11.2	115	2	S65745		NADH2 dehydrogenas
1499	46	11.2	115	2	H59153		NADH2 dehydrogenas
1500	46	11.2	125	2	AG1134		probable secreted

ALIGNMENTS

RESULT 1
T19408
hypothetical protein C18E9.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19408, T25046
R;Sims, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19120
A;Accession: T19408
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <WI1>
A;Cross-references: UNIPROT:Q9XTH1; EMBL:Z70034; PIDN:CAA93859.1; GSPDB:GN00020; CESP:C1
R;Baynes, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19973
A;Accession: T25046
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <WI2>
A;Cross-references: EMBL:Z68318; PIDN:CAA92698.1; GSPDB:GN00020; CESP:C18E9.10
A;Experimental source: clone T21B10
C;Genetics:
A;Gene: CESP:C18E9.10
A;Map position: 2
A;Introns: 39/2; 72/2; 112/3; 141/2; 180/3; 200/2

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Query Match       25.9%;  Score 106;  DB 2;  Length 235;
Best Local Similarity   35.5%;  Pred. No. 0.0011;
Matches  22;  Conservative   7;  Mismatches  33;  Indels   0;  Gaps   0;

Qy    1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCIIQSLALTWYSLSF  60
          ||| ||| |: |::|:|:||: | : |||::| : | || ||:|:|||||||
Db  146 LGPKSYLTHMASPQRRLVTVSYLSALFATLYSSLWLKSTIFTLIAAIFQGFTLVWYVLSY 205

Qy   61 IP  62
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Db  206 VP 207
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RESULT 2
T05049
hypothetical protein M3E9.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05049
R;Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hoheisel, J.; Mewes, H.W.; Mayer
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15396
A;Accession: T05049
A;Molecule type: DNA
A;Residues: 1-385 <BEV>
A;Cross-references: UNIPROT:O65579; EMBL:AL022223
A;Experimental source: cultivar Columbia; BAC clone M3E9
C;Genetics:

A;Map position: 4
A;Introns:19/2; 80/2; 180/2; 314/3; 349/3
A;Note: M3E9.20

Query Match 19.3%; Score 79; DB 2; Length 385;
Best Local Similarity 27.3%; Pred. No. 0.19;
Matches 21; Conservative 13; Mismatches 27; Indels 16; Gaps 1;

Qy 2 GPVKQLKRM-----------FEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIF 45
        ||| ||| :| :| : ||| | :::|
Db 286 GPKNQLAHMSSMEVCYTVLLCVCHALNPRRLPSTLGFIATMVGTIYVSMVLHSYILSVLF 345

Qy 46 CILQSLALTWYSLSFIP 62
        :|| ||| :| :|:|
Db 346 SVLQVIALIVYCISYFP 362

RESULT 3
S45393
probable membrane protein YBL102w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBL0812
C;Species: Saccharomyces cerevisiae
C;Date: 09-Jun-1994 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S45393; S45845; S59190
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A;Reference number: S45387
A;Accession: S45393
A;Molecule type: DNA
A;Residues: 1-215 <OBE>
A;Cross-references: UNIPROT:P38166; EMBL:X79489; NID:g496661; PID:g496667
A;Experimental source: strain S288C
R;Obermaier, B.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45816
A;Accession: S45845
A;Molecule type: DNA
A;Residues: 1-215 <DOM>
A;Cross-references: EMBL:Z35863; NID:g536171; PID:g536172; MIPS:YBL102w
A;Experimental source: strain S288C
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
Yeast 11, 1103-1112, 1995
A;Title: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevis
A;Reference number: S59184; MUID:96076635; PMID:7502586
A;Accession: S59190
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <OBW>
A;Cross-references: EMBL:X79489; NID:g496661; PIDN:CAA55993.1; PID:g496667
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C;Genetics:
A;Gene: SGD;SFT2
A;Cross-references: SGD:S0000198; MIPS:YBL102w
A;Map position: 2L
C;Keywords: transmembrane protein
F;79-107/Domain: transmembrane #status predicted <TM1>
F;111-138/Domain: transmembrane #status predicted <TM2>
F;148-166/Domain: transmembrane #status predicted <TM3>
F;168-193/Domain: transmembrane #status predicted <TM4>

Query Match 18.3%; Score 75; DB 2; Length 215;
Best Local Similarity 27.1%; Pred. No. 0.33;
Matches 19; Conservative 17; Mismatches 32; Indels 2; Gaps 2;

Qy 1 MGPVKQLKRMFEPTRL-IATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLS 59
        ||| ||| : ||| | : | :: ||| | : :|:|:| :|::| :|:|
Db 131 MGPLAYLKHLTARERLPFSMFFFATCF-WTIYFAAFSKNTVLTITCALLELVAVIYYAIS 189

Qy 60 FIPFARDAVK 69
        :| ||
Db 190 YFPFGATGLR 199

RESULT 4
T02324
hypothetical protein At2g34360 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F13P17.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Mar-1999
C;Accession: T02324; F84755
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.
A;Reference number: Z14657
A;Accession: T02324
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-466 <ROU>
A;Cross-references: UNIPROT:O80785; EMBL:AC004481; NID:g3337347; PID:g3337367
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-466 <STO>
A;Cross-references: GB:AE002093; NID:g3337367; PIDN:AAC27412.1; GSPDB:GN00139
C;Genetics:
A;Gene: F13P17.20; At2g34360
A;Map position: 2
A;Introns: 82/3; 264/2; 292/1; 306/2; 386/1; 425/3
C;Superfamily: conserved hypothetical protein HI1612

Query Match 16.2%; Score 66.5; DB 2; Length 466;
Best Local Similarity 25.6%; Pred. No. 5.8;
Matches 20; Conservative 13; Mismatches 22; Indels 23; Gaps 4;

Qy 19 TIMVLLCFALTLCSAF-------------WWHNKGLALIFCILQ--SLALTWYSLS--- 59
        ::|:|:||| | :|:|| |::|| |:||
Db 189 SLHVIICWVLVLKSGLGFRGAAVANAISYWLN--VILLSCVVKFSPSCSLTWTGFSKEAR 246

Qy 60 --FIPFARDAVKKCFAVC 75
        |:||||| |||||
Db 247 RDIIPFMKLVIPSAFWVC 264

RESULT 5
F58930
cytochrome-c oxidase (EC 1.9.3.1) chain III - Cyanidioschyzon merolae mitochondrion
C;Species: mitochondrion Cyanidioschyzon merolae
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: F58930
R;Ohta, N.; Sato, N.; Kuroiwa, T.
Nucleic Acids Res. 26, 5190-5198, 1998
A;Title: Structure and organization of the mitochondrial genome of the unicellular red al
A;Reference number: A58930; MUID:99030526; PMID:9801318
A;Accession: F58930
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <ARN>
A;Cross-references: UNIPROT:Q9ZZQ8; GB:D89861; NID:g4115781; PIDN:BAA34657.1; PID:g39278(
C;Genetics:
A;Gene: cox3
A;Genome: mitochondrion
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;

Query Match 15.9%; Score 65; DB 2; Length 272;
Best Local Similarity 32.4%; Pred. No. 5.5;
Matches 22; Conservative 13; Mismatches 13; Indels 18; Gaps 5;

Qy   10 MFEPTRL--IATIMVLLCFALTLCSAFWWH--------NKG-LALIFCILQSLAIT---W 55
         |||:||:|.:||:|| | |||:||:||| ||:||
Db   133 IFDPCVPFLNTIILL----LSGCTVTWAHHAIIHGNRNQGILALVFTILLALLFTGLQF 188

Qy   56 YSLSFIPF 63
Db   189 YEYKIAPF 196

RESULT 6
AI0825
probable 3-phenylpropionate permease STY2801 [imported] - Salmonella enterica subsp. ent
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0825
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02757.1; PIDN:g16503767; GSPDB:GN00176
C;Genetics:
A;Gene: STY2801
C;Superfamily: maltose permease

Query Match   15.7%; Score 64.5; DB 2; Length 379;
Best Local Similarity 24.4%; Pred. No. 8.2;
Matches   19; Conservative   13; Mismatches   33; Indels   13; Gaps   2;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFW------W-------HNKGLALIFCI 47
         |: :||:|||.| ||||:|| || : |
Db   54 LGSLLIAPRVSDPSRLISALRVLALLTLVPALAFWAGTHVAVLMVVMVGFNLFFSPLVPL 113

Qy   48 LQSLALTWYSLSFIPFAR 65
         :|| | |: :
Db   114 TDALANTWQKQITLDYGR 131

RESULT 7
A69826
hypothetical protein yhdK - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69826
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69826
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-96 <KUN>
A;Cross-references: UNIPROT:O07580; GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12789.
A;Experimental source: strain 168

C;Genetics:
A;Gene: yhdK

Query Match   15.6%; Score 64; DB 2; Length 96;
Best Local Similarity 36.6%; Pred. No. 3;
Matches   15; Conservative   9; Mismatches   13; Indels   4; Gaps   1;

Qy   32 SAFWWHNKGLALIFCILQSLAL---TWYSLSFIPFARDAV 68
         : |: |||| ||||:|||| :| ||:|||||| ||
Db   11 NVFGWISVGTAVLSLLLNLAIISNVTFYSYQMLPFAMAAV 51

RESULT 8
A38908
spa40 protein - Shigella flexneri plasmid pMYSH6000
C;Species: Shigella flexneri
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: A38908
R;Sasakawa, C.; Komatsu, K.; Tobe, T.; Suzuki, T.; Yoshikawa, M.
J. Bacteriol. 175, 2334-2346, 1993
A;Title: Eight genes in region 5 that form an operon are essential for invasion of epith
A;Reference number: A49846; MUID:93224456; PMID:8385666
A;Accession: A38908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-342 <SAS>
A;Cross-references: UNIPROT:P40707; GB:D13663; NID:g287439; PIDN:BAA02832.1; PID:g303896
C;Genetics:
A;Genome: plasmid
C;Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology
C;Keywords: transmembrane protein

Query Match   15.6%; Score 64; DB 2; Length 342;
Best Local Similarity 31.7%; Pred. No. 8.6;
Matches   20; Conservative   9; Mismatches   22; Indels   12; Gaps   3;

Qy   1 MGPVKQLKRMFEPTRLIATI-------MVLLCFALTLCSAFWWHNKG---LALIFCILQSLA 52
         || ||::| |: |::: |:| |||||||| | ||
Db   116 LNPVKGLKKIFS---IKTIKFFKSILLLILALTYFFWINDRKIIFSQVFSSVDGLY 171

Qy   53 LTW 55
         |||
Db   172 LIW 174

RESULT 9
T26918
hypothetical protein Y45F10B.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26918
R;McMurray, A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20286
A;Accession: T26918
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-351 <WIL>
A;Cross-references: UNIPROT:O62470; EMBL:AL021487; PIDN:CAA16356.1; GSPDB:GN00022; CESP:
A;Experimental source: clone Y45F10B
C;Genetics:
A;Gene: CESP:Y45F10B.5
A;Map position: 4
A;Introns: 94/3; 164/3; 217/3; 283/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b

Query Match   15.6%; Score 64; DB 2; Length 351;
Best Local Similarity 35.1%; Pred. No. 8.8;
Matches   20; Conservative   10; Mismatches   21; Indels   6; Gaps   4;

Qy   17 IATIMVLLCFALTL-CSAFWWHNKGLALIFCILQSLALTWYSLSFIPFARDAVKKCF 72
         :|| |: | || | |:||||| |||:||:| |
Db   267 LTALSMLLSFVTLICARF--HAKIFQLIFIIFPTMAV--YFIALRPFGNDC-EICF 318

RESULT 10
F83092
probable cytochrome b PA4430 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83092
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83092
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-403 <STO>
A;Cross-references: UNIPROT:Q9HVY5; GB:AE004091, NID:g9950654; PIDN:AAG0781
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4430
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C;Keywords: heme; iron; metalloprotein
F;87,188/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F;101,203/Binding site: heme iron (His) (axial ligands) (high potential) #status predict

Query Match   15.6%; Score 64; DB 2; Length 403;
Best Local Similarity 38.2%; Pred. No. 9.9;
Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 34 FWWHNKGLALIFCILQSLALTWYSLSFIPFARDA 67
          ||: ||: | :||::|| | :|
Db 33 FWYFFGSLALLVLVNQILTGIWLTMSFTPSAEEA 66

RESULT 11
F95885
probable iron ABC transporter permease protein SMb20364 [imported] - Sinorhizobium melil
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95885
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
o, H.; Okumura, J.; Wong, K.; Yeh, K.
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481131
A;Accession: F95885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-681 <KUR>
A;Cross-references: UNIPROT:Q92WI9; GB:AL591985; PIDN:CAC48750.1; PID:g15140223; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20364
A;Genome: plasmid

Query Match   15.6%; Score 64; DB 2; Length 681;
Best Local Similarity 37.1%; Pred. No. 15;
Matches 13; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 12 EPTRLIATIMVLLCFALT--LCSAFWWHNKGLALI 44
       :|:| ::||||||| | || :|
Db 345 DPSRAAVLAIILLCFLTAFLAQRFWLSGKNFATV 379

RESULT 12
S73803
MG256 homolog H91_orf258 - Mycoplasma pneumoniae (strain ATCC 29342)
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S73803
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73803
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-258 <HIM>
A;Cross-references: UNIPROT:P75421; EMBL:AE000047; GB:U00089; NID:g1674162; PIDN:AAB9612!
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Genetic code: SGC3

Query Match   15.4%; Score 63; DB 2; Length 258;
Best Local Similarity 26.5%; Pred. No. 8.8;
Matches 18; Conservative 12; Mismatches 12; Indels 26; Gaps 4;

Qy 4 VKQLKRMFEPTRLIATIMVLLCFALTLCSAF----WWHNKGL-----ALIFCILQSLALTW 55
      :::::: :)   : | :|: | | |||::| ||||:
Db 32 IERMRIVF------GLLIALICFSNVLCPLFIATWFSTKGFGQHYRALIFTL--------- 77

Qy 56 YSLSFIPF 63
      ||||
Db 78 ----FIPF 81

RESULT 13
S74522
hypothetical protein slr0728 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74522
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74522
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-387 <KAN>
A;Cross-references: UNIPROT:P72672; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA1674
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG

Query Match   15.4%; Score 63; DB 2; Length 387;
Best Local Similarity 24.6%; Pred. No. 12;
Matches 17; Conservative 14; Mismatches 20; Indels 18; Gaps 2;

Qy 16 LIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSL--------------SFI 61
      |:||:| ||| | : || :|||||||| :|:||
Db 149 LVACILEAIAIVLITGSRSAW---GIGLLIGIAYAIYLSWTWLVALAGGATAMVLWASFG 204

Qy 62 PFARDAVKK 70
      || :|: :::
Db 205 PFGKEPLRQ 213

RESULT 14
T16599
hypothetical protein K09F5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

```
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16599
R;Bentley, D.
submitted to the EMBL Data Library, September 1995
A;Description: The sequence of C. elegans cosmid K09F5.
A;Reference number: Z18544
A;Accession: T16599
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1022 <BEN>
A;Cross-references: UNIPROT:O17943; EMBL:U37430; NID:g1019963; PID:g1945497; PIDN:AAB526
A;Experimental source: strain Bristol N2; clone K09F5
C;Genetics:
A;Gene: CESP:K09F5.3
A;Map position: X
A;Introns: 35/2; 109/1; 156/1; 332/3; 452/3; 480/3; 558/3; 668/3; 735/2; 799/3; 919/2; 9

Query Match             15.4%;  Score 63;  DB 2;  Length 1022;
Best Local Similarity   25.8%;  Pred. No. 28;
Matches   16;  Conservative   15;  Mismatches   27;  Indels    4;  Gaps    2;

Qy      3  PVKQLKRMFE-PTRLIATIMVLLCFALTLCSAFWWHNKGLALIF---CILQSLALTWYSL  58
              ::|  |:: ||:|:|||||:  |:|    ::|:  : |||| ::   :|| :: |
Db    205  PVLMHMKLFGIPLEMVNLFIALVAPAIAYPAVFWRVSKPFSVIFSLHLVIYAAQVIWGYL 264

Qy     59  SF 60
           ||
Db    265  SF 266


RESULT 15
S49295
hypothetical protein - Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 29-Sep-1999
C;Accession: S49295
R;Turlin, E.; Gasser, F.; Biville, F.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and sequencing of an E. coli gene homologous to dioxygenase of Gr
A;Reference number: S49292
A;Accession: S49295
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <TUR>
A;Cross-references: EMBL:Z37966; NID:g550595; PIDN:CAA86021.1; PID:g550599
C;Superfamily: conserved hypothetical protein HI0308

Query Match             15.2%;  Score 62.5;  DB 2;  Length 255;
Best Local Similarity   27.9%;  Pred. No. 9.9;
Matches   19;  Conservative   10;  Mismatches   26;  Indels   13;  Gaps    2;

Qy      1  MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFW--WHNKGLALIFC----------I 47
           :|   |:::||||::|:|||||  |:||:  ||| |  :||:
Db     54  LGSLLIAPRVSDPSRLISALRVLALLTLLFAVAFWAGAHVAWLMLVMIGFNLFFSPLVPL 113

Qy     48  LQSLALTW 55
            ||:|| ||
Db    114  TDALANTW 121


Search completed: April  7, 2005, 03:30:23
Job time : 76 secs
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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    April  7, 2005, 03:17:03 ; Search time 184 Seconds
                                       (without alignments)
                       214.294 Million cell updates/sec

Title:     US-10-063-563-56
Perfect score: 410
Sequence:  1 MGPVKQLKRMFEPTRLIATI.........LSFIPFARDAVKKCFAVCLA 77

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:  1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:       1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   UniProt 03:*
        1: uniprot_sprot:*
        2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	410	100.0	77	2	Q6UWR8	Q6uwr8 homo sapien
2	410	100.0	160	2	O95562	O95562 homo sapien
3	366.5	89.4	159	2	Q8VD57	Q8vd57 mus musculu
4	324	79.0	161	2	Q7T375	Q7t375 brachydanio
5	306	74.6	159	2	Q8WV19	Q8wv19 homo sapien
6	298	72.7	178	2	Q9UIC7	Q9uic7 homo sapien
7	240	58.5	163	2	Q9VPD4	Q9vpd4 drosophila
8	225.5	55.0	113	2	Q86F94	Q86f94 schistosoma
9	167	40.7	162	2	Q7YTP0	Q7ytp0 caenorhabdi
10	159	38.8	163	2	Q9NEC2	Q9nec2 leishmania
11	157	38.3	175	2	Q9LT07	Q9lt07 arabidopsis
12	147	35.9	163	2	Q6GKX4	Q6gkx4 arabidopsis
13	144	35.1	171	2	Q6Z7E9	Q6z7e9 oryza sativ
14	142	34.6	218	2	Q9N6J5	Q9n6j5 leishmania
15	140	34.1	136	2	Q922U5	Q922u5 mus musculu
16	129	31.5	155	2	Q7YVB3	Q7yvb3 trypanosoma
17	106	25.9	235	2	Q9XTH1	Q9xth1 caenorhabdi
18	97	23.7	138	2	Q9FIP2	Q9fip2 arabidopsis
19	97	23.7	214	2	Q6BPR2	Q6bpr2 debaryomyce
20	96	23.4	198	2	Q6C220	Q6c220 yarrowia li
21	84.5	20.6	231	2	Q69V58	Q69v58 oryza sativ
22	83	20.2	212	2	Q75A53	Q75a53 ashbya goss
23	83	20.2	227	2	Q6IDC5	Q6idc5 arabidopsis
24	83	20.2	230	2	Q9FKU4	Q9fku4 arabidopsis
25	81.5	19.9	1169	2	Q7N4N7	Q7n4n7 photorhabdu
26	80.5	19.6	486	2	Q9FHB6	Q9fhb6 arabidopsis
27	79	19.3	385	2	O65579	O65579 arabidopsis
28	77	18.8	213	2	Q6FJ40	Q6fj40 candida gla
29	76.5	18.7	1769	2	Q8W0J2	Q8w0j2 oryza sativ
30	76	18.5	199	2	Q6II06	Q6ii06 drosophila
31	75	18.3	210	2	Q6BHX8	Q6bhx8 debaryomyce
32	75	18.3	215	1	SFT2_YEAST	P38166 saccharomyc
33	74	18.0	213	2	Q6CP97	Q6cp97 kluyveromyc
34	73.5	17.9	353	2	Q8GAP9	Q8gap9 lyngbya maj
35	72.5	17.7	675	2	Q6AX77	Q6ax77 xenopus lae
36	70	17.1	389	2	Q6D3I1	Q6d3i1 erwinia car
37	69.5	17.0	312	2	Q7TRN8	Q7trn8 mus musculu
38	69.5	17.0	313	2	Q7TRN9	Q7trn9 mus musculu
39	69.5	17.0	319	2	Q8VGV1	Q8vgv1 mus musculu
40	68	16.6	1033	2	Q9VCM4	Q9vcm4 drosophila
41	67	16.3	171	2	Q8SQN0	Q8sqn0 encephalito
42	67	16.3	191	2	Q6AS37	Q6as37 desulfotale
43	67	16.3	309	2	Q8VFT9	Q8vft9 mus musculu
44	67	16.3	309	2	Q7TRM3	Q7trm3 mus musculu
45	67	16.3	335	2	Q9W6Q6	Q9w6q6 gallus gall
46	66.5	16.2	466	2	O80785	O80785 arabidopsis
47	66	16.1	228	2	Q7Z0P6	Q7z0p6 paramecium
48	66	16.1	259	2	Q642V4	Q642v4 riftia pach
49	66	16.1	282	2	Q6CY96	Q6cy96 kluyveromyc
50	66	16.1	482	2	Q64C53	Q64c53 uncultured
51	66	16.1	529	2	Q6HMP1	Q6hmp1 bacillus th
52	66	16.1	546	1	FVR2_RAT	P60815 rattus norv
53	66	16.1	619	2	Q74ZK5	Q74zk5 ashbya goss
54	66	16.1	1441	2	Q9LK63	Q9lk63 arabidopsis
55	66	16.1	1466	2	Q8VZZ4	Q8vzz4 arabidopsis
56	65	15.9	136	2	Q7QQ51	Q7qq51 giardia lam
57	65	15.9	272	2	Q9ZZQ8	Q9zzq8 cyanidiosch
58	65	15.9	342	2	Q6XVW1	Q6xvw1 shigella fl
59	65	15.9	484	2	Q630H5	Q630h5 bacillus ce
60	65	15.9	484	2	Q81JM7	Q81jm7 bacillus an
61	64.5	15.7	217	2	Q89ZB3	Q89zb3 bacteroides
62	64.5	15.7	356	2	Q6LN82	Q6ln82 photobacter
63	64.5	15.7	379	2	Q7CQ09	Q7cq09 salmonella
64	64.5	15.7	379	2	Q9EZ24	Q9ez24 salmonella
65	64.5	15.7	557	2	Q6Q3H3	Q6q3h3 vitis vinif
66	64.5	15.7	626	2	Q88KQ0	Q88kq0 pseudomonas
67	64.5	15.7	1253	2	Q729R3	Q729r3 desulfovibr
68	64	15.6	96	1	YHDK_BACSU	O07580 bacillus su
69	64	15.6	96	2	Q7X2K9	Q7x2k9 bacillus su
70	64	15.6	231	2	Q64B46	Q64b46 uncultured
71	64	15.6	342	1	SPAS_SHIFL	P40707 shigella fl
72	64	15.6	390	2	Q758M8	Q758m8 ashbya goss
73	64	15.6	403	2	Q9HVY5	Q9hvy5 pseudomonas
74	64	15.6	452	2	Q83C47	Q83c47 coxiella bu
75	64	15.6	494	2	Q83DA1	Q83da1 coxiella bu
76	64	15.6	529	2	Q81UF4	Q81uf4 bacillus an
77	64	15.6	538	2	Q81H85	Q81h85 bacillus ce
78	64	15.6	570	2	Q62K30	Q62k30 burkholderi
79	64	15.6	570	2	Q63TT9	Q63tt9 burkholderi
80	64	15.6	681	2	Q92WI9	Q92wi9 rhizobium m
81	64	15.6	685	1	FZD8_MOUSE	Q61091 mus musculu
82	64	15.6	694	1	FZD8_HUMAN	Q9h461 homo sapien
83	63.5	15.5	388	2	Q6AAQ0	Q6aaq0 propionibac
84	63	15.4	148	2	Q6CC06	Q6cc06 yarrowia li
85	63	15.4	255	2	Q8DLR5	Q8dlr5 synechococc
86	63	15.4	258	1	Y256_MYCPN	P75421 mycoplasma
87	63	15.4	260	2	Q9MNJ0	Q9mnj0 helobdella
88	63	15.4	330	2	Q8TPJ8	Q8tpj8 methanosarc
89	63	15.4	387	2	P72672	P72672 synechocyst
90	63	15.4	442	2	O07845	O07845 ralstonia s
91	63	15.4	529	2	Q73CQ5	Q73cq5 bacillus ce
92	63	15.4	662	2	Q7Q4B8	Q7q4b8 anopheles g
93	63	15.4	802	2	Q95QC9	Q95qc9 caenorhabdi
94	63	15.4	1022	2	O17943	O17943 caenorhabdi
95	63	15.4	1683	2	Q86KY1	Q86ky1 dictyosteli
96	62.5	15.2	310	2	Q65269	Q65269 african swi
97	62.5	15.2	316	2	Q8KPR7	Q8kpr7 synechococc
98	62.5	15.2	347	2	Q92DJ0	Q92dj0 rickettsia
99	62.5	15.2	379	1	HCAT_ECOLI	Q47142 escherichia
100	62.5	15.2	379	2	Q8FF40	Q8ff40 escherichia
101	62.5	15.2	379	2	Q8XA77	Q8xa77 escherichia
102	62.5	15.2	438	2	Q8Z430	Q8z430 salmonella
103	62.5	15.2	2379	2	Q6UN13	Q6un13 porcine rep
104	62	15.1	97	2	Q6IE38	Q6ie38 homo sapien

No.	Accession	Name	Ct	Len	S2	S1	Description
105	Q63pz7	Q63PZ7	2	126	15.1	62	burkholderi
106	Q8g5c0	YA94_BIFLO	1	354	15.1	62	bifidobacte
107	Q6ph58	Q6PH58	2	481	15.1	62	brachydanio
108	Q7vuu8	Q7VUU8	2	498	15.1	62	bordetella
109	Q9bu25	Q9BU25	2	501	15.1	62	homo sapien
110	Q9kzf1	Q9KZF1	2	504	15.1	62	streptomyce
111		FVR2_MOUSE	1	551	15.1	62	mus musculu
112	Q96s66	Q96S66	2	551	15.1	62	homo sapien
113	Q97925	Q97925	2	1015	15.1	62	thermoplasm
114	Q98238	Q98238	2	93	15.0	61.5	molluscum c
115	Q7qbd3	Q7QBD3	2	222	15.0	61.5	anopheles g
116	Q6f9z4	Q6F9Z4	2	259	15.0	61.5	acinetobact
117	Q6cs38	Q6CS38	2	263	15.0	61.5	kluyveromyc
118	Q9wvd9	Q9WVD9	2	326	15.0	61.5	mus musculu
119	O18689	O18689	2	340	15.0	61.5	caenorhabdi
120	Q83mk7	Q83MK7	2	379	15.0	61.5	shigella fl
121	Q6d247	Q6D247	2	386	15.0	61.5	erwinia car
122	P58119	FTSW_LACLA	1	420	15.0	61.5	lactococcus
123	Q99li2	Q99LI2	2	539	15.0	61.5	mus musculu
124	Q04551	YGA4_STRCO	1	1000	15.0	61.5	streptomyce
125	P31875	RPOA_PRRSV	1	3859	15.0	61.5	porcine rep
126		CYBH_WOLSU	1	230	15.0	61.5	wolinella s
127	Q7uej1	Q7UEJ1	2	306	14.9	61	rhodopirell
128	Q8x6f9	Q8X6F9	2	373	14.9	61	escherichia
129	Q7nbi6	Q7NBI6	2	376	14.9	61	mycoplasma
130	Q8bxj5	Q8BXJ5	2	383	14.9	61	mus musculu
131	O45173	O45173	2	392	14.9	61	caenorhabdi
132	Q7pp97	Q7PP97	2	459	14.9	61	anopheles g
133	Q80vz6	Q80VZ6	2	491	14.9	61	mus musculu
134	Q870v7	Q870V7	2	554	14.9	61	neurospora
135	Q17638	YAMS_CAEEL	1	59	14.9	60.5	caenorhabdi
136	O05277	O05277	2	152	14.8	60.5	chlorante-a
137	O47946	O47946	2	159	14.8	60.5	lumbricus r
138	Q67en6	Q67EN6	2	168	14.8	60.5	callinectes
139	Q04352	Y1B2_CLOAB	1	180	14.8	60.5	clostridium
140	Q6amp6	Q6AMP6	2	223	14.8	60.5	desulfotale
141	Q8nx81	Q8NX81	2	339	14.8	60.5	staphylococ
142	Q99v11	Q99V11	2	339	14.8	60.5	staphylococ
143	Q7a684	Q7A684	2	339	14.8	60.5	staphylococ
144	Q6gac7	Q6GAC7	2	339	14.8	60.5	staphylococ
145	Q6ghz8	Q6GHZ8	2	339	14.8	60.5	staphylococ
146	Q8vif0	Q8VIF0	2	360	14.8	60.5	rattus norv
147	Q667x4	Q667X4	2	385	14.8	60.5	yersinia ps
148	Q8zcr4	Q8ZCR4	2	385	14.8	60.5	yersinia pe
149	Q6kcb7	Q6KCB7	2	394	14.8	60.5	saccharomyc
150	Q6kcb8	Q6KCB8	2	394	14.8	60.5	kluyveromyc
151	Q6kcb9	Q6KCB9	2	394	14.8	60.5	saccharomyc
152	Q8vie8	Q8VIE8	2	394	14.8	60.5	rattus norv
153	Q8vie9	Q8VIE9	2	395	14.8	60.5	rattus norv
154	Q9rmd3	Q9RMD3	2	401	14.8	60.5	acinetobact
155	Q7n0h9	Q7N0H9	2	443	14.8	60.5	photorhabdu
156	Q82cb2	Q82CB2	2	451	14.8	60.5	streptomyce
157	Q8vif1	Q8VIF1	2	507	14.8	60.5	rattus norv
158	Q6cpq7	Q6CPQ7	2	540	14.8	60.5	kluyveromyc
159	Q66hq5	Q66HQ5	2	541	14.8	60.5	rattus norv
160	Q9wu61	Q9WU61	2	541	14.8	60.5	rattus norv
161	Q6f7c5	Q6F7C5	2	1063	14.8	60.5	acinetobact
162	Q9bmq4	Q9BMQ4	2	2304	14.8	60.5	blattella g
163	Q6sri0	Q6SRI0	2	143	14.6	60	sars corona
164	Q6sri4	Q6SRI4	2	143	14.6	60	sars corona
165	Q6sri8	Q6SRI8	2	143	14.6	60	sars corona
166	Q6srj2	Q6SRJ2	2	143	14.6	60	sars corona
167	Q6srj6	Q6SRJ6	2	143	14.6	60	sars corona
168	Q6srk0	Q6SRK0	2	143	14.6	60	sars corona
169	Q6srk4	Q6SRK4	2	143	14.6	60	sars corona
170	Q6srk8	Q6SRK8	2	143	14.6	60	sars corona
171	Q6srl2	Q6SRL2	2	143	14.6	60	sars corona
172	Q6srl6	Q6SRL6	2	143	14.6	60	sars corona
173	Q6srm0	Q6SRM0	2	143	14.6	60	sars corona
174	Q6srm4	Q6SRM4	2	143	14.6	60	sars corona
175	Q6srm8	Q6SRM8	2	143	14.6	60	sars corona
176	Q6srn2	Q6SRN2	2	143	14.6	60	sars corona
177	Q6srn6	Q6SRN6	2	143	14.6	60	sars corona

No.	Accession	Name	Ct	Len	S2	S1	Description
178	Q6srp0	Q6SRP0	2	143	14.6	60	sars corona
179	Q6srp4	Q6SRP4	2	143	14.6	60	sars corona
180	Q6srp8	Q6SRP8	2	143	14.6	60	sars corona
181	Q7ncl4	Q7NCL4	2	151	14.6	60	gloeobacter
182	Q90444	Q90444	2	185	14.6	60	brachydanio
183	P59596	VME1_CVHSA	1	221	14.6	60	human coron
184	Q66vb9	Q66VB9	2	221	14.6	60	mus musculu
185	Q6gyq7	Q6GYQ7	2	221	14.6	60	sars corona
186	Q6jh34	Q6JH34	2	221	14.6	60	sars corona
187	Q6jh42	Q6JH42	2	221	14.6	60	sars corona
188	Q6r7y2	Q6R7Y2	2	221	14.6	60	molluscum c
189	Q6rcw1	Q6RCW1	2	221	14.6	60	sars corona
190	Q6rcx2	Q6RCX2	2	221	14.6	60	sars corona
191	Q6rcy3	Q6RCY3	2	221	14.6	60	sars corona
192	Q6rcz4	Q6RCZ4	2	221	14.6	60	sars corona
193	Q6rd05	Q6RD05	2	221	14.6	60	sars corona
194	Q6rd16	Q6RD16	2	221	14.6	60	sars corona
195	Q6rd27	Q6RD27	2	221	14.6	60	sars corona
196	Q6rd38	Q6RD38	2	221	14.6	60	sars corona
197	Q6rd49	Q6RD49	2	221	14.6	60	sars corona
198	Q6rd60	Q6RD60	2	221	14.6	60	sars corona
199	Q6s8d3	Q6S8D3	2	221	14.6	60	sars corona
200	Q6t1d8	Q6T1D8	2	221	14.6	60	sars corona
201	Q6tpe4	Q6TPE4	2	221	14.6	60	sars corona
202	Q6uze9	Q6UZE9	2	221	14.6	60	sars corona
203	Q6uzf3	Q6UZF3	2	221	14.6	60	sars corona
204	Q6v584	Q6V584	2	221	14.6	60	sars corona
205	Q6va74	Q6VA74	2	221	14.6	60	sars corona
206	Q6va85	Q6VA85	2	221	14.6	60	sars corona
207	Q6va96	Q6VA96	2	221	14.6	60	sars corona
208	Q80gx4	Q80GX4	2	226	14.6	60	hepatitis b
209	Q93rc4	Q93RC4	2	243	14.6	60	escherichia
210	Q6d8d7	Q6D8D7	2	285	14.6	60	erwinia car
211	P77156	YDCU_ECOLI	1	313	14.6	60	escherichia
212	Q6ecb6	Q6ECB6	2	346	14.6	60	acanthiza a
213	Q6ecc0	Q6ECC0	2	346	14.6	60	timelliopsis
214	Q8heh4	Q8HEH4	2	380	14.6	60	monochirus
215	Q96fk6	Q96FK6	2	387	14.6	60	homo sapien
216	Q93440	Q93440	2	424	14.6	60	caenorhabdi
217	Q8xs70	Q8XS70	2	435	14.6	60	ralstonia s
218	Q9u622	Q9U622	2	491	14.6	60	drosophila
219	Q7wfb2	Q7WFB2	2	498	14.6	60	bordetella
220	Q9upi3	FVR2_HUMAN	1	526	14.6	60	homo sapien
221	Q88ci6	Q88CI6	2	540	14.6	60	pseudomonas
222	Q13467	FZD5_HUMAN	1	585	14.6	60	homo sapien
223	Q6cy55	Q6CY55	2	895	14.6	60	kluyveromyc
224	Q8pd78	Q8PD78	2	994	14.6	60	xanthomonas
225	Q6kz39	Q6KZ39	2	1007	14.6	60	picrophilus
226	Q7qq48	Q7QQ48	2	1918	14.6	60	giardia lam
227	Q8cbj2	Q8CBJ2	2	142	14.6	60	mus musculu
228	Q9jwy7	Q9JWY7	2	221	14.5	59.5	neisseria m
229	Q9k1k8	Q9K1K8	2	221	14.5	59.5	neisseria m
230	P38459	YM16_MARPO	1	244	14.5	59.5	marchantia
231	Q83gu8	Q83GU8	2	256	14.5	59.5	tropheryma
232	Q83ns6	Q83NS6	2	256	14.5	59.5	tropheryma
233	Q7ncv4	Q7NCV4	2	259	14.5	59.5	gloeobacter
234	Q6fch0	Q6FCH0	2	274	14.5	59.5	acinetobact
235	Q697f7	Q697F7	2	308	14.5	59.5	neomaskelli
236	Q729w0	Q729W0	2	320	14.5	59.5	desulfovibr
237	Q72k20	Q72K20	2	325	14.5	59.5	thermus the
238	Q9vfg7	Q9VFG7	2	351	14.5	59.5	drosophila
239	Q705x0	Q705X0	2	362	14.5	59.5	scyliorhinu
240	Q7nz17	Q7NZ17	2	400	14.5	59.5	chromobacte
241	Q8gjg4	Q8GJG4	2	403	14.5	59.5	leptospira
242	Q72r73	Q72R73	2	412	14.5	59.5	leptospira
243	Q8f4k6	Q8F4K6	2	412	14.5	59.5	leptospira
244	Q7pl30	Q7PL30	2	414	14.5	59.5	drosophila
245	Q7me69	Q7ME69	2	414	14.5	59.5	vibrio vuln
246	Q8d747	Q8D747	2	414	14.5	59.5	vibrio vuln
247	Q6fdn5	Q6FDN5	2	515	14.5	59.5	acinetobact
248	Q88xr1	Q88XR1	2	577	14.5	59.5	lactobacill
249	Q98hs3	Q98HS3	2	692	14.5	59.5	rhizobium l
250	Q8ffd1	Q8FFD1	2	749	14.5	59.5	escherichia

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#	Score	Value	Len	ID	n	Organism
251	59.5	14.5	760	Q9N6L2	2	leishmania
252	59.5	14.5	858	Q74IE5	2	lactobacill
253	59.5	14.5	998	P73519	2	synechocyst
254	59.5	14.5	1031	Q9UF42	2	homo sapien
255	59.5	14.5	1777	Q9ULH0	2	homo sapien
256	59	14.4	113	Q744T2	2	mycobacteri
257	59	14.4	141	Q6FER5	2	acinetobact
258	59	14.4	141	Q9Z8U1	2	chlamydia p
259	59	14.4	205	Q6F8F8	2	acinetobact
260	59	14.4	221	Q692E0	2	sars corona
261	59	14.4	221	Q6QJ38	2	sars corona
262	59	14.4	233	YSR3_CAEEL	1	caenorhabdi
263	59	14.4	237	Q647V2	2	uncultured
264	59	14.4	239	Q64D59	2	uncultured
265	59	14.4	244	Q6QLQ4	2	mus musculu
266	59	14.4	244	Q9JI50	2	mus musculu
267	59	14.4	244	Q8KIL4	2	mus musculu
268	59	14.4	260	O63593	2	florometra
269	59	14.4	260	Q9ZHX3	2	brucella me
270	59	14.4	260	Q8G221	2	brucella su
271	59	14.4	263	Q8U0R0	2	pyrococcus
272	59	14.4	265	Q8YFV2	2	brucella me
273	59	14.4	268	Q8GSI6	2	arabidopsis
274	59	14.4	269	Q7MFQ4	2	vibrio vuln
275	59	14.4	299	O47578	2	onchocerca
276	59	14.4	301	Q8H3H8	2	oryza sativ
277	59	14.4	328	P2Y6_HUMAN	1	homo sapien
278	59	14.4	359	IL8B_MOUSE	1	mus musculu
279	59	14.4	386	Q8ZFC4	2	yersinia pe
280	59	14.4	403	Q20067	2	caenorhabdi
281	59	14.4	471	P72122	2	pseudomonas
282	59	14.4	483	Q6BW26	2	debaryomyce
283	59	14.4	489	Q6YXZ6	2	oryza sativ
284	59	14.4	564	Q7R692	2	giardia lam
285	59	14.4	624	Q7XMU9	2	oryza sativ
286	59	14.4	629	Q86H95	2	dictyosteli
287	59	14.4	680	Q6BSW5	2	debaryomyce
288	59	14.4	683	Q84L74	2	arabidopsis
289	59	14.4	763	Q8RWT0	2	arabidopsis
290	59	14.4	780	Q8XEA2	2	escherichia
291	59	14.4	795	Q64552	2	arabidopsis
292	59	14.4	815	O44385	2	caenorhabdi
293	59	14.4	1028	Q67J93	2	symbiobacte
294	59	14.4	1089	Q7JK70	2	caenorhabdi
295	58.5	14.3	1139	Q9U280	2	caenorhabdi
296	58.5	14.3	1591	Q7QRS0	2	giardia lam
297	58.5	14.3	147	Q8HNS0	2	schistosoma
298	58.5	14.3	237	O82L92	2	streptomyce
299	58.5	14.3	250	Q72I15	2	listeria mo
300	58.5	14.3	261	Q87P44	2	vibrio para
301	58.5	14.3	282	Q9Y682	2	homo sapien
302	58.5	14.3	311	Q8R2A3	2	mus musculu
303	58.5	14.3	333	Q757U1	2	ashbya goss
304	58.5	14.3	356	Q86XG6	2	homo sapien
305	58.5	14.3	358	FLHB_HELPY	1	helicobacte
306	58.5	14.3	365	Q7MJE1	2	vibrio vuln
307	58.5	14.3	387	Q20012	2	caenorhabdi
308	58.5	14.3	428	Q6C4S2	2	yarrowia li
309	58.5	14.3	433	Q6U1N6	2	biomphalari
310	58.5	14.3	476	O08635	2	bos taurus
311	58.5	14.3	499	CIK2_HUMAN	1	homo sapien
312	58.5	14.3	518	O87771	2	legionella
313	58.5	14.3	538	Q6K9X7	2	oryza sativ
314	58.5	14.3	718	Q9XXF4	2	caenorhabdi
315	58.5	14.3	843	Q923J8	2	mus musculu
316	58.5	14.3	843	Q925I4	2	mus musculu
317	58.5	14.3	1170	Q9PNZ5	2	campylobact
318	58	14.1	100	Q8QGG7	2	gallus gall
319	58	14.1	115	Q8A1T5	2	bacteroides
320	58	14.1	123	Q6A270	2	haemophilus
321	58	14.1	126	Q62GJ1	2	burkholderi
322	58	14.1	144	Q89CT2	2	bradyrhizob
323	58	14.1	169	Q9PIM9	2	campylobact

#	Score	Value	Len	ID	n	Accession	Organism
324	58	14.1	170	Q8T9C6	2	Q8t9c6	drosophila
325	58	14.1	216	Q6G597	2	Q6g597	bartonella
326	58	14.1	217	FZD8_CHICK	1	Q91a03	gallus gall
327	58	14.1	222	Q6G1C5	2	Q6g1c5	bartonella
328	58	14.1	226	Q6NWF9	2	Q6nwf9	brachydanio
329	58	14.1	227	Q06498	2	Q06498	lactate deh
330	58	14.1	230	O58111	1	O58111	pyrococcus
331	58	14.1	232	COBS_PYRHO	2	Q9v2n1	pyrococcus
332	58	14.1	239	COBS_PYRAB	2	Q90447	brachydanio
333	58	14.1	239	Q90447	2	Q6n0k7	rhodopseudo
334	58	14.1	256	Q6N0K7	2	Q8ie98	plasmodium
335	58	14.1	259	Q81E98	2	Q9cb55	platynereis
336	58	14.1	259	Q9TB55	2	Q832n8	enterococcu
337	58	14.1	264	Q832N8	2	Q923z9	mus musculu
338	58	14.1	264	Q923Z9	2	Q09081	oryctolagus
339	58	14.1	273	CIK2_RABIT	1	Q7n9z0	photorhabdu
340	58	14.1	293	Q7N9Z0	2	Q88dh2	pseudomonas
341	58	14.1	293	Q88DH2	2	Q8vqk4	brucella ab
342	58	14.1	314	Q8VQK4	2	Q8fux0	brucella su
343	58	14.1	314	Q8FUX0	2	Q8ydg7	brucella me
344	58	14.1	315	Q8YDG7	2	Q9phs9	campylobact
345	58	14.1	334	Q9PHS9	2	Q88pj8	pseudomonas
346	58	14.1	335	Q88PJ8	2	Q7n4z0	photorhabdu
347	58	14.1	341	Q7N4Z0	2	Q6ecb3	gergyone ch
348	58	14.1	346	Q65CB3	2	Q28519	macaca mula
349	58	14.1	353	IL8B_MACMU	1	P35407	rattus norv
350	58	14.1	359	IL8B_RAT	1	Q9x8k5	streptomyce
351	58	14.1	370	Q9X8K5	1	O56886	yersinia en
352	58	14.1	383	FLHB_YEREN	1	Q6ca15	yarrowia li
353	58	14.1	414	Q6CA15	2	Q9v6q3	drosophila
354	58	14.1	417	Q9V6Q3	2	Q9v6q4	drosophila
355	58	14.1	417	Q9V6Q4	2	P31435	escherichia
356	58	14.1	460	YICJ_ECOLI	1	Q8xqe9	ralstonia s
357	58	14.1	476	Q8XQE9	2	Q6cpy8	kluyveromyc
358	58	14.1	479	Q6CPY8	2	Q93se8	escherichia
359	58	14.1	479	Q93SE8	2	Q8fc70	escherichia
360	58	14.1	479	Q8FC70	2	Q8xca5	escherichia
361	58	14.1	479	Q8XCA5	2	Q9kj74	staphylococ
362	58	14.1	498	Q9KJ74	2	Q9la06	gallus gall
363	58	14.1	523	FZD2_CHICK	1	Q9vly4	drosophila
364	58	14.1	523	Q9VLY4	2	Q9yl7	brachydanio
365	58	14.1	550	Q9YL7	2	Q9puu6	xenopus lae
366	58	14.1	551	FZD2_XENLA	1	Q66ka3	xenopus tro
367	58	14.1	553	Q66KA3	2	Q6wj01	gallus gall
368	58	14.1	558	Q6WJ01	2	Q14332	mus musculu
369	58	14.1	565	FZD2_HUMAN	1	Q9jip6	mus musculu
370	58	14.1	570	FZD2_MOUSE	1	Q832k0	enterococcu
371	58	14.1	575	Q832K0	2	Q9pwk6	brachydanio
372	58	14.1	576	Q9PWK6	2	Q9pwn8	brachydanio
373	58	14.1	576	Q9PWN8	2	Q9yi49	brachydanio
374	58	14.1	576	Q9YI49	2	Q9eqd0	mus musculu
375	58	14.1	577	FZD5_MOUSE	1	Q9ptt7	brachydanio
376	58	14.1	579	Q9PTT7	2	Q9yi00	brachydanio
377	58	14.1	579	Q9YI00	2	Q7y1v1	melaleuca a
378	58	14.1	583	Q7Y1V1	2	Q8chk9	mus musculu
379	58	14.1	584	Q8CHK9	2	Q8bmr2	mus musculu
380	58	14.1	585	Q8BMR2	2	Q8chl0	rattus norv
381	58	14.1	585	Q8CHL0	2	Q6i7z0	sceloporus
382	58	14.1	600	Q6I7Z0	2	O08463	rattus norv
383	58	14.1	641	FZD1_RAT	1	Q86uz8	homo sapien
384	58	14.1	641	Q86UZ8	2	O70421	mus musculu
385	58	14.1	642	FZD1_MOUSE	1	Q7ts82	mus musculu
386	58	14.1	642	Q7TS82	2	Q9up38	homo sapien
387	58	14.1	648	FZD1_HUMAN	1	Q68d41	homo sapien
388	58	14.1	681	Q68D41	2	Q92cv4	listeria in
389	58	14.1	696	Q92CV4	2	Q8u6m2	agrobacteri
390	58	14.1	743	Q8U6M2	2	Q7cvv3	agrobacteri
391	58	14.1	747	Q7CVV3	2	Q8vxb4	oryza sativ
392	58	14.1	788	Q8VXB4	2	Q7xiv8	oryza sativ
393	58	14.1	788	Q7XIV8	2	Q6asz9	oryza sativ
394	58	14.1	1723	Q6ASZ9	2	Q08983	sus scrofa
395	57.5	14.0	2476	ZAN_PIG	1	Q00145	ictalurid h
396	57.5	14.0	136	VG40_ICHV1	1	Q6zpb5	homo sapien
			146	Q62PB5	2		

No.	n	Length			Accession	Organism	ID
397	2	150	14.0	57.5	Q7S4F1	neurospora	Q7S4F1
398	2	157	14.0	57.5	Q9VJR2	drosophila	Q9VJR2
399	2	189	14.0	57.5	Q7YWX1	caenorhabdi	Q7YWX1
400	2	230	14.0	57.5	Q6ZlV2	oryza sativ	Q6ZIV2
401	2	231	14.0	57.5	Q9V4G4	drosophila	Q9V4G4
402	2	250	14.0	57.5	Q8Y8C8	listeria mo	Q8Y8C8
403	2	252	14.0	57.5	Q7RP58	plasmodium	Q7RP58
404	2	254	14.0	57.5	Q69LF7	oryza sativ	Q69LF7
405	2	295	14.0	57.5	Q6CZ32	erwinia car	Q6CZ32
406	1	328	14.0	57.5	LGT_BORBU	borrelia bu	LGT_BORBU
407	2	333	14.0	57.5	Q66lQ7	borrelia ga	Q66IQ7
408	2	336	14.0	57.5	Q9MNJ4	helobdella	Q9MNJ4
409	2	353	14.0	57.5	O44697	caenorhabdi	O44697
410	2	353	14.0	57.5	O93247	cyprinus ca	O93247
411	2	372	14.0	57.5	Q9PTF7	brachydanio	Q9PTF7
412	1	387	14.0	57.5	CYB_TRYBO	trypanoplas	CYB_TRYBO
413	2	408	14.0	57.5	O49632	arabidopsis	O49632
414	2	410	14.0	57.5	Q73TQ1	mycobacteri	Q73TQ1
415	2	417	14.0	57.5	Q7M9R9	wolinella s	Q7M9R9
416	2	419	14.0	57.5	Q825M6	streptomyce	Q825M6
417	2	435	14.0	57.5	Q7NQW0	chromobacte	Q7NQW0
418	2	437	14.0	57.5	Q64VY8	bacteroides	Q64VY8
419	2	445	14.0	57.5	Q94AL2	arabidopsis	Q94AL2
420	2	479	14.0	57.5	O16548	caenorhabdi	O16548
421	2	481	14.0	57.5	Q65lL0	oryza sativ	Q65lL0
422	2	530	14.0	57.5	Q72V77	leptospira	Q72V77
423	1	533	14.0	57.5	Q7UlI7	rhodopirell	Q7ULI7
424	2	533	14.0	57.5	P07018	escherichia	MCP4_ECOLI
425	1	534	14.0	57.5	Q7UAB7	shigella fl	Q7UAB7
426	2	538	14.0	57.5	Q8XCF7	escherichia	Q8XCF7
427	2	729	14.0	57.5	Q83KP5	shigella fl	Q83KP5
428	2	729	14.0	57.5	Q69XM6	oryza sativ	Q69XM6
429	1	742	14.0	57.5	P23842	escherichia	YFEA_ECOLI
430	2	750	14.0	57.5	Q7ABU5	escherichia	Q7ABU5
431	2	822	14.0	57.5	Q8XBN6	escherichia	Q8XBN6
432	2	851	14.0	57.5	Q8N3U2	homo sapien	Q8N3U2
433	1	1002	14.0	57.5	Q09225	giardia lam	NRF6_CAEEL
434	1	1015	14.0	57.5	P55018	rattus norv	S123_RAT
435	2	1057	14.0	57.5	Q8MRT3	drosophila	Q8MRT3
436	2	1077	14.0	57.5	Q9A5Q7	caulobacter	Q9A5Q7
437	2	1077	14.0	57.5	Q62C80	burkholderi	Q62C80
438	2	2379	14.0	57.5	Q63LH4	burkholderi	Q63LH4
439	2	96	14.0	57.5	Q6U9W8	porcine rep	Q6U9W8
440	1	120	13.9	57	NULM_MYXGL	myxine glut	NULM_MYXGL
441	2	120	13.9	57	Q6Q900	uncultured	Q6Q900
442	2	120	13.9	57	Q6SG60	uncultured	Q6SG60
443	2	157	13.9	57	Q6UCX0	uncultured	Q6UCX0
444	1	159	13.9	57	P24834	rhesus papi	VE5_RHPV1
445	2	170	13.9	57	Q6QHU8	bos taurus	Q6QHU8
446	2	173	13.9	57	Q6A8P8	propionibac	Q6A8P8
447	2	185	13.9	57	Q66PD3	rhizobium m	Q66PD3
448	2	210	13.9	57	Q08786	saccharomyc	Q08786
449	2	231	13.9	57	O63546	bodo saltan	O63546
450	2	242	13.9	57	Q6YR58	onion yello	Q6YR58
451	1	261	13.9	57	Q44261	alcaligenes	CRTW_ALCSP
452	2	264	13.9	57	Q9MIA3	typhlonecte	Q9MIA3
453	2	268	13.9	57	Q8G0N2	brucella su	Q8G0N2
454	2	300	13.9	57	Q6YN12	agrobacteri	Q6YN12
455	2	300	13.9	57	Q93DS7	streptococc	Q93DS7
456	2	300	13.9	57	Q8E0K2	streptococc	Q8E0K2
457	2	305	13.9	57	Q8E675	streptococc	Q8E675
458	2	305	13.9	57	Q8Y5K2	listeria mo	Q8Y5K2
459	2	305	13.9	57	Q929V9	listeria in	Q929V9
460	2	309	13.9	57	Q71XV6	listeria mo	Q71XV6
461	2	311	13.9	57	Q9FJP9	arabidopsis	Q9FJP9
462	2	311	13.9	57	Q9F0G9	arabidopsis	Q9F0G9
463	2	311	13.9	57	Q8VFT7	mus musculu	Q8VFT7
464	2	315	13.9	57	Q7TRM2	mus musculu	Q7TRM2
465	2	316	13.9	57	Q9WVD8	mus musculu	Q9WVD8
466	2	325	13.9	57	Q9WVD7	mus musculu	Q9WVD7
467	2	356	13.9	57	Q6D712	erwinia car	Q6D712
468	1	—	13.9	57	Q97571	canis famil	IL8B_CANFA
469	1	—	13.9	57	Q97571	canis famil	IL8B_CANFA

No.	n	Length			ID	Organism
470	2	359	13.9	57	Q887b9	pseudomonas
471	2	361	13.9	57	Q88sz2	lactobacill
472	2	367	13.9	57	Q927f5	listeria in
473	2	382	13.9	57	Q66vy6	leishmania
474	2	404	13.9	57	Q8ej63	shewanella
475	2	415	13.9	57	Q8bgz8	m mus muscu
476	2	476	13.9	57	Q8pu48	methanosarc
477	2	515	13.9	57	Q6ty91	xiphinema a
478	2	548	13.9	57	Q7rzg7	neurospora
479	2	548	13.9	57	Q8avj9	xenopus lae
480	1	581	13.9	57	O93274 (FZD8_XENLA)	xenopus lae
481	1	583	13.9	57	O57428 (HASS_XENLA)	xenopus lae
482	2	583	13.9	57	Q6azi0	caenorhabdi
483	2	598	13.9	57	O93247 (Q9AQU2)	oryza sativ
484	2	604	13.9	57	Q9fv73	perilla fru
485	2	604	13.9	57	Q9fv75	perilla cit
486	2	604	13.9	57	Q9m5a4	perilla cit
487	2	654	13.9	57	Q8euq4	mycoplasma
488	2	674	13.9	57	Q9ht30	pseudomonas
489	2	710	13.9	57	Q653b8	oryza sativ
490	2	712	13.9	57	Q66ce7	yersinia ps
491	2	712	13.9	57	Q8zg74	yersinia pe
492	1	745	13.9	57	P05164 (PERM_HUMAN)	homo sapien
493	1	754	13.9	57	P37443 (YCAI_ECOLI)	escherichia
494	2	756	13.9	57	Q8s7x4	oryza sativ
495	2	756	13.9	57	Q7xha3	oryza sativ
496	2	923	13.9	57	Q6hm90	bacillus th
497	2	952	13.9	57	Q9xim1	arabidopsis
498	2	953	13.9	57	Q7ptc2	arabidopsis
499	2	991	13.9	57	Q6r5n8	anopheles g
500	2	999	13.9	57	Q93jy2	mus musculu
501	2	1028	13.9	57	Q8mkk5	erwinia chr
502	2	1043	13.9	57	Q9w1g6	drosophila
503	2	1059	13.9	57	Q9w1g5	drosophila
504	2	1074	13.9	57	Q8mlq5	drosophila
505	2	1431	13.9	57	Q9xyh6	drosophila
506	2	1526	13.9	57	Q9vvk6	cryptospori
507	2	1967	13.9	57	Q65652	drosophila
508	2	3471	13.9	57	Q91pp5	blueberry s
509	2	3473	13.9	57	Q83034	rice tungro
510	2	89	13.8	56.5	Q7m3s6	rice tungro
511	2	135	13.8	56.5	Q71bb4	leishmania
512	2	156	13.8	56.5	Q88ol4	branchiosto
513	2	170	13.8	56.5	Q9mr45	pseudomonas
514	2	171	13.8	56.5	Q62f52	echinococcu
515	2	171	13.8	56.5	Q63xt8	burkholderi
516	2	224	13.8	56.5	Q6sn52	burkholderi
517	2	229	13.8	56.5	O53651	callithrix
518	2	229	13.8	56.5	Q7u2l0	mycobacteri
519	2	250	13.8	56.5	Q92d41	mycobacteri
520	1	253	13.8	56.5	TNFA_SPAAU	listeria in
521	2	257	13.8	56.5	Q8jfg3	sparus aura
522	2	260	13.8	56.5	Q8cut4	oceanobacil
523	2	260	13.8	56.5	Q7rdx0	plasmodium
524	2	308	13.8	56.5	Q92m69	rhizobium m
525	2	310	13.8	56.5	Q7m5m9	mus musculu
526	2	328	13.8	56.5	Q89lk3	simian aden
527	2	339	13.8	56.5	Q9psy2	bradyrhizob
528	2	339	13.8	56.5	Q00331	carassius a
529	2	373	13.8	56.5	Q7vcr6	salmonella
530	2	405	13.8	56.5	Q91gi4	prochloroco
531	2	437	13.8	56.5	Q31600	epiphyas po
532	2	465	13.8	56.5	O26645	bacillus su
533	2	467	13.8	56.5	Q41793	methanobact
534	2	475	13.8	56.5	Q75c40	zea mays (m
535	2	494	13.8	56.5	Q8ym67	ashbya gos
536	2	506	13.8	56.5	Q9i830	anabaena sp
537	2	514	13.8	56.5	Q80xm3	oncorhynchu
538	2	515	13.8	56.5	Q9xaj9	mus musculu
539	2	516	13.8	56.5	Q6abi2	streptomyce
540	2	519	13.8	56.5	Q729l5	propionibac
541	2	533	13.8	56.5	Q9v546	desulfovibr
542	1	541	13.8	56.5	GT10_HUMAN	homo sapien

Left table (rank 543–615):

#	%	score	length	n	code	organism
543	56.5	13.8	546	2	Q9MA18	arabidopsis
544	56.5	13.8	564	2	Q9LMD3	oryza sativ
545	56.5	13.8	596	2	Q66SK2	bipes bipor
546	56.5	13.8	607	2	Q9XL01	aythya amer
547	56.5	13.8	647	2	Q7QDZ1	anopheles amer
548	56.5	13.8	648	2	Q64WT0	bacteroides g
549	56.5	13.8	653	1	CIK4_HUMAN	homo sapien
550	56.5	13.8	654	1	CIK4_MOUSE	mus musculu
551	56.5	13.8	654	1	CIK4_MUSPF	mustela put
552	56.5	13.8	654	2	Q8CBF8	mus musculu
553	56.5	13.8	655	1	CIK4_RAT	rattus norv
554	56.5	13.8	658	2	Q09946	caenorhabdi
555	56.5	13.8	802	2	Q7UWT0	rhodopirell
556	56.5	13.8	938	2	Q7RNR9	plasmodium
557	56.5	13.8	955	2	Q7V7J0	prochloroco
558	56.5	13.8	971	2	Q88KR0	pseudomonas
559	56.5	13.8	1051	2	Q9ALR2	pseudomonas
560	56.5	13.8	1202	1	YE01_SCHPO	schizosacch
561	56.5	13.8	1247	2	Q8T6H5	dictyosteli
562	56.5	13.8	1284	2	Q9Y8G2	emericella
563	56.5	13.8	1334	2	Q8ST87	dictyosteli
564	56	13.7	74	2	Q35990	trypanosoma
565	56	13.7	98	2	Q6IE46	rattus norv
566	56	13.7	100	2	Q8EHU0	shewanella
567	56	13.7	122	2	Q8BNC5	mus musculu
568	56	13.7	161	2	Q65Z26	caenorhabdi
569	56	13.7	172	2	Q6BWE7	debaryomyce
570	56	13.7	182	2	Q6GLU5	xenopus lae
571	56	13.7	193	2	Q7LZC6	clarias mac
572	56	13.7	198	2	Q8DSR6	streptococc
573	56	13.7	201	2	Q9P6K1	schizosacch
574	56	13.7	242	2	Q7VR92	candidatus
575	56	13.7	260	2	Q952F1	phascolopsi
576	56	13.7	269	1	RBN_HAEIN	haemophilus
577	56	13.7	300	2	Q8P1Y3	streptococc
578	56	13.7	300	2	Q9A0X1	streptococc
579	56	13.7	300	2	Q7CFC7	streptococc
580	56	13.7	309	2	Q6ZMA1	rattus norv
581	56	13.7	315	2	Q7RI45	plasmodium
582	56	13.7	321	2	O18046	caenorhabdi
583	56	13.7	324	2	Q98526	paramecium
584	56	13.7	346	2	Q6ECA9	sericornis
585	56	13.7	347	2	Q9B6G1	thryonomys
586	56	13.7	351	2	O17520	caenorhabdi
587	56	13.7	355	2	Q8HZN5	macaca mula
588	56	13.7	360	2	Q6DOI0	erwinia car
589	56	13.7	363	2	Q8FHX9	escherichia
590	56	13.7	380	2	Q9ZY33	raja radiat
591	56	13.7	393	2	Q9KTX2	vibrio chol
592	56	13.7	417	2	Q8PN58	xanthomonas
593	56	13.7	429	2	O25682	helicobacte
594	56	13.7	452	2	Q7QHX7	anopheles g
595	56	13.7	454	2	Q875K7	coprinus ci
596	56	13.7	468	2	Q6N0G9	rhodopseudo
597	56	13.7	506	2	Q7QRD6	giardia lam
598	56	13.7	527	2	P73863	synechocyst
599	56	13.7	558	2	Q9KB83	bacillus ha
600	56	13.7	603	2	Q953H1	volemys kik
601	56	13.7	621	2	Q9XWG9	caenorhabdi
602	56	13.7	667	2	O35267	rattus norv
603	56	13.7	674	2	O61456	schistocerc
604	56	13.7	684	2	Q9UAQ8	caenorhabdi
605	56	13.7	694	2	Q9VVX3	drosophila
606	56	13.7	804	2	Q6LPK5	photobacter
607	56	13.7	815	2	Q9P6R5	schizosacch
608	56	13.7	824	2	Q9CM56	pasteurella
609	56	13.7	869	2	Q63ER5	bacillus ce
610	56	13.7	869	2	Q8IU13	bacillus an
611	56	13.7	1300	2	Q6ZR22	homo sapien
612	56	13.7	1352	2	Q6LUC6	photobacter
613	56	13.7	1682	1	CIN7_HUMAN	homo sapien
614	56	13.7	1962	2	Q75RX9	homo sapien
615	56	13.7	1966	2	Q925G6	rattus norv

Right table (rank 616–688):

#	%	score	length	n	code	organism
616	56	13.7	2013	2	Q865W3	canis famil
617	56	13.7	2015	2	Q81ZC9	homo sapien
618	56	13.7	2015	2	Q96J69	homo sapien
619	56	13.7	2016	2	Q86UR3	homo sapien
620	56	13.7	2019	2	Q14524	homo sapien
621	56	13.7	2016	2	Q75RY0	rattus norv
622	56	13.7	2019	1	CIN5_HUMAN	homo sapien
623	56	13.7	2019	1	CIN5_RAT	rattus norv
624	56	13.7	2022	2	Q9JJV9	mus musculu
625	55.5	13.5	52	2	Q8WMP8	bos taurus
626	55.5	13.5	99	2	Q952F2	phascolopsi
627	55.5	13.5	100	2	Q6AIB9	desulfotale
628	55.5	13.5	134	2	Q92HI4	rickettsia
629	55.5	13.5	152	2	Q8CBT0	mus musculu
630	55.5	13.5	155	2	Q8EWD2	mycoplasma
631	55.5	13.5	186	2	Q85H93	austrochlus
632	55.5	13.5	191	2	Q7X2T8	uncultured
633	55.5	13.5	198	2	Q82ZK2	enterococcu
634	55.5	13.5	191	2	Q73MB3	treponema d
635	55.5	13.5	198	1	FTSW_LACLC	lactococcus
636	55.5	13.5	203	1	P11788	crithidia f
637	55.5	13.5	210	1	COX2_TRYCR	trypanosoma
638	55.5	13.5	223	2	Q6SNH5	colobus gue
639	55.5	13.5	224	2	Q6SMZ6	aotus azara
640	55.5	13.5	224	2	Q6SN23	pongo pygma
641	55.5	13.5	224	2	Q6SNF6	gorilla gor
642	55.5	13.5	233	2	Q7SSN2	neurospora
643	55.5	13.5	261	2	Q94RG2	heterodontu
644	55.5	13.5	268	1	ESL1_MYCGE	mycoplasma
645	55.5	13.5	271	2	Q6L537	oryza sativ
646	55.5	13.5	277	2	Q84BI5	streptococc
647	55.5	13.5	281	2	Q8T4H4	drosophila
648	55.5	13.5	281	2	Q7JN87	drosophila
649	55.5	13.5	292	1	FX16_HUMAN	homo sapien
650	55.5	13.5	298	1	XIST_MOUSE	mus musculu
651	55.5	13.5	310	1	OXA2_STRA5	streptococc
652	55.5	13.5	313	1	OZA4_HUMAN	homo sapien
653	55.5	13.5	322	2	Q9I5Z3	pseudomonas
654	55.5	13.5	345	2	Q8NT14	corynebacte
655	55.5	13.5	349	2	Q883X6	pseudomonas
656	55.5	13.5	352	2	Q7M7X9	wolinella s
657	55.5	13.5	355	2	Q8HZN6	pongo pygma
658	55.5	13.5	355	2	Q8UBK7	agrobacteri
659	55.5	13.5	359	2	Q66660	equid herpe
660	55.5	13.5	360	2	O70600	rattus norv
661	55.5	13.5	360	2	Q8VHM2	mus musculu
662	55.5	13.5	362	2	Q8CBB9	mus musculu
663	55.5	13.5	362	2	Q9JHD4	mus musculu
664	55.5	13.5	362	2	Q6PEU4	mus musculu
665	55.5	13.5	365	2	Q6IFK7	homo sapien
666	55.5	13.5	388	2	Q6M7N5	corynebacte
667	55.5	13.5	397	2	Q7MSS9	wolinella s
668	55.5	13.5	421	2	Q92NF6	bacillus li
669	55.5	13.5	423	2	Q9VHG8	drosophila
670	55.5	13.5	476	1	RFBP_SALTY	salmonella
671	55.5	13.5	476	2	Q54OI6	salmonella
672	55.5	13.5	498	2	Q7MH85	vibrio vuln
673	55.5	13.5	498	2	Q8DCL9	vibrio vuln
674	55.5	13.5	516	2	Q86P46	drosophila
675	55.5	13.5	523	2	Q21538	caenorhabdi
676	55.5	13.5	532	2	Q9SEG9	nicotiana t
677	55.5	13.5	539	2	Q20236	caenorhabdi
678	55.5	13.5	561	2	Q64K29	populus bal
679	55.5	13.5	609	2	Q70RT9	platanista
680	55.5	13.5	611	2	Q94YR4	engraulis j
681	55.5	13.5	612	2	Q8HLX8	hypoatherin
682	55.5	13.5	621	2	Q95PS1	leishmania
683	55.5	13.5	628	2	Q98CC4	rhizobium l
684	55.5	13.5	685	2	Q6BP35	debaryomyce
685	55.5	13.5	720	2	Q9PAU8	nicotiana t
686	55.5	13.5	734	2	Q94056	xylella fas
687	55.5	13.5	843	2	Q9ZOR7	caenorhabdi
688	55.5	13.5	972	2	Q87ZF8	rattus norv
	55.5	13.5	1001	2	Q62439	pseudomonas / mus musculu

No.	Score1	Score2	Len	N	Name	Accession	Organism
689	55.5	13.5	1002	1	S123_MOUSE	P59158	mus musculu
690	55.5	13.5	1063	1	CZCA_ALCEU	P13511	alcaligenes
691	55.5	13.5	1063	1	CZCA_ALCSC	P94177	alcaligenes
692	55.5	13.5	1267	2	Q88IA8	Q88IA8	pseudomonas
693	55.5	13.5	1275	2	Q668S7	Q668S7	yersinia ps
694	55.5	13.5	1275	2	Q8ZD68	Q8ZD68	yersinia pe
695	55.5	13.5	1380	2	Q84T60	Q84T60	oryza sativ
696	55.5	13.5	1403	2	Q75IQ7	Q75IQ7	oryza sativ
697	55.5	13.5	1605	2	Q6CUF0	Q6CUF0	kluyveromyc
698	55.5	13.5	1618	2	Q8MMC7	Q8MMC7	drosophila
699	55.5	13.5	2327	2	Q9W0Y8	Q9W0Y8	drosophila
700	55.5	13.5	3063	2	Q8QXN1	Q8QXN1	sugarcane m
701	55	13.4	63	2	Q832S1	Q832S1	enterococcu
702	55	13.4	71	1	BRI1_ASHGO	Q75D30	ashbya goss
703	55	13.4	98	1	Q9XLI0	Q9XLI0	falco pereg
704	55	13.4	111	2	Q88AM1	Q88AM1	pseudomonas
705	55	13.4	117	2	P71212	P71212	escherichia
706	55	13.4	128	1	COXE_CAEEL	Q20779	caenorhabdi
707	55	13.4	130	2	Q87TZ5	Q87TZ5	pseudomonas
708	55	13.4	145	2	Q7YCW1	Q7YCW1	arion flage
709	55	13.4	157	2	Q6HWM2	Q6HWM2	bacillus an
710	55	13.4	161	2	Q8Y196	Q8Y196	ralstonia s
711	55	13.4	167	2	Q9MDD4	Q9MDD4	grallaria r
712	55	13.4	176	2	Q97XE0	Q97XE0	sulfolobus
713	55	13.4	189	2	Q6TUR0	Q6TUR0	yaba monkey
714	55	13.4	221	2	Q6SNF1	Q6SNF1	gorilla gor
715	55	13.4	229	2	Q9JRM7	Q9JRM7	actinobacil
716	55	13.4	241	2	Q8XMU6	Q8XMU6	clostridium
717	55	13.4	242	1	CRTW_AGRAU	P54972	agrobacteri
718	55	13.4	249	2	Q8D479	Q8D479	vibrio vuln
719	55	13.4	260	2	Q93PP3	Q93PP3	campylobact
720	55	13.4	261	2	Q94SS9	Q94SS9	danaceticht
721	55	13.4	263	2	Q64ZA5	Q64ZA5	bacteroides
722	55	13.4	292	1	E434_ADE09	P89083	human adeno
723	55	13.4	294	2	Q8RNV6	Q8RNV6	brevibacill
724	55	13.4	301	1	Q7TY09	Q7TY09	mycobacteri
725	55	13.4	301	2	Q8DUY3	Q8DUY3	streptococc
726	55	13.4	309	2	Q6MFX0	Q6MFX0	rattus norv
727	55	13.4	320	2	P94346	P94346	bacillus st
728	55	13.4	321	2	O54386	O54386	brucella ab
729	55	13.4	321	2	Q8YH82	Q8YH82	brucella me
730	55	13.4	321	2	Q8G0M5	Q8G0M5	brucella su
731	55	13.4	340	2	Q8YSR7	Q8YSR7	anabaena sp
732	55	13.4	346	2	Q6ECB2	Q6ECB2	gerygone ch
733	55	13.4	347	1	CB2R_MOUSE	P47936	mus musculu
734	55	13.4	347	2	Q8M161	Q8M161	arctocephal
735	55	13.4	347	2	Q678W1	Q678W1	arctocephal
736	55	13.4	353	1	IL8B_GORGO	Q28422	gorilla gor
737	55	13.4	353	1	IL8B_PANTR	Q28807	pan troglod
738	55	13.4	355	1	IL8A_RABIT	P21109	oryctolagus
739	55	13.4	355	2	Q8HZN7	Q8HZN7	gorilla gor
740	55	13.4	355	2	Q8HZN8	Q8HZN8	pan troglod
741	55	13.4	359	2	O85098	O85098	pseudomonas
742	55	13.4	359	2	Q6QQC6	Q6QQC6	pseudomonas
743	55	13.4	360	1	IL8B_HUMAN	P25025	homo sapien
744	55	13.4	375	2	Q9V2E0	Q9V2E0	pyrococcus
745	55	13.4	383	2	Q81BN5	Q81BN5	bacillus ce
746	55	13.4	383	2	Q6HGU3	Q6HGU3	bacillus th
747	55	13.4	395	1	SOTB_ERWCH	Q9S3J9	erwinia chr
748	55	13.4	411	2	Q6WJ00	Q6WJ00	gallus gall
749	55	13.4	437	2	Q8R8S1	Q8R8S1	thermoanaer
750	55	13.4	439	1	BRNQ_ECOLI	P37011	escherichia
751	55	13.4	439	2	Q7UDK1	Q7UDK1	shigella fl
752	55	13.4	439	2	Q83SH0	Q83SH0	shigella fl
753	55	13.4	440	2	Q8FKC8	Q8FKC8	escherichia
754	55	13.4	440	2	Q6NG43	Q6NG43	corynebacte
755	55	13.4	449	2	O31658	O31658	bacillus su
756	55	13.4	459	2	Q7P7A3	Q7P7A3	fusobacteri
757	55	13.4	459	2	Q8X5V8	Q8X5V8	escherichia
758	55	13.4	459	2	Q83P84	Q83P84	shigella fl
759	55	13.4	467	2	Q8LBF1	Q8LBF1	arabidopsis
760	55	13.4	480	2	Q6KIC9	Q6KIC9	mycoplasma
761	55	13.4	481	2	Q9XI53	Q9XI53	arabidopsis
762	55	13.4	485	2	Q64Z90	Q64Z90	bacteroides
763	55	13.4	496	2	Q68X09	Q68X09	rickettsia
764	55	13.4	500	1	Q989D1	Q989D1	rhizobium l
765	55	13.4	503	1	ALG6_CAEEL	Q09226	caenorhabdi
766	55	13.4	513	2	Q638Z8	Q638Z8	bacillus ce
767	55	13.4	513	2	Q6HGK6	Q6HGK6	bacillus th
768	55	13.4	534	2	Q9N571	Q9N571	caenorhabdi
769	55	13.4	567	1	PZD7_CHICK	Q57329	gallus gall
770	55	13.4	576	2	Q84LB2	Q84LB2	malus domes
771	55	13.4	581	1	FRZ3_DROME	Q77438	drosophila
772	55	13.4	592	1	PZD1_CHICK	Q57328	gallus gall
773	55	13.4	600	2	Q66SU8	Q66SU8	amphisbaena
774	55	13.4	623	2	Q6CDZ1	Q6CDZ1	yarrowia li
775	55	13.4	706	2	O45283	O45283	caenorhabdi
776	55	13.4	761	2	Q6UD08	Q6UD08	uncultured
777	55	13.4	808	2	Q62KR6	Q62KR6	burkholderi
778	55	13.4	809	2	Q63UK2	Q63UK2	burkholderi
779	55	13.4	813	2	Q86HP1	Q86HP1	dictyosteli
780	55	13.4	814	1	GUNE_CLOTM	P10477	clostridium
781	55	13.4	856	2	Q73NF9	Q73NF9	treponema d
782	55	13.4	883	2	Q9VZY7	Q9VZY7	drosophila
783	55	13.4	911	2	Q73C88	Q73C88	bacillus ce
784	55	13.4	944	2	Q6N7N7	Q6N7N7	rhodopseudo
785	55	13.4	1010	2	Q9V0B3	Q9V0B3	pyrococcus
786	55	13.4	1013	1	PRML_DROME	P82295	drosophila
787	55	13.4	1017	1	A1A2_CHICK	P24797	gallus gall
788	55	13.4	1030	2	Q7S8D2	Q7S8D2	neurospora
789	55	13.4	1091	2	Q6CKH9	Q6CKH9	kluyveromyc
790	55	13.4	1139	2	Q8ZC91	Q8ZC91	yersinia pe
791	55	13.4	1156	2	Q74WP6	Q74WP6	yersinia pe
792	55	13.4	1445	2	Q75LT9	Q75LT9	oryza sativ
793	55	13.4	1554	2	Q80SX9	Q80SX9	mus musculu
794	55	13.4	1709	2	Q7R4H3	Q7R4H3	giardia lam
795	55	13.4	2134	2	Q6WQ42	Q6WQ42	avian encep
796	55	13.4	2134	2	Q9YLS4	Q9YLS4	avian encep
797	54.5	13.3	66	2	Q887R7	Q887R7	pseudomonas
798	54.5	13.3	96	2	Q75L86	Q75L86	oryza sativ
799	54.5	13.3	136	2	Q7U6F0	Q7U6F0	synechococc
800	54.5	13.3	155	2	Q85CQ7	Q85CQ7	austrochlus
801	54.5	13.3	155	2	Q85CQ9	Q85CQ9	austrochlus
802	54.5	13.3	162	2	Q8KMC4	Q8KMC4	methylocyst
803	54.5	13.3	165	2	Q934M2	Q934M2	uncultured
804	54.5	13.3	165	2	Q934N4	Q934N4	uncultured
805	54.5	13.3	169	1	VG12_SHV21	P24915	salmirine
806	54.5	13.3	170	2	Q953M7	Q953M7	echinococcu
807	54.5	13.3	174	2	Q26857	Q26857	trypanosoma
808	54.5	13.3	174	2	Q98PD3	Q98PD3	rhizobium l
809	54.5	13.3	185	2	Q7MP11	Q7MP11	vibrio vuln
810	54.5	13.3	193	2	Q89FF3	Q89FF3	bradyrhizob
811	54.5	13.3	204	2	Q94QB4	Q94QB4	opisthoteut
812	54.5	13.3	217	2	Q6SWR7	Q6SWR7	human cytom
813	54.5	13.3	224	2	Q6SMR7	Q6SMR7	lagothrix l
814	54.5	13.3	224	2	Q6SNB0	Q6SNB0	eulemur mon
815	54.5	13.3	224	2	Q6SNE6	Q6SNE6	gorilla gor
816	54.5	13.3	224	2	Q6SNK3	Q6SNK3	pan troglod
817	54.5	13.3	226	2	Q6WYZ0	Q6WYZ0	hepatitis b
818	54.5	13.3	229	2	Q8KRY3	Q8KRY3	actinobacil
819	54.5	13.3	234	2	Q97LF0	Q97LF0	clostridium
820	54.5	13.3	244	2	Q9LWC5	Q9LWC5	oryza sativ
821	54.5	13.3	245	1	T4S6_HUMAN	Q43657	homo sapien
822	54.5	13.3	274	2	Q75DJ2	Q75DJ2	ashbya goss
823	54.5	13.3	277	2	Q9TUK6	Q9TUK6	oryctolagus
824	54.5	13.3	284	2	Q9PEH9	Q9PEH9	xylella fas
825	54.5	13.3	284	2	Q6D0P1	Q6D0P1	erwinia car
826	54.5	13.3	287	1	OXA1_LISIN	Q8Y3I2	listeria in
827	54.5	13.3	287	1	OXA1_LISMO	Q71VQ8	listeria mo
828	54.5	13.3	287	2	Q71VQ8	Q71VQ8	listeria mo
829	54.5	13.3	290	2	Q6MFW9	Q6MFW9	rattus norv
830	54.5	13.3	297	2	Q64SW7	Q64SW7	caenorhabdi
831	54.5	13.3	300	2	P91076	P91076	bacteroides
832	54.5	13.3	300	2	Q66GA9	Q66GA9	yersinia ps
833	54.5	13.3	300	2	Q8ZJL7	Q8ZJL7	yersinia pe
834	54.5	13.3	302	2	Q9MAQ8	Q9MAQ8	arabidopsis

No.	Score	%	Length	R	Identifier	Accession	Organism
835	54.5	13.3	314	1	O2A1_HUMAN		homo sapien
836	54.5	13.3	315	1	NU1M_MOUSE	P03888	mus musculu
837	54.5	13.3	318	2	Q61FL0	Q61FL0	homo sapien
838	54.5	13.3	318	2	Q8SEZ8	Q8eez8	rattus norv
839	54.5	13.3	318	2	Q7JD06	Q7jd06	mus musculu
840	54.5	13.3	318	2	Q8HID1	Q8hid1	rattus norv
841	54.5	13.3	318	2	Q9G0S6	Q9g0s6	mus musculu
842	54.5	13.3	328	2	O93550	O93550	carassius a
843	54.5	13.3	331	2	Q67ES4	Q67es4	rattus norv
844	54.5	13.3	346	2	Q6N8W0	Q6n8w0	rhodopseudo
845	54.5	13.3	348	2	O99939	O99939	cyprinella
846	54.5	13.3	348	2	O99948	O99948	notropis at
847	54.5	13.3	350	1	C5AR_RABIT		oryctolagus
848	54.5	13.3	350	2	Q8F131	Q8f131	leptospira
849	54.5	13.3	362	2	O83562	O83562	treponema p
850	54.5	13.3	363	2	Q9KA51	Q9ka51	bacillus ha
851	54.5	13.3	371	2	Q8VZN9	Q8vzn9	arabidopsis
852	54.5	13.3	374	1	G23B_DROME	P83292	drosophila
853	54.5	13.3	377	2	Q9ZI98	Q9zi98	lactobacill
854	54.5	13.3	378	2	Q22722	Q22722	caenorhabdi
855	54.5	13.3	383	2	Q83CN5	Q83cn5	coxiella bu
856	54.5	13.3	387	2	Q630M9	Q630m9	bacillus ce
857	54.5	13.3	387	2	Q72X77	Q72x77	bacillus ce
858	54.5	13.3	387	2	Q81JS9	Q81js9	bacillus an
859	54.5	13.3	387	2	Q6HAR4	Q6har4	bacillus th
860	54.5	13.3	396	2	Q9LP12	Q9lp12	arabidopsis
861	54.5	13.3	397	2	Q81C11	Q81c11	bacillus ce
862	54.5	13.3	398	2	Q969F8	Q969f8	homo sapien
863	54.5	13.3	398	2	Q96QG0	Q96qg0	homo sapien
864	54.5	13.3	403	1	GC5B_HUMAN		homo sapien
865	54.5	13.3	413	2	O24946	O24946	helicobacte
866	54.5	13.3	414	2	Q9HJD5	Q9hjd5	thermoplasm
867	54.5	13.3	416	2	Q7QCI6	Q7qci6	anopheles g
868	54.5	13.3	416	2	Q65FY1	Q65fy1	bacillus li
869	54.5	13.3	419	2	Q961E7	Q961e7	drosophila
870	54.5	13.3	421	2	Q8YSL9	Q8ysl9	anabaena sp
871	54.5	13.3	428	2	Q7MTK8	Q7mtk8	porphyromon
872	54.5	13.3	438	1	FUCP_ECOLI	P11551	escherichia
873	54.5	13.3	438	1	Q8FEE8	Q8fee8	escherichia
874	54.5	13.3	438	2	Q83QC8	Q83qc8	shigella fl
875	54.5	13.3	438	2	Q8X6R7	Q8x6r7	escherichia
876	54.5	13.3	442	1	PUS3_YEAST	P31115	saccharomyc
877	54.5	13.3	443	2	Q98C40	Q98c40	rhizobium l
878	54.5	13.3	450	2	Q67119	Q67119	influenza a
879	54.5	13.3	461	1	Y061_MYCGE	P47307	mycoplasma
880	54.5	13.3	480	2	Q63FH4	Q63fh4	bacillus ce
881	54.5	13.3	483	1	CLK1_MOUSE	P22518	mus musculu
882	54.5	13.3	483	2	Q9PWM8	Q9pwm8	gallus gall
883	54.5	13.3	485	2	Q7PQT4	Q7pqt4	anopheles g
884	54.5	13.3	488	2	O61865	O61865	caenorhabdi
885	54.5	13.3	490	2	Q65II6	Q65ii6	oryza sativ
886	54.5	13.3	492	2	Q9ZZQ1	Q9zzq1	cyanidiosch
887	54.5	13.3	493	2	O17395	O17395	caenorhabdi
888	54.5	13.3	499	1	CIK2_MOUSE		mus musculu
889	54.5	13.3	499	1	CIK2_RAT	P63141	rattus norv
890	54.5	13.3	499	2	Q28293	Q28293	canis famil
891	54.5	13.3	499	2	Q9MYX3	Q9myx3	oryctolagus
892	54.5	13.3	499	2	Q8C8W4	Q8c8w4	mus musculu
893	54.5	13.3	499	2	Q7T1A0	Q7t1a0	gallus gall
894	54.5	13.3	502	2	Q9I7D0	Q9i7d0	drosophila
895	54.5	13.3	510	2	Q87BQ9	Q87bq9	xylella fas
896	54.5	13.3	510	2	Q9PAY3	Q9pay3	xylella fas
897	54.5	13.3	533	2	Q6KHI0	Q6khi0	mycoplasma
898	54.5	13.3	548	2	Q84LG0	Q84lg0	nicotiana a
899	54.5	13.3	560	2	Q7K4Y9	Q7k4y9	drosophila
900	54.5	13.3	560	2	Q9VYV7	Q9vyv7	drosophila
901	54.5	13.3	566	2	Q6FRJ2	Q6frj2	candida gla
902	54.5	13.3	589	2	Q6LM81	Q6lm81	photobacter
903	54.5	13.3	593	2	Q14931	Q14931	homo sapien
904	54.5	13.3	595	2	Q8W1N8	Q8w1n8	oryza sativ
905	54.5	13.3	595	2	Q8W5S2	Q8w5s2	oryza sativ
906	54.5	13.3	596	2	Q6AU53	Q6au53	oryza sativ
907	54.5	13.3	598	2	Q66SS9	Q66ss9	geocalamus
908	54.5	13.3	602	1	N05M_DIDMA	P41309	didelphis m
909	54.5	13.3	608	2	Q72H22	Q72h22	thermus the
910	54.5	13.3	612	2	Q8H1Z1	Q8h1z1	melanotaeni
911	54.5	13.3	612	2	Q8HMF9	Q8hmf9	sirembo imb
912	54.5	13.3	616	1	YG02_YEAST	P30777	saccharomyc
913	54.5	13.3	660	1	CIK4_BOVIN	O05037	bos taurus
914	54.5	13.3	661	2	Q9GLF1	Q9glf1	bos taurus
915	54.5	13.3	662	2	Q9YGX8	Q9ygx8	gallus gall
916	54.5	13.3	672	2	Q6G0V1	Q6g0v1	bartonella
917	54.5	13.3	672	2	Q6G521	Q6g521	bartonella
918	54.5	13.3	686	2	Q84Z01	Q84z01	oryza sativ
919	54.5	13.3	697	1	BYN_DROME	P55965	drosophila
920	54.5	13.3	729	2	Q8ESC5	Q8escs	oceanobacil
921	54.5	13.3	799	2	Q7S005	Q7s005	neurospora
922	54.5	13.3	931	1	EMR1_MOUSE	Q61549	mus musculu
923	54.5	13.3	940	2	Q7XQ41	Q7xq41	oryza sativ
924	54.5	13.3	1012	2	Q84ZR7	Q84zr7	oryza sativ
925	54.5	13.3	1022	2	Q62Q49	Q62q49	oryza sativ
926	54.5	13.3	1274	2	Q9E168	Q9e168	grass carp
927	54.5	13.3	1274	2	Q9E3V9	Q9e3v9	grass carp
928	54.5	13.3	1435	2	Q9DSQ0	Q9dsq0	colorado ti
929	54.5	13.3	2820	1	NF1_RAT	P97526	rattus norv
930	54.5	13.3	2839	1	NF1_HUMAN	P21359	homo sapien
931	54.5	13.3	2841	1	NF1_MOUSE	Q04690	mus musculu
932	54.5	13.3	3063	2	Q8QXN2	Q8qxn2	sugarcane m
933	54.5	13.3	3063	2	Q8QXN3	Q8qxn3	sugarcane m
934	54.5	13.3	3064	2	Q8QXN4	Q8qxn4	sugarcane m
935	54	13.2	82	2	Q6LL67	Q6ll67	photobacter
936	54	13.2	115	2	Q9G3S9	Q9g3s9	pteropus sc
937	54	13.2	116	2	Q8SC58	Q8sc58	stx2 conver
938	54	13.2	116	2	Q7Y2N5	Q7y2n5	stx2 conver
939	54	13.2	116	2	Q7Y346	Q7y346	stx1 conver
940	54	13.2	133	2	Q62M75	Q62m75	brachydanio
941	54	13.2	140	2	Q7PA91	Q7pa91	rickettsia
942	54	13.2	152	2	Q9R1Q7	Q9r1q7	m proteolip
943	54	13.2	165	2	Q8WGE5	Q8wges	callichirus
944	54	13.2	167	1	YMW1_YEAST	Q04767	saccharomyc
945	54	13.2	175	2	Q90448	Q90448	brachydanio
946	54	13.2	188	2	Q8CAG5	Q8cag5	escherichia
947	54	13.2	192	2	Q9BH50	Q9bh50	babesia bov
948	54	13.2	193	2	O99985	O99985	porphyra pu
949	54	13.2	206	2	Q75IQ7	Q75iq7	ashbya goss
950	54	13.2	220	2	Q6LQG6	Q6lqg6	photobacter
951	54	13.2	223	2	Q8ZW91	Q8zw91	pyrobaculum
952	54	13.2	225	2	Q7YIH2	Q7yih2	pemphigus b
953	54	13.2	242	2	Q9RLH7	Q9rlh7	paracoccus
954	54	13.2	244	2	Q6XYV8	Q6xyv8	spiroplasma
955	54	13.2	254	2	Q8MYB2	Q8myb2	ciona intes
956	54	13.2	257	2	Q7YX63	Q7yx63	caenorhabdi
957	54	13.2	259	1	COX3_LUMTE	Q34943	lumbricus t
958	54	13.2	261	2	Q94TA0	Q94ta0	myctophum a
959	54	13.2	261	2	Q6446S6	Q6446s6	plethodon p
960	54	13.2	264	2	Q8YUJ0	Q8yuj0	arabidopsis
961	54	13.2	265	2	Q61LT1	Q61lt1	anabaena sp
962	54	13.2	265	2	Q9K018	Q9k018	neisseria m
963	54	13.2	277	2	Q82UI3	Q82ui3	nitrosomona
964	54	13.2	283	2	Q6MBY2	Q6mby2	canis famil
965	54	13.2	295	2	Q65V68	Q65v68	mus musculu
966	54	13.2	304	2	Q6MKC6	Q6mkc6	parachlamyd
967	54	13.2	308	2	Q7YVE9	Q7yve9	mannheimia
968	54	13.2	310	2	Q8VG91	Q8vg91	bdellovibri
969	54	13.2	315	1	PSTC_METJA	Q58420	methanococc
970	54	13.2	325	2	O61969	O61969	trypanosoma
971	54	13.2	325	2	Q87466	Q87466	methanosarc
972	54	13.2	330	2	Q8QOX6	Q8qox6	clostridium
973	54	13.2	337	2	Q97EUO	Q97euo	pseudomonas
974	54	13.2	338	2	Q9SZU0	Q9szu0	arabidopsis
975	54	13.2	339	2	Q8G686	Q8g686	bifidobacte
976	54	13.2	346	2	Q6ECC1	Q6ecc1	timeliopsis
977	54	13.2	346	2	Q6SCI3	Q6sci3	thryothorus
978	54	13.2	347	2	Q9HXJ3	Q9hxj3	pseudomonas
979	54	13.2	348	2	P91860	P91860	caenorhabdi
980	54	13.2	358	1	IL8B_RABIT	P35344	oryctolagus

Left panel (SEQ 981–1052):

No.	Score	Eval	Entry Name	Count	Length	Accession	Organism
981	54	13.2	GP15_MACMU	1	360	O97663	macaca mula
982	54	13.2	GP15_MACNE	2	360	P56412	macaca neme
983	54	13.2	Q884W1	2	378	Q884W1	pseudomonas
984	54	13.2	Q7NPU9	2	379	Q7HPU9	chromobacte
985	54	13.2	Q9GKZ7	2	385	Q9GKZ7	tenrec ecau
986	54	13.2	Q631D6	2	385	Q631D6	bacillus ce
987	54	13.2	Q8YU77	2	387	Q8YU77	anabaena sp
988	54	13.2	Q8CMF9	2	402	Q8CMF9	shewanella
989	54	13.2	Q8CLZ2	2	404	Q8CLZ2	shewanella
990	54	13.2	Q8E957	2	404	Q8E957	shewanella
991	54	13.2	Q8EBL3	2	404	Q8EBL3	shewanella
992	54	13.2	Q8EHH7	2	404	Q8EHH7	shewanella
993	54	13.2	Q8D4U1	2	408	Q8D4U1	vibrio vuln
994	54	13.2	Q639H1	2	409	Q639H1	bacillus ce
995	54	13.2	Q6AGK0	2	416	Q6AGK0	leifsonia x
996	54	13.2	Q62EV7	2	417	Q62EV7	burkholderi
997	54	13.2	Q98M33	2	428	Q98M33	rhizobium l
998	54	13.2	Q63YE0	2	430	Q63YE0	burkholderi
999	54	13.2	Q6LUN8	2	435	Q6LUN8	photobacter
1000	54	13.2	Q8K2A8	2	438	Q8K2A8	mus musculu
1001	54	13.2	Q755U5	2	447	Q755U5	ashbya goss
1002	54	13.2	Q8FB33	2	459	Q8FB33	escherichia
1003	54	13.2	Q86AR0	2	463	Q86AR0	dictyosteli
1004	54	13.2	Q62BK7	2	469	Q62BK7	burkholderi
1005	54	13.2	Q94GS8	2	473	Q94GS8	oryza sativ
1006	54	13.2	Q6V5E7	2	478	Q6V5E7	capsella ru
1007	54	13.2	Q6N4J2	2	480	Q6N4J2	rhodopseudo
1008	54	13.2	Q8XIN7	2	482	Q8XIN7	clostridium
1009	54	13.2	Q6TMC9	2	483	Q6TMC9	coprinus ci
1010	54	13.2	Q8NU24	2	498	Q8NU24	staphylococ
1011	54	13.2	Q99RJ0	2	498	Q99RJ0	staphylococ
1012	54	13.2	Q7A3Q5	2	498	Q7A3Q5	staphylococ
1013	54	13.2	Q6G6M9	2	498	Q6G6M9	staphylococ
1014	54	13.2	LNT_RICCN	1	499	Q92IC5	rickettsia
1015	54	13.2	Q7NAT3	2	500	Q7NAT3	mycoplasma
1016	54	13.2	Q9VPD9	2	504	Q9VPD9	drosophila
1017	54	13.2	Q7PBL4	2	504	Q7PBL4	rickettsia
1018	54	13.2	Q6EVS3	2	507	Q6EVS3	yersinia ps
1019	54	13.2	Q9VCO2	2	527	Q9VCO2	drosophila
1020	54	13.2	Q8WF37	2	541	Q8WF37	venerupis (
1021	54	13.2	Q9VRM0	2	542	Q9VRM0	drosophila
1022	54	13.2	Q8I3H5	2	548	Q8I3H5	plasmodium
1023	54	13.2	FZD7_XENLA	1	549	Q6NV44	xenopus lae
1024	54	13.2	Q6NV44	2	554	Q6NV44	brachydanio
1025	54	13.2	Q7SZR7	2	554	Q7SZR7	brachydanio
1026	54	13.2	Q8YCG4	2	558	Q8YCG4	brucella me
1027	54	13.2	FZD1_XENLA	1	559	Q919M5	xenopus lae
1028	54	13.2	FZD5_XENLA	2	559	P58421	xenopus lae
1029	54	13.2	Q90ZT3	2	559	Q90ZT3	brachydanio
1030	54	13.2	Q98SI2	2	559	Q98SI2	brachydanio
1031	54	13.2	Q7Y684	2	563	Q7Y684	venerupis (
1032	54	13.2	Q7YF46	2	563	Q7YF46	venerupis (
1033	54	13.2	Q7YF49	2	563	Q7YF49	venerupis (
1034	54	13.2	HEMA_IAGU2	1	566	P13103	influenza a
1035	54	13.2	Q6FTB1	1	567	Q6FTB1	candida gla
1036	54	13.2	FZD7_MOUSE	1	570	Q08464	rattus norv
1037	54	13.2	Q6P551	2	572	Q61090	mus musculu
1038	54	13.2	Q871A0	1	572	Q6P551	mus musculu
1039	54	13.2	FZD7_HUMAN	1	573	Q871A0	neurospora
1040	54	13.2	Q7RZI9	2	574	O75084	homo sapien
1041	54	13.2	Q7T5Q9	2	589	Q7RZI9	neurospora
1042	54	13.2	Q9F409	2	592	Q7T5Q9	cryptophleb
1043	54	13.2	Q8LX55	2	594	Q9F409	mycobacteri
1044	54	13.2	Q40322	2	598	Q8LX55	cynocephalu
1045	54	13.2	Q9SW76	2	599	Q40322	mentha spic
1046	54	13.2	Q6AY92	2	599	Q9SW76	mentha long
1047	54	13.2	Q9PEB4	2	604	Q6AY92	rattus norv
1048	54	13.2	Q9SJA2	2	662	Q9PEB4	xylella fas
1049	54	13.2	Q7XWQ1	2	690	Q9SJA2	arabidopsis
1050	54	13.2	Q8FVV4	2	694	Q7XWQ1	oryza sativ
1051	54	13.2	Q8I0L8	2	741	Q8FVV4	brucella su
1052	54	13.2	Q6CTQ2	2	750	Q8I0L8	mus musculu
1053	54	13.2	Q6CTQ2	2	775	Q6CTQ2	kluyveromyc

Right panel (SEQ 1054–1126):

No.	Score	Eval	Entry Name	Count	Length	Accession	Organism
1054	54	13.2	Q7VEF1	2	779	Q7vef1	prochloroco
1055	54	13.2	POT6_ARATH	1	782	Q8w4i4	arabidopsis
1056	54	13.2	Q94KC6	2	788	Q94kc6	mesembryant
1057	54	13.2	Q8Y3B8	2	801	Q8y3b8	ralstonia s
1058	54	13.2	Q72UY4	2	845	Q72uy4	leptospira
1059	54	13.2	Q8EZY9	2	845	Q8ezy9	leptospira
1060	54	13.2	Q7X7Q3	2	868	Q7x7q3	oryza sativ
1061	54	13.2	Q9NL45	2	872	Q9nl45	ciona intes
1062	54	13.2	Q8A929	2	883	Q8a929	bacteroides
1063	54	13.2	YN86_YEAST	1	894	P27514	saccharomyc
1064	54	13.2	Q9HKX3	2	1018	Q9hkx3	thermoplasm
1065	54	13.2	Q64TN7	2	1040	Q64tn7	bacteroides
1066	54	13.2	Q72G02	2	1046	Q72g02	desulfovibr
1067	54	13.2	Q8IAQ8	2	1053	Q8iaq8	plasmodium
1068	54	13.2	Q8CFG5	2	1085	Q8cfg5	rattus norv
1069	54	13.2	Q66EN6	2	1164	Q66en6	yersinia ps
1070	54	13.2	Q8CKD9	2	1164	Q8ckd9	yersinia pe
1071	54	13.2	022731	2	1272	022731	arabidopsis
1072	54	13.2	TSC2_MOUSE	1	1814	Q61037	mus musculu
1073	54	13.2	Q9PT63	2	2065	Q9pt63	xenopus lae
1074	54	13.2	CU05_HUMAN	1	2298	Q9y3r5	homo sapien
1075	53.5	13.0	Q8LDK7	2	112	Q8ldk7	arabidopsis
1076	53.5	13.0	Q6ZNG3	2	132	Q6zng3	homo sapien
1077	53.5	13.0	Q8SUV0	2	149	Q8suv0	encephalito
1078	53.5	13.0	Q6W051	2	149	Q6w051	mus musculu
1079	53.5	13.0	Q8TNK2	2	162	Q8tnk2	methanosarc
1080	53.5	13.0	Q9S4C1	2	165	Q9s4c1	uncultured
1081	53.5	13.0	Q85H72	2	184	Q85h72	dasyhelea s
1082	53.5	13.0	P74727	2	184	P74727	synechocyst
1083	53.5	13.0	Q9DHK4	2	191	Q9dhk4	yaba-like d
1084	53.5	13.0	Q8DUQ8	2	195	Q8duq8	streptococc
1085	53.5	13.0	Q8G4H2	2	219	Q8g4h2	bifidobacte
1086	53.5	13.0	Q69598	2	226	Q69598	hepatitis b
1087	53.5	13.0	Q69599	2	226	Q69599	hepatitis b
1088	53.5	13.0	090305	2	233	090305	breda virus
1089	53.5	13.0	Q8Z8X0	2	263	Q8z8x0	salmonella
1090	53.5	13.0	Q7PXC7	2	264	Q7pxc7	anopheles g
1091	53.5	13.0	P96065	2	265	P96065	salmonella
1092	53.5	13.0	Q9VK02	2	273	Q9vk02	photobacter
1093	53.5	13.0	Q87EH8	2	281	Q87eh8	xylella fas
1094	53.5	13.0	Q73E92	2	284	Q73e92	bacillus ce
1095	53.5	13.0	Q9KBJ0	2	290	Q9kbj0	bacillus ha
1096	53.5	13.0	HTPX_STRPN	1	298	Q97qd6	streptococc
1097	53.5	13.0	Q8UY66	2	299	Q8uy66	simian aden
1098	53.5	13.0	Q6QP87	2	301	Q6qp87	simian aden
1099	53.5	13.0	Q6QPC3	2	301	Q6qpc3	simian aden
1100	53.5	13.0	Q6QPF9	2	301	Q6qpf9	simian aden
1101	53.5	13.0	Q6FF49	2	305	Q6ff49	acinetobact
1102	53.5	13.0	Q6UAG7	2	309	Q6uag7	mus musculu
1103	53.5	13.0	Q8WHX9	2	310	Q8whx9	psilotum nu
1104	53.5	13.0	Q8VFE1	2	310	Q8vfe1	mus musculu
1105	53.5	13.0	Q9PSJ5	2	313	Q9psj5	ictalurus p
1106	53.5	13.0	Q87WK8	2	315	Q87wk8	pseudomonas
1107	53.5	13.0	Q82DA1	2	319	Q82da1	streptomyce
1108	53.5	13.0	Q7TN51	2	330	Q7tn51	mus musculu
1109	53.5	13.0	RIR2_TRYBB	1	337	015910	trypanosoma
1110	53.5	13.0	Q8CPN5	2	338	Q8cpn5	staphylococ
1111	53.5	13.0	P91219	2	343	P91219	caenorhabdi
1112	53.5	13.0	Q9WR47	2	346	Q6wr47	treron sieb
1113	53.5	13.0	Q39980	2	350	Q39980	hyoscyamus
1114	53.5	13.0	Q66F72	2	355	Q66f72	yersinia ps
1115	53.5	13.0	Q83ZY2	2	355	Q83zy2	yersinia ps
1116	53.5	13.0	Q8ZBB0	2	355	Q8zbb0	yersinia pe
1117	53.5	13.0	RAI3_MOUSE	1	356	Q8bh14	mus musculu
1118	53.5	13.0	Q9T9H3	2	362	Q9t9h3	halocynthia
1119	53.5	13.0	Q7P9U4	2	362	Q7p9u4	rattus norv
1120	53.5	13.0	Q92GC4	2	362	Q92gc4	rickettsia
1121	53.5	13.0	Q68VX9	2	362	Q68vx9	rickettsia
1122	53.5	13.0	Q9ZCH3	2	362	Q9zch3	rickettsia
1123	53.5	13.0	Q8SJ48	2	369	Q8sj48	pfiesteria
1124	53.5	13.0	Q8M4X4	2	373	Q8m4x4	pfiesteria
1125	53.5	13.0	Q6FG00	2	374	Q6fg00	acinetobact

Index	Col A	Col B	Length	Copies	ID	Accession	Organism
1127	53.5	13.0	380	2	Q8M4L5	Q8m4l5	gymnocraniu
1128	53.5	13.0	381	2	CYB_ISUPA	P34871	isurus pauc
1129	53.5	13.0	385	2	Q81WZ9	Q81wz9	bacillus an
1130	53.5	13.0	385	2	Q6HB69	Q6hb69	bacillus th
1131	53.5	13.0	385	2	Q6KK53	Q6kk53	bacillus an
1132	53.5	13.0	389	2	Q6IE78	Q6ie78	herpesvirus
1133	53.5	13.0	395	2	Q81932	Q81932	paralichthy
1134	53.5	13.0	400	1	BMR2_BACSU	P39843	bacillus su
1135	53.5	13.0	410	2	Q8SGQ4	Q8sgq4	encephalito
1136	53.5	13.0	417	2	Q81AN4	Q81an4	bacillus ce
1137	53.5	13.0	419	2	Q8E200	Q8e200	streptococc
1138	53.5	13.0	424	2	Q64W69	Q64w69	bacteroides
1139	53.5	13.0	446	2	Q8E7F8	Q8e7f8	streptococc
1140	53.5	13.0	452	1	YCDT_ECOLI	P75908	escherichia
1141	53.5	13.0	455	2	Q70EC6	Q70ec6	bufo melano
1142	53.5	13.0	458	2	Q7Y8U9	Q7y8u9	andrias dav
1143	53.5	13.0	476	2	Q8Z5J2	Q8z5j2	salmonella
1144	53.5	13.0	478	2	Q8SW72	Q8sw72	encephalito
1145	53.5	13.0	500	2	Q9DY00	Q9dy00	avian leuko
1146	53.5	13.0	523	1	NU4M_PROWI	Q37617	prototheca
1147	53.5	13.0	529	2	Q8U2T6	Q8u2t6	pyrococcus
1148	53.5	13.0	537	2	Q8W118	Q8w118	arabidopsis
1149	53.5	13.0	537	2	Q8GWB7	Q8gwb7	arabidopsis
1150	53.5	13.0	546	2	Q8G6N6	Q8g6n6	bifidobacte
1151	53.5	13.0	549	2	Q9VPP9	Q9vpp9	drosophila
1152	53.5	13.0	571	2	Q9DLK2	Q9dlk2	avian leuko
1153	53.5	13.0	571	2	Q9DLK3	Q9dlk3	avian leuko
1154	53.5	13.0	578	1	OXAA_PSEAE	Q9ht06	pseudomonas
1155	53.5	13.0	580	2	Q85MD7	Q85md7	harpochytri
1156	53.5	13.0	602	2	Q70XH5	Q70xh5	caenolestes
1157	53.5	13.0	603	1	NU5M_HYLLA	P03919	hylobates l
1158	53.5	13.0	603	2	Q9GA20	Q9ga20	tupaia glis
1159	53.5	13.0	608	2	Q76HR3	Q76hr3	leiognathus
1160	53.5	13.0	610	2	Q6CKZ6	Q6ckz6	kluyveromyc
1161	53.5	13.0	627	1	RRN3_YEAST	P36070	saccharomyc
1162	53.5	13.0	628	2	Q6C697	Q6c697	yarrowia li
1163	53.5	13.0	706	2	Q9JWZ2	Q9jwz2	neisseria m
1164	53.5	13.0	706	2	Q9K1K3	Q9k1k3	neisseria m
1165	53.5	13.0	720	2	Q87BN6	Q87bn6	rhodopirell
1166	53.5	13.0	734	2	Q7UL18	Q7ul18	synechocyst
1167	53.5	13.0	770	2	P74677	P74677	burkholderi
1168	53.5	13.0	772	2	Q62CR6	Q62cr6	drosophila
1169	53.5	13.0	926	2	Q9W2L4	Q9w2l4	homo sapien
1170	53.5	13.0	1021	2	S123_HUMAN	P55017	oryctolagus
1171	53.5	13.0	1028	2	O18886	O18886	pseudomonas
1172	53.5	13.0	1053	2	Q88RT6	Q88rt6	nitrosomona
1173	53.5	13.0	1072	2	Q820K8	Q820k8	mycobacteri
1174	53.5	13.0	1083	1	EMBB_MYCLE	Q8cda9	mus musculu
1175	53.5	13.0	1112	2	Q8CGT8	Q8cgt8	leishmania
1176	53.5	13.0	1488	2	O15849	O15849	sugarcane m
1177	53.5	13.0	3064	2	Q8B388	Q8b388	eptatretus
1178	53	12.9	96	2	Q94ZD5	Q94zd5	blastophaga
1179	53	12.9	96	2	Q9B980	Q9b980	panulirus j
1180	53	12.9	117	2	Q8HD87	Q8hd87	pagurus lon
1181	53	12.9	117	2	Q9MNX9	Q9mnx9	sulfolobus
1182	53	12.9	119	2	Q9UWS9	Q9uws9	giardia lam
1183	53	12.9	126	2	Q7QY76	Q7qy76	drosophila
1184	53	12.9	141	2	Q6AWG3	Q6awg3	bacteroides
1185	53	12.9	147	2	Q8AA90	Q8aa90	anopheles g
1186	53	12.9	158	2	Q7PFM6	Q7pfm6	giardia lam
1187	53	12.9	158	2	Q7R5K3	Q7r5k3	pyrobaculum
1188	53	12.9	170	2	Q8ZTG7	Q8ztg7	trypanosoma
1189	53	12.9	174	2	Q26856	Q26856	trypanosoma
1190	53	12.9	174	2	Q27227	Q27227	caenorhabdi
1191	53	12.9	175	2	Q7YZV6	Q7yzv6	eulimnogamm
1192	53	12.9	188	2	Q96177	Q96177	arabidopsis
1193	53	12.9	192	2	Q6NM06	Q6nm06	eulimnogamm
1194	53	12.9	195	2	Q9G727	Q9g727	carassius a
1195	53	12.9	200	2	Q90WB6	Q90wb6	streptococc
1196	53	12.9	206	2	Q8DZ55	Q8dz55	brucella su
1197	53	12.9	213	2	Q8FYP4	Q8fyp4	chromobacte
1198	53	12.9	221	2	Q7P1V8	Q7p1v8	triatoma di
1199	53	12.9	227	2	Q9G807	Q99807	triatoma di

Index	Col A	Col B	Length	Copies	ID	Accession	Organism
1200	53	12.9	228	2	Q98RJ6	Q98rj6	mycoplasma
1201	53	12.9	229	2	CEMA_ATRBE	Q88w5	atropa bel
1202	53	12.9	229	1	CEMA_TOBAC	P12213	nicotiana t
1203	53	12.9	231	1	COBS_PYRKO	O52454	pyrococcus
1204	53	12.9	235	2	Q8TDV3	Q8tdv3	homo sapien
1205	53	12.9	236	2	Q6A9U4	Q6a9u4	propionibac
1206	53	12.9	242	2	Q74EF1	Q74ef1	geobacter s
1207	53	12.9	252	2	Q71U75	Q71u75	homo sapien
1208	53	12.9	252	2	Q8W1N7	Q8w1n7	oryza sativ
1209	53	12.9	253	2	Q8ISN8	Q81sn8	chasmagnath
1210	53	12.9	255	2	Q8YH75	Q8yh75	brucella me
1211	53	12.9	261	2	Q68SY9	Q68sy9	rhineura fl
1212	53	12.9	261	2	Q8E7F8	Q8e7f8	platytrocte
1213	53	12.9	261	2	Q85D01	Q85d01	dallia pect
1214	53	12.9	262	2	Q85D66	Q85d66	escherichia
1215	53	12.9	268	2	Q8KZ64	Q8kz64	bufo melano
1216	53	12.9	268	2	Q6YN06	O6yn06	rhizobium e
1217	53	12.9	268	2	Q6YN08	O6yn08	rhizobium g
1218	53	12.9	268	2	Q6YN11	O6yn11	agrobacteri
1219	53	12.9	271	2	Q6YN14	O6yn14	rhizobium e
1220	53	12.9	288	2	Q9TAK6	Q9tak6	cafeteria r
1221	53	12.9	292	2	Q9HUW4	Q9huw4	pseudomonas
1222	53	12.9	297	2	Q88AY2	Q88ay2	pseudomonas
1223	53	12.9	297	2	Q8RZ29	Q8rz29	oryza sativ
1224	53	12.9	297	2	Q6H663	Q6h663	oryza sativ
1225	53	12.9	300	2	Q66D50	Q66d50	yersinia ps
1226	53	12.9	300	2	Q8ZGV6	Q8zgv6	yersinia pe
1227	53	12.9	300	2	Q6CZ45	Q6cz45	erwinia car
1228	53	12.9	301	2	Q8UUP6	Q8uup6	tetraodon n
1229	53	12.9	301	2	Q7D6P5	Q7d6p5	mycobacteri
1230	53	12.9	305	2	O33234	O33234	mycobacteri
1231	53	12.9	305	2	Q6BA71	O6ba71	uncultured
1232	53	12.9	312	2	Q7P5R9	Q7p5r9	fusobacteri
1233	53	12.9	316	2	Q7YZV7	Q7yzv7	caenorhabdi
1234	53	12.9	328	1	YBA8_SHEON	Q8e8f7	shewanella
1235	53	12.9	330	1	P2Y6_MOUSE	Q9erk9	mus musculu
1236	53	12.9	332	2	Q66673	O66673	equid herpe
1237	53	12.9	335	2	Q83A71	Q83a71	coxiella bu
1238	53	12.9	336	2	Q87ZQ3	Q87zq3	pseudomonas
1239	53	12.9	337	2	Q9FV74	Q9fv74	perilla fru
1240	53	12.9	338	2	Q8UJL6	Q8ujl6	agrobacteri
1241	53	12.9	346	2	Q9XV78	Q9xv78	caenorhabdi
1242	53	12.9	346	2	Q6ECG5	Q6ecg5	certhionyx
1243	53	12.9	346	2	Q6Y050	Q6y050	amazona far
1244	53	12.9	347	2	Q644K3	Q644k3	batrachosep
1245	53	12.9	348	2	O21636	O21636	darevskia c
1246	53	12.9	350	2	Q9B2I2	Q9b2i2	limia versi
1247	53	12.9	350	1	IL8A_GORGO	P55919	gorilla gor
1248	53	12.9	350	2	IL8A_HUMAN	P25024	homo sapien
1249	53	12.9	350	1	IL8A_PANTR	P55920	pan troglod
1250	53	12.9	350	2	Q8N6T6	Q8n6t6	homo sapien
1251	53	12.9	353	2	Q6IN95	Q6in95	homo sapien
1252	53	12.9	353	2	Q95P47	Q95p47	epiphyas po
1253	53	12.9	355	2	Q9C9B6	Q9c9b6	arabidopsis
1254	53	12.9	359	2	Q8HZN3	Q8hzn3	papio hamad
1255	53	12.9	360	2	Q83HX7	Q83hx7	tropheryma
1256	53	12.9	360	1	CB2R_HUMAN	P34972	homo sapien
1257	53	12.9	360	2	Q6B0G7	Q6b0g7	homo sapien
1258	53	12.9	361	2	Q6NSY0	Q6nsy0	homo sapien
1259	53	12.9	364	2	O60150	O60150	schizosacch
1260	53	12.9	364	2	Q9AFH7	Q9afh7	streptococc
1261	53	12.9	367	2	Q8DZD6	Q8dzd6	streptococc
1262	53	12.9	368	2	Q95YA8	Q95ya8	caenorhabdi
1263	53	12.9	368	2	O69131	O69131	burkholderi
1264	53	12.9	368	2	Q62HQ8	Q62hq8	burkholderi
1265	53	12.9	377	2	Q63RK1	Q63rk1	burkholderi
1266	53	12.9	378	2	Q87B8	Q87b8	streptococc
1267	53	12.9	381	2	Q75V45	Q75v45	monochirus
1268	53	12.9	384	2	Q8BKU9	Q8bku9	mus musculu
1269	53	12.9	394	2	Q6CB93	Q6cb93	yarrowia li
1270	53	12.9	397	2	Q7W2B3	Q7w2b3	bordetella
1271	53	12.9	397	2	Q7MDA0	Q7mda0	vibrio vuln
1272	53	12.9	398	2	Q8D6E7	Q8d6e7	vibrio vuln
				2	Q83G95	Q83g95	tropheryma

Left half of the listing (columns: No. | Score | E | Name | n | Accession | Length | Organism):

No.	Score	E	Name	n	Accession	Length	Organism
1273	53	12.9	Q81C85	2	q81c85	400	bacillus ce
1274	53	12.9	Q830N1	2	q830n1	400	enterococcu
1275	53	12.9	Q7QDD3	2	q7qdd3	404	anopheles g
1276	53	12.9	Q8G4Q5	2	q8g4q5	405	bifidobacte
1277	53	12.9	CB2R_RAT	1	cb2r_rat	410	rattus norv
1278	53	12.9	Q6DD05	2	q6dd05	410	xenopus lae
1279	53	12.9	Q9PNV8	2	q9pnv8	415	caenorhabdi
1280	53	12.9	Q7MCZ4	2	q7mcz4	417	vibrio vuln
1281	53	12.9	Q8D5X7	2	q8d5x7	417	vibrio vuln
1282	53	12.9	Q6QT97	2	q6qt97	419	trypanosoma
1283	53	12.9	Q725X7	2	q725x7	419	desulfovibr
1284	53	12.9	Q8HN35	2	q8hn35	420	paragonimus
1285	53	12.9	Q9MLH8	2	q9mlh8	420	paragonimus
1286	53	12.9	Q6AUA6	2	q6aua6	421	oryza sativ
1287	53	12.9	CISY_RHITR	1	p51037	429	rhizobium t
1288	53	12.9	CISZ_RHITR	1	p51038	429	rhizobium t
1289	53	12.9	Q92M38	2	q92m38	429	helicobacte
1290	53	12.9	NQOB_THETH	1	q56229	431	thermus the
1291	53	12.9	Q8TDT8	1	q8tdt8	433	homo sapien
1292	53	12.9	Q9KL99	2	q9kl99	440	vibrio chol
1293	53	12.9	NUON_RICCN	1	q92hh5	458	rickettsia
1294	53	12.9	Q7P8U7	2	q7p8u7	458	rickettsia
1295	53	12.9	Q7P049	2	q7p049	461	chromobacte
1296	53	12.9	Q684E6	2	q684e6	468	sulfolobus
1297	53	12.9	Q75AS5	2	q75as5	486	ashbya goss
1298	53	12.9	O29976	1	o29976	490	archaeoglob
1299	53	12.9	Q8T7W0	2	q8t7w0	492	drosophila
1300	53	12.9	Q8FJ30	2	q8fj30	496	escherichia
1301	53	12.9	Q6AV67	2	q6av67	497	oryza sativ
1302	53	12.9	Q800U0	2	q800u0	500	ictalurus p
1303	53	12.9	Q9LMM4	2	q9lmm4	509	arabidopsis
1304	53	12.9	Q9HVA7	2	q9hva7	512	pseudomonas
1305	53	12.9	Q6A592	2	q6a592	513	caenorhabdi
1306	53	12.9	Q6NJW0	2	q6njw0	517	corynebacte
1307	53	12.9	P91840	2	p91840	520	caenorhabdi
1308	53	12.9	Q9BHW0	2	q9bhw0	522	leishmania
1309	53	12.9	FZD4_XENLA	1	q9pt62	523	xenopus lae
1310	53	12.9	FZD4_CHICK	1	q9ia05	525	gallus gall
1311	53	12.9	Q98C28	2	q98c28	526	rhizobium l
1312	53	12.9	Q6P8H8	2	q6p8h8	527	mus musculu
1313	53	12.9	O16923	1	o16923	537	caenorhabdi
1314	53	12.9	FZD4_HUMAN	1	q9ulv1	537	homo sapien
1315	53	12.9	FZD4_MOUSE	1	q61088	537	mus musculu
1316	53	12.9	Q6S9E4	2	q6s9e4	537	homo sapien
1317	53	12.9	Q8BKS3	2	q8bks3	538	mus musculu
1318	53	12.9	Q8BLL2	2	q8bll2	541	mus musculu
1319	53	12.9	FZD4_RAT	1	q9qzh0	545	rattus norv
1320	53	12.9	BBR1_SCHCO	1	p78741	546	schizophyll
1321	53	12.9	Q85IJ1	2	q85ij1	546	oryza sativ
1322	53	12.9	Y61B_MYCPN	1	p75040	553	mycoplasma
1323	53	12.9	Q7QA61	2	q7qa61	555	anopheles g
1324	53	12.9	Q9JXN7	2	q9jxn7	555	neisseria m
1325	53	12.9	CSTA_AQUAE	1	o67304	556	aquifex aeo
1326	53	12.9	Q04162	2	q04162	557	saccharomyc
1327	53	12.9	Q7ZU08	2	q7zu08	558	brachydanio
1328	53	12.9	Q8QFM3	2	q8qfm3	558	brachydanio
1329	53	12.9	Q9JW86	2	q9jw86	567	neisseria m
1330	53	12.9	Q8TEN4	2	q8ten4	571	homo sapien
1331	53	12.9	Q93GF4	2	q93gf4	579	staphylococ
1332	53	12.9	Q9W6E4	2	q9w6e4	588	brachydanio
1333	53	12.9	Q8H038	2	q8h038	590	oryza sativ
1334	53	12.9	Q34192	2	q34192	590	crithidia o
1335	53	12.9	O81193	2	o81193	592	salvia offi
1336	53	12.9	Q9W6E2	2	q9w6e2	603	brachydanio
1337	53	12.9	O04806	2	o04806	603	perilla fru
1338	53	12.9	Q9FV72	2	q9fv72	604	perilla fru
1339	53	12.9	Q9AXM7	2	q9axm7	611	perilla fru
1340	53	12.9	NU5M_LATCH	1	o03174	643	latimeria c
1341	53	12.9	Q8H6J2	2	q8h6j2	649	zea mays (m
1342	53	12.9	Q8IT87	2	q8it87	655	drosophila
1343	53	12.9	O23675	2	o23675	666	arabidopsis
1344	53	12.9	FZD3_HUMAN	1	q9npg1	667	homo sapien
1345	53	12.9	Q757W1	2	q757w1	667	ashbya goss

Right half of the listing (columns: No. | Score | E | Name | n | Accession | Length | Organism):

No.	Score	E	Name	n	Accession	Length	Organism
1346	53	12.9	Q9LJP4	2	q91jp4	673	arabidopsis
1347	53	12.9	Q6ZGM7	2	q6zgm7	683	oryza sativ
1348	53	12.9	Q6L538	2	q61538	688	oryza sativ
1349	53	12.9	Q9SB75	2	q9sb75	692	arabidopsis
1350	53	12.9	Q8Y0N1	2	q8y0n1	696	ralstonia s
1351	53	12.9	Q75IY3	2	q75iy3	706	oryza sativ
1352	53	12.9	Q9BL30	2	q9b130	716	caenorhabdi
1353	53	12.9	Q8Z7R8	2	q8z7r8	717	salmonella
1354	53	12.9	Q90Z26	2	q90z26	743	sternopygus
1355	53	12.9	Q92BN1	2	q92bn1	746	listeria in
1356	53	12.9	Q6NG44	2	q6ng44	748	corynebacte
1357	53	12.9	Q9V5H6	2	q9v5h6	807	drosophila
1358	53	12.9	Q8IGU8	2	q8igu8	840	drosophila
1359	53	12.9	Q87Y21	2	q87y21	880	pseudomonas
1360	53	12.9	Q6CIC7	2	q6cic7	923	kluyveromyc
1361	53	12.9	Q7RDK2	2	q7rdk2	947	plasmodium
1362	53	12.9	Q6XGE6	2	q6xge6	964	escherichia
1363	53	12.9	Q9V5H7	2	q9v5h7	992	drosophila
1364	53	12.9	Q75CL2	2	q75cl2	1010	ashbya goss
1365	53	12.9	Q6V495	2	q6v495	1026	drosophila
1366	53	12.9	Q7Q240	2	q7q240	1083	anopheles g
1367	53	12.9	Q9Z1L5	2	q9z1l5	1091	mus musculu
1368	53	12.9	Q7XQT5	2	q7xqt5	1120	oryza sativ
1369	53	12.9	Q66DQ6	2	q66dq6	1139	yersinia ps
1370	53	12.9	Q6B377	2	q6b377	1159	uncultured
1371	53	12.9	Q95022	2	q95022	1321	tetrahymena
1372	53	12.9	Q9GRK2	2	q9grk2	1341	leishmania
1373	53	12.9	Q7QDJ1	2	q7qdj1	1348	anopheles g
1374	53	12.9	Q7PDM5	2	q7pdm5	1467	plasmodium
1375	53	12.9	Q756V3	2	q756v3	1502	ashbya goss
1376	53	12.9	Q6AT77	2	q6at77	1672	oryza sativ
1377	53	12.9	Q80TG7	2	q80tg7	1693	mus musculu
1378	53	12.9	Q90519	2	q90519	1717	fugu rubrip
1379	53	12.9	Q75IX6	2	q75ix6	1724	oryza sativ
1380	53	12.9	Q9DF53	2	q9df53	1949	brachydanio
1381	52.5	12.8	Q9SKG6	2	q9skg6	83	arabidopsis
1382	52.5	12.8	N36A_SOYBN	1	q02918	90	glycine max
1383	52.5	12.8	Q6ETG0	2	q6etg0	104	oryza sativ
1384	52.5	12.8	Q705E0	2	q705e0	107	human papil
1385	52.5	12.8	Q8YPY4	2	q8ypy4	111	anabaena sp
1386	52.5	12.8	DYLX_BOVIN	1	p63171	113	bos taurus
1387	52.5	12.8	DYLX_HUMAN	1	p63172	113	homo sapien
1388	52.5	12.8	DYLX_RAT	1	q92336	113	rattus norv
1389	52.5	12.8	Q970J2	2	q970j2	125	sulfolobus
1390	52.5	12.8	Q8CAT5	2	q8cat5	129	mus musculu
1391	52.5	12.8	Q8UIF8	2	q8uif8	133	agrobacteri
1392	52.5	12.8	Q98QT1	2	q98qt1	137	mycoplasma
1393	52.5	12.8	Q8TP69	2	q8tp69	138	methanosarc
1394	52.5	12.8	Q9HK88	2	q9hk88	138	thermoplasm
1395	52.5	12.8	Q85H90	2	q85h90	141	austrochlus
1396	52.5	12.8	Q7YCV9	2	q7ycv9	145	arion irati
1397	52.5	12.8	Q66CB6	2	q66cb6	148	yersinia ps
1398	52.5	12.8	Q8ZG73	2	q8zg73	148	yersinia pe
1399	52.5	12.8	Q85H91	2	q85h91	154	austrochlus
1400	52.5	12.8	Q85H92	2	q85h92	155	austrochlus
1401	52.5	12.8	Q65Z03	2	q65z03	162	megabalanus
1402	52.5	12.8	Q934N3	2	q934n3	165	uncultured
1403	52.5	12.8	Q934N5	2	q934n5	165	uncultured
1404	52.5	12.8	Q50283	2	q50283	169	methylocyst
1405	52.5	12.8	Q6V0T5	2	q6v0t5	170	uncultured
1406	52.5	12.8	Q9TGJ3	2	q9tgj3	175	taenia cras
1407	52.5	12.8	Q8DKB9	2	q8dkb9	177	synechococc
1408	52.5	12.8	Q6RW20	2	q6rw20	177	uncultured
1409	52.5	12.8	Q6RW21	2	q6rw21	183	uncultured
1410	52.5	12.8	SIEB_LAMBD	1	p03762	190	bacteriopha
1411	52.5	12.8	Q7NCD9	2	q7ncd9	195	gloeobacter
1412	52.5	12.8	O59004	2	o59004	214	pyrococcus
1413	52.5	12.8	Q9GCA6	2	q9gca6	214	litoria pea
1414	52.5	12.8	Q9GCB0	2	q9gcb0	216	litoria spe
1415	52.5	12.8	Q8P901	2	q8p901	219	xanthomonas
1416	52.5	12.8	Q8VCL0	2	q8vcl0	219	mus musculu
1417	52.5	12.8	Q9D7S1	2	q9d7s1	224	mus musculu
1418	52.5	12.8	Q6SMZ5	2	q6smz5	224	aotus azara

ALIGNMENTS

RESULT 1
Q6UWR8

ID   Q6UWR8   PRELIMINARY;   PRT;   77 AA.
AC   Q6UWR8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   GPVK512.
GN   ORFNames=UNQ512;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358675; AAQ89038.1; -.
SQ   SEQUENCE   77 AA; 8772 MW; 11OCBCF87CCC4B86 CRC64;

Query Match   100.0%; Score 410; DB 2; Length 77;
Best Local Similarity   100.0%; Pred. No. 1e-37;
Matches   77; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFAJTLCSAFWFNKGLALIFCIIQSLALTWYSLSF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPVKQLKRMFEPTRLIATIMVLLCFAJTLCSAFWFNKGLALIFCIIQSLALTWYSLSF 60

Qy   61 IPFARDAVKKCFAVCLA 77
              |||||||||||||||||
Db   61 IPFARDAVKKCFAVCLA 77

RESULT 2
O95562

ID   O95562   PRELIMINARY;   PRT;   160 AA.
AC   O95562;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.

RA   Rhodes S.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Kojima Y., Kondo H., Konno H., Kouda M., Koya S.,
RA   Katoh H., Kawai J., Kawai G., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

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RA   Rhodes S.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL035297; CAA22897.1; -.
DR   EMBL; BC068098; AAH68098.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 160 AA; 17779 MW; F05C57532B7593BD CRC64;

Query Match   100.0%;   Score 410;   DB 2;   Length 160;
Best Local Similarity 100.0%;   Pred. No. 1.9e-37;
Matches   77; Conservative   0; Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 143

Qy   61 IPFARDAVKKCFAVCLA   77
         |||||||||||||||||
Db 144 IPFARDAVKKCFAVCLA 160

RESULT 3
ID   Q8VD57   PRELIMINARY;   PRT;   159 AA.
AC   Q8VD57;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   RIKEN cDNA 2010005O13 (Mus musculus adult male bone cDNA, RIKEN full-
DE   length enriched library, clone:9830137K19 product:hypothetical
DE   protein, full insert sequence).
GN   Name=2010005O13Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saito H., Sakai C., Sakai K., Sakazume N., Sano.H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017549; AAH17549.1; -.
DR   EMBL; AK036578; BAC29488.1; -.
DR   MGD; MGI:1917362; 2010005013Rik.
KW   Hypothetical protein.
SQ   SEQUENCE 159 AA; 17499 MW; B30B7BB5FE82A0B6 CRC64;

Query Match   89.4%; Score 366.5; DB 2; Length 159;
Best Local Similarity   92.2%; Pred. No. 1.2e-32;
Matches   71; Conservative   4; Mismatches   4; Indels   1; Gaps   1;

Qy   1 MGPVKVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
           |||:||||||||||||||||| |:||||||| |||||||||||||||||||||||||||||
Db   84 MGPLKVKQLKRMFEPTRLIATIIVLLCFALTLCSAFLW-NKKGLALIFCILQSLALTWYSLSY 142

Qy   61 IPFARDAVKKCFAVCLA 77
           | :|||||||||||||
Db   143 IPYARDAVKKCFAVCLA 159

RESULT 4
Q7T375
ID   Q7T375   PRELIMINARY;   PRT;   161 AA.
AC   Q7T375;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein zgc:64053.
GN   ORFNames=zgc:64053;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053226; AAH53226.1; -.
DR   ZFIN; ZDB-GENE-040426-1350; zgc:64053.
KW   Hypothetical protein.
SQ   SEQUENCE 161 AA; 18025 MW; 5BACAB7DDACDB634 CRC64;

RESULT 6

Query Match   79.0%; Score 324; DB 2; Length 161;
Best Local Similarity   76.6%; Pred. No. 6.1e-28;
Matches   59; Conservative   8; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MGPVKVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
           |||||||||||||||||||||||| |:||||| |||||||||||:|||||||||||||||:
Db   85 MGPVKVKQLKRMFEPTRLIATIVLLVLLFLVLTLCAVFWWNKKGLAIIFCILQFLAMTWYSISY 144

Qy   61 IPFARDAVKKCFAVCLA 77
           |||||||| ||:
Db   145 IPFARDAVIKCCTTCLS 161

RESULT 5
Q8WV19
ID   Q8WV19   PRELIMINARY;   PRT;   159 AA.
AC   Q8WV19;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Chromosome 6 open reading frame 83.
GN   Name=C6orf83;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018969; AAH18969.1; -.
DR   EMBL; BC018969; AAH18969.1; -. 0EC8A9CED7EF27E0 CRC64;
SQ   SEQUENCE 159 AA; 17804 MW; 0EC8A9CED7EF27E0 CRC64;

Query Match   74.6%; Score 306; DB 2; Length 159;
Best Local Similarity   70.1%; Pred. No. 5.9e-26;
Matches   54; Conservative   13; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MGPVKVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
           |||||||||||||||||:||| |||| ||| ||||||||||||:|||:|||||||||||||:
Db   83 MGPVKVKQLKKMFEATRLLATIVMLLCFIFTLCALWHHKKGLAVLFCIIQFLSMTWYSLSY 142

Qy   61 IPFARDAVKKCFAVCLA 77
           |||||||| |||:
Db   143 IPYARDAVIKCCSSLLS 159

RESULT 6

```
Q9UIC7
ID   Q9UIC7          PRELIMINARY;      PRT;   178 AA.
AC   Q9UIC7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PRGR1 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hu Y.F., Mao X.H., Zhuang M., Lu C.D.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF041429; AAF18564.1; -.
DR   Genew; HGNC:21102; C6orf83.
FT   NON_TER       1      1
SQ   SEQUENCE   178 AA;  19879 MW;  72C1E2BA35F3C6EA CRC64;

Query Match             72.7%;   Score 298;  DB 2;  Length 178;
Best Local Similarity   68.8%;   Pred. No. 5e-25;
Matches  53;   Conservative  13;  Mismatches  11;  Indels  0;  Gaps  0;

Qy     1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWHNKGLALIFCILQSLALTWYSLSF  60
           ||||||||| | |||:||||||||||||| ||| ||| ||||||| :|||||||||||:|
Db   102 MGPVKQLKMCEATRLLATIVMLLCFIFTLCAALMWHHKGLAVLFCILQFLSMTWYSLSY 161

Qy    61 IPFARDAVKKCFAVCLA  77
           |:|||||| | ||  |:
Db   162 IPYARDAVIKCCCSSLS 178


RESULT 7
Q9VPD4
ID   Q9VPD4          PRELIMINARY;      PRT;   163 AA.
AC   Q9VPD4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CG5104-PB (RH26504p).
GN   ORFNames=CG5104;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson R.C., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.B.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003591; AAN12138.1; -.
DR   EMBL; AY18429; AAM48458.1; -.
DR   IntAct; Q9VPD4; -.
DR   FlyBase; FBgn0037009; CG5104.
SQ   SEQUENCE   163 AA;  18180 MW;  FD8D4B8A588EPD0F CRC64;
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Query Match        58.5%;   Score 240;  DB 2;  Length 163;
Best Local Similarity   61.8%;  Pred. No. 1.2e-18;
Matches  47;  Conservative  10;  Mismatches  19;  Indels  0;  Gaps  0;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
         ||||:||:||  ||||||:|||:||  ||||||||||||:||||||||||||||||:||||
Db  86 MGPFKQIKKMFAETRLIATIIVLVMMVLTFIAAIVWKKAGLTLIFIIIQSLAMTWYSLSY 145

Qy  61 IPFARDAVKKCFAVCL 76
         ||:||||||
Db 146 IPYARDAVKKTMSAIL 161
```

RESULT 8
Q86F94
ID   Q86F94;   PRELIMINARY;   PRT;   113 AA.
AC   Q86F94;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Clone ZZZ409 mRNA sequence.
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RA   Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA   Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA   Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA   Xue C.L., Feng Z., Chen Z., Han Z.G.;
RT   "Evolutionary and biomedical implications of a Schistosoma japonicum
RT   complementary DNA resource.";
RL   Nat. Genet. 35:139-147(2003).
DR   EMBL; AY222969; AAP05981.1; -.
SQ   SEQUENCE 113 AA; 12524 MW; 2FF26F707A512D73 CRC64;

```
Query Match        55.0%;   Score 225.5;  DB 2;  Length 113;
Best Local Similarity   57.9%;  Pred. No. 3.4e-17;
Matches  44;  Conservative  15;  Mismatches  16;  Indels  1;  Gaps  1;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
         |||:|| |||||||||||:||  |:|  |:|| |  ||||||||:|  ||||||||||||||
Db  38 MGPMNQLKRMFQETRIIAAVIMLVCLVLTTVFALLGF-RLLCLIFCILQSLSLTWYSLSY 96

Qy  61 IPFARDAVKKCFAVCL 76
         ||:||||||||
Db  97 IPYARDAVKRLCSSCI 112
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RESULT 9
Q7YTP0
ID   Q7YTP0;   PRELIMINARY;   PRT;   162 AA.
AC   Q7YTP0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein F27D4.7.
GN   ORFNames=F27D4.7;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditina;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   none.
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilkinson J.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z79695; CAE17789.1; -.
DR   WormBase; WBGene00009191; F27D4.7.
DR   WormPep; F27D4.7; CE34829.
KW   Hypothetical protein.
SQ   SEQUENCE 162 AA; 17849 MW; C540FE86696A9489 CRC64;

```
Query Match        40.7%;   Score 167;  DB 2;  Length 162;
Best Local Similarity   48.6%;  Pred. No. 1.3e-10;
Matches  35;  Conservative  13;  Mismatches  24;  Indels  0;  Gaps  0;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
         |||:|| ||  ||||  |:|  |:||  |:|||||||||||:|||| ||:  |||:||||:
Db  90 MGPIGQIKKMFDKSRWIASSMYILFITLLSGLVLKNSLLAIICTAGQYIAMAWYSLSY 149

Qy  61 IPFARDAVKKCF 72
         ||:|| || |
Db 150 IPYARRAVSKIF 161
```

RESULT 10
Q9NEC2
ID   Q9NEC2;   PRELIMINARY;   PRT;   163 AA.
AC   Q9NEC2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2001 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Possible hypothetical 17.8 Kd protein.
GN   Name=L8325.06;
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Friedlin;
RX   MEDLINE=98146435; PubMed=9477341;
RA   Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA   Smith D.F.;
RT   "A physical map of the Leishmania major Friedlin genome.";
RL   Genome Res. 8:135-145(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Friedlin;
RA   Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
RA   Barrell B.G.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL157415; CAB75633.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 163 AA; 17766 MW; CE8464549DEB6AEC CRC64;

```
Query Match        38.8%;   Score 159;  DB 2;  Length 163;
Best Local Similarity   45.8%;  Pred. No. 1e-09;
Matches  33;  Conservative  11;  Mismatches  28;  Indels  0;  Gaps  0;

Qy   2 GPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFI 61
         |  :|||  ||  || |:||||  |  ||    |  ||||||:|||| |:||:||||| |:
Db  87 GPARQPKSMFNEGRWIASTVVIITMVLTLLCAVLLHSGLLTLMSIIQLLALAWYILSYI 146

Qy  62 PFARDAVKKCFA 73
         || ||||
Db 147 PFARDIVKGAFS 158
```

RESULT 11
Q9LT07
ID   Q9LT07;   PRELIMINARY;   PRT;   175 AA.
AC   Q9LT07;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```
DE   Similarity to unknown protein (Hypothetical protein At5g23550/MQM1_18)
DE   (Hypothetical protein At5g23550).
GN   Name=At5g23550/MQM1_18; Synonyms=At5g23550;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20181125; PubMed=10718197;
RA   Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT   features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:31-63(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA   Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA   Hayashizaki Y., Shinozaki K.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB025633; BAA97245.1; -.
DR   EMBL; AK117540; BAC42201.1; -.
DR   EMBL; BT005168; AAO50701.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  175 AA;  19736 MW;  CCAB351EB9155232 CRC64;

Query Match             38.3%;  Score 157;  DB 2;  Length 175;
Best Local Similarity   42.7%;  Pred. No. 1.8e-09;
Matches  32;  Conservative  11;  Mismatches  32;  Indels   0;  Gaps   0;

Qy          1  MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
               |||:..|:..:|: |||||||||||||||||||||||||| :|   :|||:|:||:||:
Db         96  IGPQRQVTMMLDPARIYATALYLASIIIALFCALVRNKLLTLLAIILEFTGLIWYSLSY 155

Qy         61  IPFARDAVKKCFAVC 75
               ||||   :  |||
Db        156  IPFARTMVSKIFMTC 170

RESULT 12
Q6GKX4
ID   Q6GKX4            PRELIMINARY;   PRT;   163 AA.
AC   Q6GKX4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   At5g24170.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RT   "Arabidopsis ORF clones.";
```

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RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT014940; AAR47791.1; -.
DR   EMBL; BT015632; AAU15131.1; -.
SQ   SEQUENCE  163 AA;  17751 MW;  A71DD2D77C8330F3 CRC64;

Query Match             35.9%;  Score 147;  DB 2;  Length 163;
Best Local Similarity   41.4%;  Pred. No. 2.2e-08;
Matches  29;  Conservative  14;  Mismatches  27;  Indels   0;  Gaps   0;

Qy          1  MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
               |||:..|:..:|: ||||||||||||||:|   ::.||.::::: ||:||:| |:||:|
Db         84  MGPEQQMSMFDPVRFLATSIYIGCVVVALICALLIHSKIITVLAIICEICALIWYSLSY 143

Qy         61  IPFARDAVKK 70
               ||||||
Db        144  IPFARRMVSE 153

RESULT 13
Q6Z7E9
ID   Q6Z7E9            PRELIMINARY;   PRT;   171 AA.
AC   Q6Z7E9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative pRGR1.
GN   Name=P0020C11.16;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP004865; BAD15819.1; -.
SQ   SEQUENCE  171 AA;  19016 MW;  97B49A7A3A3694A7 CRC64;

Query Match             35.1%;  Score 144;  DB 2;  Length 171;
Best Local Similarity   40.0%;  Pred. No. 4.9e-08;
Matches  30;  Conservative  12;  Mismatches  33;  Indels   0;  Gaps   0;

Qy          1  MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSF 60
               |||:..|:...|.:.|||||||||||||||||||||||||:   |:::::|||.|:||:
Db         92  IGPKRQFDMMLDSVRIYATAVVIASIIIALFCALFVHSKLLTLLAIILEFGALVWYSLSY 151

Qy         61  IPFARDAVKKCFAVC 75
               |||||   |||
Db        152  IPFARSVVSKVMTSC 166

RESULT 14
Q9N6J5
ID   Q9N6J5            PRELIMINARY;   PRT;   218 AA.
AC   Q9N6J5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=Chr3_0830;
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Friedlin;
RX   MEDLINE=22738071; PubMed=12853638; DOI=10.1093/nar/gkg469;
RA   Worthey E.A., Martinez-Calvillo S., Schnaufer A., Aggarwal G.,
RA   Cawthra J., Fazelinia G., Fong C., Fu G., Hasebrock M., Hixson G.,
RA   Ivens A.C., Kiser P., Marsolini F., Rickell E., Salavati R., Sisk E.,
RA   Sunkin S.M., Stuart K.D., Myler P.J.;
RT   "Leishmania major chromosome 3 contains two long convergent
```

RT   polycistronic gene clusters separated by a tRNA gene.";
RL   Nucleic Acids Res. 31:4201-4210(2003).
DR   EMBL; AC125735; AAM69057.1; -.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   218 AA;   24440 MW; 5106FC662012AA19 CRC64;

Query Match   34.6%; Score 142; DB 2; Length 218;
Best Local Similarity   38.2%; Pred. No. 1e-07;
Matches   26; Conservative 15; Mismatches 27; Indels   0; Gaps   0;

Qy   2 GPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFI 61
               | :||: ||| || | : :: ::||| | ||| :|| | :|: | |: |||:|
Db   121 GCAQQLRSMFEANRFEAACLYVISIVMTLLSALWLQSKLLCVLFALAQLACILWYALSYI 180

Qy   62 PFARDAVK 69
               |:||| :|
Db   181 PYARQTLK 188

RESULT 15
Q922U5
ID   Q922U5   PRELIMINARY;   PRT;   136 AA.
AC   Q922U5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update).
DE   RIKEN cDNA 5630401J11 (Similar to CG5104).
GN   Name=5630401J11Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129S6/SvEvTac;
RA   Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA   Nagaraja R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006777; AAH06777.1; -.
DR   EMBL; AF466883; AAM21003.1; -.
DR   MGD; MGI:1918689; 5630401J11Rik.
DR   GO; GO:0016021; C:integral to membrane; TAS.

SQ   SEQUENCE   136 AA;   15085 MW; 3FBAF412B5E9840C CRC64;

Query Match   34.1%; Score 140; DB 2; Length 136;
Best Local Similarity   71.4%; Pred. No. 1.1e-07;
Matches   25; Conservative   5; Mismatches   5; Indels   0; Gaps   0;

Qy   1 MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFW 35
               ||||||||:||| |||:||:||: ::||| ||:|
Db   83 MGPVKQLKKMFETTRLLATIIMLLCLVFTLCAALW 117

Search completed: April 7, 2005, 03:34:39
Job time : 281 secs

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OM protein - protein search, using sw model
Run on:          April 7, 2005, 03:12:32 ; Search time 175 Seconds
                                         (without alignments)
                                         170.175 Million cell updates/sec

Title:          US-10-063-563-56
Perfect score:  410
Sequence:       1 MGPVKQLKRMFEPTRLIATI........LSFIPFARDAVKKCFAVCLA 77
Scoring table:  BLOSUM62

                Gapop 10.0, Gapext 0.5
Searched:       2105692 seqs, 38676038l residues
Total number of hits satisfying chosen parameters:    2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :      A_Geneseq_16Dec04:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result,being printed,
      and is derived by analysis of the total score distribution.
                            SUMMARIES

No.   Score  Match  Length  DB  ID                              Description

RESULT 1
ID   AAY6715 standard; protein; 77 AA.
DE   Membrane-bound protein PRO1027.
PN   WO963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
     Query Match       100.0%;   Score 410; DB 3;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 2
ID   AAU29130 standard; protein; 77 AA.
DE   Human PRO polypeptide sequence #107.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
     Query Match       100.0%;   Score 410; DB 4;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 3
ID   AAB87553 standard; protein; 77 AA.
DE   Human PRO1027.
PN   WO20011618-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
     Query Match       100.0%;   Score 410; DB 4;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 4
ID   AAB65238 standard; protein; 77 AA.
DE   Human PRO1027 (UNQ512) protein sequence SEQ ID NO:283.
PN   WO20007354-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
     Query Match       100.0%;   Score 410; DB 4;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 5
ID   ABG95878 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
     Query Match       100.0%;   Score 410; DB 5;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 6
ID   ABU58506 standard; protein; 77 AA.
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DE   Human PRO polypeptide #107.
PN   US2003027272-A1.
PD   06-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 7
ID   ABU88054 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003032127-A1.
PD   13-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 8
ID   ABU84369 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003033112-A1.
PD   13-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 9
ID   ABR66243 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027278-A1.
PD   06-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 10
ID   ABR65633 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036159-A1.
PD   20-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 11
ID   ABU99573 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040070-A1.
PD   27-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 12
ID   ABU58053 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003027163-A1.
PD   06-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 13
ID   ABU59131 standard; protein; 77 AA.
DE   Novel human secreted or transmembrane protein PRO1027.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 14
ID   ABU82643 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003032023-A1.
PD   13-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 15
ID   ABU82812 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032113-A1.
PD   13-FEB-2003.
     Query Match       100.0%;   Score 410; DB 6;  Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 16
ID   ABU89933 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036147-A1.
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PD   20-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 17
ID   ABR68182 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027264-A1.
PD   06-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 18
ID   ABU60562 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein, #115.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 19
ID   ABU96235 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036144-A1.
PD   20-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 20
ID   ABU92666 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036149-A1.
PD   20-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 21
ID   ABO08743 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044923-A1.
PD   06-MAR-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 22
ID   ABO02795 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040062-A1.
PD   27-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 23
ID   ABR74949 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040056-A1.
PD   27-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 24
ID   ABR94711 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044926-A1.
PD   06-MAR-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 25
ID   ABU13944 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH ) GENENTECH LTD.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 26
ID   ABU5684 standard; protein; 77 AA.
DE.  Human PRO polypeptide #107.
PN   US2003035140-A1.
PD   20-FEB-2003.

PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 27
ID   ABU98844 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003013153-A1.
PD   16-JAN-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 28
ID   ABU98059 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003017544-A1.
PD   23-JAN-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 29
ID   ABU91765 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003022277-A1.
PD   06-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 30
ID   ABU89458 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003036141-A1.
PD   20-FEB-2003.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 31
ID   ABU86299 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 32
ID   ABU67512 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 33
ID   ABU80540 standard; protein; 77 AA.
DE   Human PRO protein #107.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 34
ID   ABU72529 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003003531-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 35
ID   ABU90903 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match     100.0%;   Score 410;  DB 6;   Length 77;
  Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 36
ID   ABO33962 standard; protein; 77 AA.
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DE Human secreted/transmembrane protein PRO1027.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 37
ID ABR99458 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040063-A1.
PD 27-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 38
ID ABR98848 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040064-A1.
PD 27-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 39
ID AB016371 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003027267-A1.
PD 06-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 40
ID ABR92271 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003035160-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 41
ID AB018912 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003044925-A1.
PD 06-MAR-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 42
ID ABR78333 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 410; DB 6; Length'77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 43
ID ABU71979 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 44
ID ABU85069 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032114-A1.
PD 13-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 45
ID AB000208 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032101-A1.
PD 13-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 46
ID AB011540 standard; protein; 77 AA.

DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036124-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 47
ID AB002185 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003040054-A1.
PD 27-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 48
ID ABU88759 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036133-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 49
ID ABU83454 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036134-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 50
ID AB006255 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003022294-A1.
PD 30-JAN-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 51
ID ABR59291 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027275-A1.
PD 06-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 52
ID AB009953 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003027324-A1.
PD 06-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 53
ID AB019217 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 54
ID AB011235 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036123-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 55
ID ABR66853 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003036148-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 56
ID AB016066 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003040060-A1.

PD 27-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 57
ID ABO13772 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003044916-A1.
PD 06-MAR-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 58
ID ABU71533 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
RESULT 59
ID ABU65675 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, SEQ ID 214.
PN US2003036156-A1.
PD 20-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 60
ID ABO07523 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032117-A1.
PD 13-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 61
ID ABO03710 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036128-A1.
PD 20-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 62
ID ABR67158 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027266-A1.
PD 06-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 63
ID ABO15761 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 64
ID ABU56042 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, PRO1027.
PN US2002182638-A1.
PD 05-DEC-2002.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 65
ID ABU72314 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003022298-A1.
PD 30-JAN-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 66
ID ABU65370 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032102-A1.

PD 13-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 67
ID ABU95315 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036117-A1.
PD 20-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 68
ID ABU71218 standard; protein.
DE Human PRO1027 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 69
ID ABO07828 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032130-A1.
PD 13-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 70
ID ABR70069 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
RESULT 71
ID ABR69402 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003036132-A1.
PD 20-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 72
ID ABO01543 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
RESULT 73
ID ABU81345 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003017542-A1.
PD 23-JAN-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 74
ID ABR60142 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032137-A1.
PD 13-FEB-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 75
ID ABU90987 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003018168-A1.
PD 23-JAN-2003.
  Query Match   100.0%;   Score 410; DB 6; Length 77;
  Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 76
ID ABR67877 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027269-A1.

PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 77
ID ABR65265 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 78
ID ABR68487 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 79
ID ABR71899 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 80
ID ABU59278 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, #115.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 81
ID ABU85379 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 82
ID ABU89069 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 83
ID ABU83149 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 84
ID ABU95005 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 85
ID ABU90553 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 86
ID ABU84064 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;

Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 87
ID ABU93715 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 88
ID ABO25975 standard; protein; 77 AA.
DE Human PRO1027 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 89
ID ABR64960 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 90
ID ABO27308 standard; protein; 77 AA.
DE Human secreted/transmembrane polypeptide PRO1027.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 91
ID ABR68792 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 92
ID ABO06608 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 93
ID ABR99153 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 94
ID ABU57037 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 95
ID ABU85989 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;
Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 96
ID ABU82276 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 97
ID ABU87287 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 98
ID ABU3759 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 99
ID ABO08133 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 100
ID ABU92503 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 101
ID ABU81844 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 102
ID ABU66008 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 103
ID ABU1173 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 104
ID ABR59837 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 105
ID ABU94025 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 106
ID ABU99878 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 107
ID ABR66548 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 108
ID ABR90966 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 109
ID ABO53288 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 110
ID ABU58984 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, #115.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 111
ID ABU94393 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 112
ID ABU79275 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 113
ID ABU86604 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 114
ID ABU86909 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 115
ID ABU94698 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 116
ID ABO04625 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

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RESULT 117
ID   ABR70374 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032139-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 118
ID   ABU92362 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003022187-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 119
ID   ABU98539 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003022301-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 120
ID   ABR65938 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 121
ID   ABR64655 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027262-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 122
ID   ABU59427 standard; protein; 77 AA.
DE   Novel human secreted or transmembrane protein PRO1107.
PN   US2003027985-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 123
ID   ABU79580 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032110-Al.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 124
ID   ABU92971 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036142-Al.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 125
ID   ABU5930 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003036145-Al.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 126
ID   ABU1150 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036154-Al.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 127
ID   ABU90243 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036153-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 128
ID   ABO09658 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044931-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 129
ID   ABO10930 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036150-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 130
ID   ABR70984 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040069-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 131
ID   ABU98290 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 132
ID   ABU87592 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003022293-Al.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 133
ID   ABU91460 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003032128-Al.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 134
ID   ABU89295 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 135
ID   ABU84674 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032116-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 136
ID   ABR69764 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032122-Al.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-44;

RESULT 137
ID   ABU80141 standard; protein; 77 AA.
DE   Human PRO protein #107.
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PN   US200303139-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 138
ID   ABU82502 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US200218494-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 139
ID   ABU92193 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US200301747 6-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 140
ID   ABU93410 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US200301 7541-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 141
ID   ABO09963 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US200301 7543-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 142
ID   ABO09048 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US200303 6152-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 143
ID   ABU96466 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US200302 7993-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 144
ID   ABU10899 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US200212463-A1.
PD   05-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 145
ID   ABU10616 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein #107.
PN   US200212 7584-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 146
ID   ABU81651 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US200217 7164-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 147

ID   ABU72136 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US200303 3042-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 148
ID   ABU95625 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US200303 2115-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 149
ID   ABU96834 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US200303 2140-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 150
ID   ABR70679 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US200304 0076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 151
ID   ABO05030 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US200300 8352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 152
ID   ABO08438 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US200304 4922-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 153
ID   ABU88590 standard; protein; 77 AA.
DE   Human secreted and transmembrane polypeptide PRO1027.
PN   US200219 7615-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 154
ID   ABO34104 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US200301 7981-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 155
ID   ABO05645 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US200303 2118-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 156
ID   ABR74034 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US200303 6135-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
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RESULT 157
ID   ABR95626 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 158
ID   ABR80923 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 159
ID   ABR81228 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 160
ID   ABM00924 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 161
ID   ABR88526 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 162
ID   ABM77347 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 163
ID   ABO28831 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 164
ID   ABO31576 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 165
ID   ABM07993 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 166
ID   ABO40473 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 167
ID   ABO35898 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 168
ID   ABO44037 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 169
ID   ADA77966 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 170
ID   ABM24832 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104539-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 171
ID   ABO03100 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036131-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 172
ID   ABR90356 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040075-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 173
ID   ABM17270 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 174
ID   ABR95016 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044930-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 6; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 175
ID   ABR95321 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.

Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 176
ID ADB17113 standard; protein; 77 AA.
DE Human transmembrane PRO polypeptide (SeqID 56).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 177
ID ABO21559 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 178
ID ABR97823 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027-A1.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 179
ID ABR87611 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 180
ID ABM77652 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 181
ID ABM27882 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 182
ID ABM06163 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 183
ID ABM03669 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 184
ID ABM35120 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;

RESULT 185
ID ABM26357 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 186
ID ABO48139 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 187
ID ABR92881 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027-A1.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 188
ID ABO24642 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 189
ID ADA37794 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 190
ID ABM11653 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027-A1.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 191
ID ABM02754 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 192
ID ABM16050 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 193
ID ABO27611 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 410; DB 6; Length 77;
Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 194

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ID   ABM29102 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 195
ID   ABM07078 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 196
ID   ABM21172 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 197
ID   ABM09518 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 198
ID   ABO41388 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 199
ID   ABO36203 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 200
ID   ABO43732 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 201
ID   ABM76432 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104548-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 202
ID   ABM76128 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 203
ID   ABM25747 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.


PN   US2003104542-A1.
PD   05-JUN-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 204
ID   ABM26052 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104543-A1.
PD   05-JUN-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 205
ID   ADA21480 standard; protein; 77 AA.
DE   Human secreted/transmembrane polypeptide PRO1027.
PN   US2003054404-A1.
PD   20-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 206
ID   ABO03405 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036127-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 207
ID   ABO02490 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040061-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 208
ID   ABO44266 standard; protein; 77 AA.
DE   Human secreted/transmembrane polypeptide PRO 1027.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 209
ID   ABR90661 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036130-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 210
ID   ABR73729 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 211
ID   ABO16981 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054470-A1.
PD   20-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 212
ID   ABR94406 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044917-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 213
ID   ABR75913 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 214
ID ABR71289 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 215
ID ABR93186 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 216
ID ABR93491 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 217
ID ADA10267 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, PRO1027.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 218
ID ABR87916 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 219
ID ABO27916 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 220
ID ABO30051 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003064461-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 221
ID ABO3260 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 222
ID ABM04948 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 223
ID ABM08908 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 224
ID ABO36508 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 225
ID ABO35593 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 226
ID ABO39558 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 227
ID ABM10433 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 228
ID ABM11958 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 229
ID ABO52104 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 230
ID ABO52409 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 231
ID ADA19918 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 6; Length 77

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  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 232
ID   ABO23727 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032134-A1.
PD   13-FEB-2003.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 233
ID   ADB17301 standard; protein; 77 AA.
DE   Human transmembrane PRO polypeptide (SeqID 56).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 234
ID   ADA17811 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 235
ID   ABR97213 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 236
ID   ABR87001 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 237
ID   ABM11043 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 238
ID   ABM28187 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 239
ID   ABO32186 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 240
ID   ABM15313 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 241
ID   ABM06468 standard; protein; 77 AA.

DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 242
ID   ABM04279 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 243
ID   ABM22392 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 244
ID   ABM07688 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 245
ID   ABO40778 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 246
ID   ABM35425 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 247
ID   ABM33188 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 248
ID   ABO52714 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 249
ID   ABO50274 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 410;  DB 6;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 250
ID   ABU99268 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040055-A1.
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PD  27-FEB-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 251
ID  ABO04320 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003036164-A1.
PD  20-FEB-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 252
ID  ABO05950 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003044074-A1.
PD  27-FEB-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 253
ID  ABM18490 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003054480-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 254
ID  ADA27919 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein PRO1027.
PN  US2003054359-A1.
PD  20-MAR-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 255
ID  ABR97518 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003059885-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 256
ID  ABR80618 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003049740-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 257
ID  ABM01229 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003049770-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 258
ID  ABR88831 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003073169-A1.
PD  17-APR-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 259
ID  ABM13483 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064457-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 260
ID  ABM20867 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068711-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 261
ID  ABO41998 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049745-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 262
ID  ABO42608 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049751-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 263
ID  ABM10128 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003067478-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 264
ID  ABO38643 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003068773-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 265
ID  ABM32883 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003073185-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 266
ID  ABM22697 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003087373-A1.
PD  08-MAY-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 267
ID  ADA79758 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003073173-A1.
PD  17-APR-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 268
ID  ABM74908 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003096353-A1.
PD  22-MAY-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
    Best Local Similarity  100.0%;   Pred. No. 2.3e-44;
RESULT 269
ID  ABR96298 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003054458-A1.
PD  20-MAR-2003.
    Query Match       100.0%;   Score 410; DB 6; Length 77;
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                Best Local Similarity    100.0%;  Score  410;  DB  6;  Length 77;
                                                  Pred. No.  2.3e-44;
RESULT 270
ID   ABM02449 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 271
ID   ABR86391 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 272
ID   ABR86696 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 273
ID   ABM16660 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 274
ID   ABM29712 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 275
ID   ABO29136 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 276
ID   ABM23917 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 277
ID   ABM33307 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 278
ID   ABM22087 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;


RESULT 279
ID   ABO37728 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 280
ID   ABM28492 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003082715-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 281
ID   ABM28797 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003082716-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 282
ID   ABM66441 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 283
ID   ABM75823 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 284
ID   ABM34103 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096355-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 285
ID   ABM34408 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003100061-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 286
ID   ABO20339 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032125-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 287
ID   ABO21254 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054454-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
                Query Match           100.0%;  Score  410;  DB  6;  Length 77;
                Best Local Similarity 100.0%;   Pred. No.  2.3e-44;
RESULT 288
ID   ABO22169 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054477-A1.
PD   20-MAR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 289
ID   ADA20090 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 290
ID   ABO34194 standard; protein; 77 AA.
DE   Human secreted/transmembrane polypeptide PRO 1027.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 291
ID   ABR96603 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054460-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 292
ID   ADA94499 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003059832-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 293
ID   ABR85781 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049753-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 294
ID   ABR99763 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049763-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 295
ID   ABM00314 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073172-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 296
ID   ABM00619 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003073172-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 297
ID   ABO29746 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068700-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 298


ID   ABM23612 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068736-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 299
ID   ABM29407 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068679-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 300
ID   ABO38338 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068767-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 301
ID   ABO45638 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003073182-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 302
ID   ABM20562 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104557-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 303
ID   ADA81485 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003092121-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 304
ID   ABO16676 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003027276-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 305
ID   ABO18302 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044920-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 306
ID   ABO22729 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003027265-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 6;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 307
ID   ABO23034 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003054461-A1.
PD   20-MAR-2003.
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PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 308
ID  ABR92576 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064446-A1.
PD  03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 309
ID  ABR81533 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003049744-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 310
ID  ABM77957 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003049783-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 311
ID  ABR89746 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003073171-A1.
PD  17-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 312
ID  ABM26662 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003032121-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 313
ID  ABM13788 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003064458-A1.
PD  03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 314
ID  ABO28526 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003064460-A1.
PD  03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 315
ID  ABO30356 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003064464-A1.
PD  03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 316
ID  ABM07383 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068702-A1.
PD  10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Best Local Similarity    100.0%;  Score 410; DB 6;  Length 77;


RESULT 317
ID  ABM03974 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003068734-A1.
PD  10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 318
ID  ABO37118 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003068719-A1.
PD  10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 319
ID  ABO41693 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003068729-A1.
PD  10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 320
ID  ABO35288 standard; protein; 77 AA.
DE  Human PRO polypeptide #107.
PN  US2003068738-A1.
PD  10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 321
ID  ABM25137 standard; protein; 77 AA.
DE  Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN  US2003104540-A1.
PD  05-JUN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 322
ID  ABO47529 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049742-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 323
ID  ABO47834 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049747-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 324
ID  ABO48444 standard; protein; 77 AA.
DE  Human secreted/transmembrane protein (PRO) #107.
PN  US2003049750-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 325
ID  ABO51494 standard; protein; 77 AA.
DE  Human PRO polypeptide #107.
PN  US2003049766-A1.
PD  13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match              100.0%;  Score 410; DB 6;  Length 77;
      Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 326
ID  ABO51799 standard; protein; 77 AA.
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DE   Human PRO polypeptide #107.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 327
ID   ABO50579 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 328
ID   ABR79703 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040059-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 329
ID   ABM16965 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044078-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 330
ID   ABO17997 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044918-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 331
ID   ABO20949 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032132-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 332
ID   ABR96908 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 333
ID   ADA38724 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003059780-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 334
ID   ABM12263 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 335
ID   ABM16355 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;

     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 336
ID   ABM24222 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064441-A1.
PD   03-APR-2003.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 337
ID   ABM14703 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068696-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 338
ID   ABM04584 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 339
ID   ABM06773 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 340
ID   ABM09213 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073174-A1.
PD   17-APR-2003.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 341
ID   ABO39253 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 342
ID   ABM75518 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104545-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 343
ID   ABM25442 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104541-A1.
PD   05-JUN-2003.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 344
ID   ABM19952 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104554-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 410, DB 6;   Length 77;
     Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 345
ID   ABO46858 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
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PN   US2003049762-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 346
ID   ABO47163 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length,77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 347
ID   ADA83283 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 348
ID   ABR71594 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032133-A1.
PD   13-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 349
ID   ABR72204 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003032136-A1.
PD   13-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 350
ID   ABR98543 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036129-A1.
PD   20-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 351
ID   ABO06913 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040053-A1.
PD   27-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 352
ID   ABR84866 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040057-A1.
PD   27-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 353
ID   ABR73424 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054467-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 354
ID   ABR76518 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044932-A1.
PD   06-MAR-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 355
ID   ABR73119 standard; protein; 77 AA.

DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003027270-A1.
PD   06-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 356
ID   ABM18185 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 357
ID   ABO20644 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032126-A1.
PD   13-FEB-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 358
ID   ABO25387 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003054463-A1.
PD   20-MAR-2003
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 359
ID   ABO25692 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003054466-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 360
ID   ABR94101 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059879-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 361
ID   ADA92845 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003060407-A1.
PD   27-MAR-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 362
ID   ABR80008 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049738-A1.
PD   13-MAR-2003.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 363
ID   ABM11348 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064469-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 364
ID   ABO32955 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003064453-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410;  DB 6;   Length 77;
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Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 365
ID   ABO30661 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064466-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 366
ID   ABO30966 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064468-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 367
ID   ABM27272 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068760-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 368
ID   ABM30017 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068769-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 369
ID   ABM05553 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003045700-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 370
ID   ABM15618 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068698-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 371
ID   ABM08603 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068759-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 372
ID   ABO42303 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049748-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 373
ID   ABO38033 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068765-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
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RESULT 374
ID   ABO45943 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049754-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 375
ID   ABM66746 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068688-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 376
ID   ADB20326 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003082767-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 377
ID   ABM19647 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104552-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 378
ID   ABO49359 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049774-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 379
ID   ABO49664 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049775-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 380
ID   ADA78578 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003073181-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 381
ID   ABR88221 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068720-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 382
ID   ADA00387 standard; protein; 77 AA.
DE   Human secreted polypeptide polypeptide PRO 1027.
PN   US2003027992-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 383
ID   ABM26967 standard; protein; 77 AA.
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DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 384
ID   ABM03364 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068763-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 6;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 385
ID   AB039863 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068689-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 386
ID   AB049969 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 387
ID   AB050884 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 388
ID   AB005340 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036126-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 389
ID   ABR74644 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044924-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 390
ID   ABR77123 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044927-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 391
ID   ABM17880 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040072-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 392
ID   ABR95931 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040073-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;

RESULT 393
ID   AB021864 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054475-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 394
ID   AB020034 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003032124-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 395
ID   AB024337 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064467-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 396
ID   ABR86086 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049759-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 397
ID   ABM10738 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 398
ID   ABM76737 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 399
ID   ABR89441 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073170-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 400
ID   ABM12568 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 401
ID   ABM05858 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068717-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;   Pred. No. 2.3e-44;
RESULT 402
ID   AB034983 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.

PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 403
ID   ABM03059 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 404
ID   ABM19037 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 405
ID   ABM19342 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 406
ID   ABO46553 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 407
ID   ABO49054 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 408
ID   ABR69097 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003022273-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 409
ID   ABR89136 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036119-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 410
ID   ABR72509 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036120-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 411
ID   ABR74339 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;

     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 412
ID   ABO18607 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044921-A1.
PD   06-MAR-2003.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 413
ID   ABR80313 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 414
ID   ABM01534 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 415
ID   ABM02144 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 416
ID   ABR87306 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 417
ID   ABM12873 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 418
ID   ABM30627 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 419
ID   ABM24527 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 420
ID   ABO29441 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 7; Length 77;
     Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 421

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ID   AB031271 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 422
ID   ABM14398 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 423
ID   ABM09823 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 424
ID   AB038948 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 425
ID   ABM34713 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104538-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 426
ID   AB051189 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 427
ID   AB004015 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003036158-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 428
ID   AB053190 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003044806-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 429
ID   AB010485 standard; protein; 77 AA.
DE   Human PRO polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036151-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 430
ID   ABR77728 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040067-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
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     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 431
ID   ABR78938 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054456-A1.
PD   20-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 432
ID   AB024032 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 433
ID   ABR93796 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 434
ID   ABM01839 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 435
ID   ABM78262 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 436
ID   ABR90051 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 437
ID   ADA22406 standard; protein; 77 AA.
DE   Human secreted/transmembrane polypeptide PRO1027.
PN   US2003040473-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 438
ID   ABM27577 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 439
ID   ABM13178 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 440
ID   AB031881 standard; protein; 77 AA.
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DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068731-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 441
ID   ABM14093 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068683-A1.
PD   10-APR-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 442
ID   ABM08298 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068754-A1.
PD   10-APR-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 443
ID   ABO40168 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068681-A1.
PD   10-APR-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 444
ID   ABM74603 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096351-A1.
PD   22-MAY-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 445
ID   ABM33798 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096358-A1.
PD   22-MAY-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 446
ID   ABM20257 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104556-A1.
PD   05-JUN-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 447
ID   ABO48749 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 448
ID   ABO22560 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027
PN   US2003017982-A1.
PD   23-JAN-2003.
     Best Local Similarity   100.0%;   Score 410; DB 7; Length 77;
Query Match   100.0%;   Pred. No. 2.3e-44;
RESULT 449
ID   ABR72814 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003036122-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 410; DB 7; Length 77;

     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 450
ID   ABO15456 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 451
ID   ABR85171 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003040065-A1.
PD   27-FEB-2003.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 452
ID   ABO15151 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003044919-A1.
PD   06-MAR-2003.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 453
ID   ABO17286 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003040077-A1.
PD   27-FEB-2003.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 454
ID   ABM17575 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003044928-A1.
PD   06-MAR-2003.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 455
ID   ADA06572 standard; protein; 77 AA.
DE   Human secreted/transmembrane PRO polypeptide #85.
PN   US2003049638-A1.
PD   13-MAR-2003.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 456
ID   ADA39265 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003059782-A1.
PD   27-MAR-2003.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 457
ID   ABR85476 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003049746-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 458
ID   ABM77042 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003054464-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 410; DB 7; Length 77;
     Best Local Similarity   100.0%;   Pred. No. 2.3e-44;
RESULT 459
ID   ABO28221 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003064459-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.

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          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 460
ID   ABM23002 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 461
ID   ABM30322 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068723-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 462
ID   ABM21782 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068741-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 463
ID   ABM21477 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003066744-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 464
ID   ABM15008 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068766-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 465
ID   ABO41083 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068694-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 466
ID   ABO16813 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068715-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 467
ID   ABO37423 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003068726-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 468
ID   ABM75213 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003104544-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;


          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 469
ID   ABM33493 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003096357-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 470
ID   ABO46248 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003049760-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 471
ID   ADA82649 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003049755-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 472
ID   ADB85629 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003049735-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 473
ID   ADB96291 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003054403-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 474
ID   ABM31847 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068680-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 475
ID   ABM31237 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 476
ID   ADB89957 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003054472-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 477
ID   ABM32152 standard; protein; 77 AA.
DE   Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN   US2003068708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          100.0%;  Score 410;  DB 7;  Length 77;
          Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 478
ID   ABM32457 standard; protein; 77 AA.
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DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 479
ID ADB68308 standard; protein; 77 AA.
DE Human PRO1027 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 480
ID ADB68115 standard; protein; 77 AA.
DE Human PRO1027 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 481
ID ABM31542 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 482
ID ABM30932 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 483
ID ADB90932 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 484
ID ADC57763 standard; protein; 77 AA.
DE Human PRO polypeptide #85.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 485
ID ADC55127 standard; protein; 77 AA.
DE Human PRO polypeptide #85.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 486
ID ADC11994 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 487
ID ADC07012 standard; protein; 77 AA.
DE Human PRO1027 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 488
ID ADC56416 standard; protein; 77 AA.
DE Human PRO polypeptide #85.
PN US2003064375-A1.
PD 03-APR-2003.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 489
ID ADC17191 standard; protein; 77 AA.
DE Mammalian PRO polypeptide (SeqID 56).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 490
ID ADC07471 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003068647-A1.
PD 10-APR-2003.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 491
ID ADC11461 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003069403-A1.
PD 10-APR-2003.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 492
ID ADC14889 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 493
ID ADC52384 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 494
ID ADC14583 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003082546-A1.
PD 01-MAY-2003.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 495
ID ADD08115 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003068623-A1.
PD 10-APR-2003.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 496
ID ADC81940 standard; protein; 77 AA.
DE Human PRO polypeptide #85.
PN US2003083461-A1.
PD 01-MAY-2003.
    Query Match   100.0%; Score 410; DB 7; Length 77;
    Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 497
ID ADD07582 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2002193299-A1.
PD 19-DEC-2002.

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PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 498
ID   ADC82473 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003059833-A1.
PD   27-MAR-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 499
ID   ADD05687 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 500
ID   ADD08653 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003073090-A1.
PD   17-APR-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 501
ID   ADD06902 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 502
ID   ADC83149 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003059783-A1.
PD   27-MAR-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 503
ID   ADD55256 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003077593-A1.
PD   24-APR-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 504
ID   ADD36060 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 505
ID   ADD56214 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003077594-A1.
PD   24-APR-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 506
ID   ADD54652 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2002112253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 507
ID   ADE26806 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.

PN   US2003087304-A1.
PD   08-MAY-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 508
ID   ADE26273 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003087305-A1.
PD   08-MAY-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 509
ID   ADF67210 standard; protein; 77 AA.
DE   Human PRO1027 amino acid sequence SEQ ID NO:283.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 510
ID   ADG01061 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 511
ID   ADG08614 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 512
ID   ADG02682 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 513
ID   ADG01389 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 514
ID   ADF95564 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 515
ID   ADF95235 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
     Best Local Similarity 100.0%;  Pred. No. 2.3e-44;
RESULT 516
ID   ADG12379 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207392-A1.
PD   06-NOV-2003.
     Query Match         100.0%;   Score 410; DB 7;   Length 77;
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        Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 517
ID   ADH24088 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180918-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 518
ID   ADH34114 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180858-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 519
ID   ADH29947 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180859-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 520
ID   ADH23918 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180919-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 521
ID   ADH09039 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 522
ID   ADG85322 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180904-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 523
ID   ADH24598 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180907-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 524
ID   ADH37454 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 525
ID   ADH02043 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180837-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;

RESULT 526
ID   ADH37624 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 527
ID   ADG85662 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180905-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 528
ID   ADH24258 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180914-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 529
ID   ADH38552 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181643-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 530
ID   ADG83673 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180794-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 531
ID   ADH29481 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180860-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 532
ID   ADH27597 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180906-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 533
ID   ADH37794 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181647-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 534
ID   ADH37971 standard; protein; 77 AA.
DE   Human secreted and transmembrane protein PRO1027.
PN   US2003181649-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;  Score 410; DB 7; Length 77;
     Best Local Similarity    100.0%;  Pred. No. 2.3e-44;
RESULT 535
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ID   ADH57391 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180920-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 536
ID   ADH53533 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181636-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 537
ID   ADH53703 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181641-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 538
ID   ADH52039 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181638-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 539
ID   ADH49894 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181639-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 540
ID   ADI25404 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181696-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 541
ID   ADH90197 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181698-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 542
ID   ADI25574 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181669-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 543
ID   ADH97748 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181672-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 544
ID   ADI35464 standard; protein; 77 AA.
DE   Human PRO polypeptide #85.
PN   US2003050457-A1.
PD   13-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 545
ID   ADI03596 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181656-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 546
ID   ADI11953 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181686-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 547
ID   ADH90027 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181697-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 548
ID   ADH99956 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003049682-A1.
PD   13-MAR-2003.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 549
ID   ADH98428 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181707-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 550
ID   ADI11103 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181682-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 551
ID   ADI11613 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181684-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 552
ID   ADH98258 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181709-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 410;  DB 7;  Length 77;
     Best Local Similarity   100.0%;  Pred. No. 2.3e-44;
RESULT 553
ID   ADH98598 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181708-A1.
PD   25-SEP-2003.
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RESULT 554
ID ADH98088 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 555
ID ADI05076 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 556
ID ADI03426 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 557
ID ADI04821 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 558
ID ADH78275 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 559
ID ADI19619 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 560
ID ADH90367 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 561
ID ADI03086 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 562
ID ADH77935 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 563
ID ADH97918 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 564
ID ADI01303 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 565
ID ADI01998 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 566
ID ADI03256 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 567
ID ADI11443 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 568
ID ADI02345 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 569
ID ADI11783 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 570
ID ADI05420 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 571
ID ADH79492 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 7; Length 77;

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        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 572
ID   ADI9449 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181675-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 573
ID   ADI05250 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181677-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 574
ID   ADH79662 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003191288-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 575
ID   ADI01488 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 576
ID   ADI01658 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 577
ID   ADI01828 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 578
ID   ADH79832 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003191289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 579
ID   ADI04650 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 580
ID   ADI02786 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;

RESULT 581
ID   ADH78105 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 582
ID   ADI25744 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 583
ID   ADI25914 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 584
ID   ADK65426 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 585
ID   ADH98768 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 586
ID   ADH80009 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 587
ID   ADL32820 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 588
ID   ADM30354 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 589
ID   ADL93740 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
        Query Match             100.0%;  Score 410;  DB 7;  Length 77;
        Best Local Similarity  100.0%;  Pred. No. 2.3e-44;
RESULT 590
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ID   ADC52194 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003110483-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 591
ID   ADE74351 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003211572-A1.
PD   13-NOV-2003.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 592
ID   ADE74963 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein (PRO) #107.
PN   US2003211574-A1.
PD   13-NOV-2003.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 593
ID   ADF35409 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003194760-A1.
PD   16-OCT-2003.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 594
ID   ADF11659 standard; protein; 77 AA.
DE   Human PRO1027 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 595
ID   ADF96176 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003215909-A1.
PD   20-NOV-2003.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 596
ID   ADG04447 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003215912-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 597
ID   ADG00607 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003215911-A1.
PD   20-NOV-2003.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 598
ID   ADH06626 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180852-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 599
ID   ADH06456 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 600
ID   ADG68877 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 601
ID   ADH27767 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 602
ID   ADH25108 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 603
ID   ADH33740 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181645-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 604
ID   ADG82863 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2003215910-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 605
ID   ADH02383 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180839-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 606
ID   ADH07990 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180845-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 607
ID   ADG69387 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;
     Best Local Similarity   100.0%; Pred. No. 2.3e-44;
RESULT 608
ID   ADH39208 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180917-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 410; DB 8; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 609
ID ADH26144 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 610
ID ADG83948 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 611
ID ADH19529 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 612
ID ADG85492 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 613
ID ADH06286 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 614
ID ADH30116 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 615
ID ADH24428 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 616
ID ADH33113 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003180910-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 617
ID ADG69557 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 618
ID ADH07820 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 619
ID ADG85832 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 620
ID ADH39378 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 621
ID ADH33570 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 622
ID ADH33910 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 623
ID ADH01120 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 624
ID ADG69727 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 625
ID ADH21022 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 626
ID ADH02213 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 627
ID ADG69217 standard; protein; 77 AA.

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DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180847-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 628
ID   ADG86002 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180862-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 629
ID   ADH24938 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180909-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 630
ID   ADH39555 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180915-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 631
ID   ADH20062 standard; protein; 77 AA.
DE   Human secreted/transmembrane protein PRO1027.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 632
ID   ADH02553 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003180840-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 633
ID   ADG69047 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180849-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 634
ID   ADH07650 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180850-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 635
ID   ADG86172 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180863-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 636
ID   ADH24768 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.


PN   US2003180908-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 637
ID   ADH25816 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180911-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 638
ID   ADH38382 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180922-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 639
ID   ADH57221 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181642-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 640
ID   ADH52208 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180921-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 641
ID   ADH49575 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003180857-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 642
ID   ADH90537 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181700-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 643
ID   ADI11273 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003181683-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 644
ID   ADH98938 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003190698-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 410;   DB 8;   Length 77;
     Best Local Similarity   100.0%;    Pred. No. 2.3e-44;
RESULT 645
ID   ADI02168 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003190699-A1.
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PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 646
ID   ADH90707 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 647
ID   ADJ54852 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2004023321-A1.
PD   05-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 648
ID   ADJ98582 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 649
ID   ADH78911 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 650
ID   ADJ99145 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 651
ID   ADJ99315 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 652
ID   ADJ98933 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 653
ID   ADH79081 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003181702-A1.
PD   25-SEP-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 655
ID   ADK00941 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2003186407-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 656
ID   ADK14462 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2003187229-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 657
ID   ADJ64623 standard; protein; 77 AA.
DE   Human PRO polypeptide #107.
PN   US2004038337-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 658
ID   ADM31519 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004048334-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 659
ID   ADM36566 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004053358-A1.
PD   18-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 660
ID   ADM40371 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004048335-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 661
ID   ADM80911 standard; protein; 77 AA.
DE   Human PRO polypeptide #28.
PN   US2004058411-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 662
ID   ADN37979 standard; protein; 77 AA.
DE   Novel human secreted and transmembrane protein PRO1027.
PN   US2004091959-A1.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 410;   DB 8;   Length 77;
     Best Local Similarity    100.0%;   Pred. No. 2.3e-44;
RESULT 663
ID   AAB12126 standard; protein; 160 AA.
DE   Hydrophobic domain protein isolated from HT-1080 cells.
PN   WO200029448-A2.
PD   25-MAY-2000.
PA   (SAGA ) SAGAMI CHEM RES CENT.
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PA (PROT-) PROTEGENE INC.
    Query Match   100.0%; Score 410; DB 3; Length 160;
    Best Local Similarity 100.0%; Pred. No. 5.2e-44;
RESULT 664
ID ABB11987 standard; peptide; 170 AA.
DE Human secreted protein homologue, SEQ ID NO:2357.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   100.0%; Score 410; DB 4; Length 170;
    Best Local Similarity 100.0%; Pred. No. 5.5e-44;
RESULT 665
ID AAY35997 standard; protein; 160 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 382.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
    Query Match   98.5%; Score 404; DB 2; Length 160;
    Best Local Similarity 98.7%; Pred. No. 3e-43;
RESULT 666
ID ADP19305 standard; protein; 160 AA.
DE Human secreted polypeptide #156.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
    Query Match   98.5%; Score 404; DB 8; Length 160;
    Best Local Similarity 98.7%; Pred. No. 3e-43;
RESULT 667
ID ABP75976 standard; protein; 77 AA.
DE Human GENSET protein SEQ ID 183.
PN WO20028389B-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
    Query Match   96.1%; Score 394; DB 6; Length 77;
    Best Local Similarity 97.4%; Pred. No. 2.5e-42;
RESULT 668
ID ABP76142 standard; protein; 77 AA.
DE Human GENSET protein SEQ ID 468.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
    Query Match   96.1%; Score 394; DB 6; Length 77;
    Best Local Similarity 97.4%; Pred. No. 2.5e-42;
RESULT 669
ID ABB89647 standard; protein; 124 AA.
DE Human polypeptide SEQ ID NO 2023.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   74.6%; Score 306; DB 5; Length 124;
    Best Local Similarity 70.1%; Pred. No. 7.1e-31;
RESULT 670
ID AAM39275 standard; protein; 159 AA.
DE Human polypeptide SEQ ID NO 2420.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   74.6%; Score 306; DB 4; Length 159;
    Best Local Similarity 70.1%; Pred. No. 9.4e-31;
RESULT 671
ID AAG89299 standard; protein; 159 AA.
DE Human secreted protein, SEQ ID NO: 419.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST) GENSET.
    Query Match   74.6%; Score 306; DB 4; Length 159;
    Best Local Similarity 70.1%; Pred. No. 9.4e-31;
RESULT 672
ID ADP55700 standard; protein; 159 AA.
DE Human PRO protein sequence SEQ ID NO:1676.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match   74.6%; Score 306; DB 8; Length 159;
Best Local Similarity 70.1%; Pred. No. 9.4e-31;
RESULT 673
ID AAM41061 standard; protein; 203 AA.
DE Human polypeptide SEQ ID NO 5992.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   74.6%; Score 306; DB 4; Length 203;
    Best Local Similarity 70.1%; Pred. No. 1.2e-30;
RESULT 674
ID ADF76452 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein SeqID 126.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   72.7%; Score 298; DB 7; Length 178;
    Best Local Similarity 68.8%; Pred. No. 1.1e-29;
RESULT 675
ID ADR14033 standard; protein; 178 AA.
DE Human NF-kappaB pathway-associated protein SeqID34.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
    Query Match   72.7%; Score 298; DB 8; Length 178;
    Best Local Similarity 68.8%; Pred. No. 1.1e-29;
RESULT 676
ID ABB71351 standard; protein; 163 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40845.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   58.5%; Score 240; DB 4; Length 163;
    Best Local Similarity 61.8%; Pred. No. 2.5e-22;
RESULT 677
ID AAY31835 standard; protein; 179 AA.
DE Human foetal kidney secreted protein pk266_4.
PN WO947555-A1.
PD 23-SEP-1999.
PA (GEMY) GENETICS INST INC.
    Query Match   52.7%; Score 216; DB 2; Length 179;
    Best Local Similarity 74.5%; Pred. No. 3.3e-19;
RESULT 678
ID AAG41866 standard; protein; 126 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52142.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   35.9%; Score 147; DB 3; Length 126;
    Best Local Similarity 41.4%; Pred. No. 1.4e-10;
RESULT 679
ID AAG41865 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52141.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   35.9%; Score 147; DB 3; Length 163;
    Best Local Similarity 41.4%; Pred. No. 1.9e-10;
RESULT 680
ID AAG41864 standard; protein; 165 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52140.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   35.9%; Score 147; DB 3; Length 165;
    Best Local Similarity 41.4%; Pred. No. 1.9e-10;
RESULT 681
ID AAG52603 standard; protein; 573 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66888.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   21.0%; Score 86; DB 3; Length 573;
    Best Local Similarity 32.8%; Pred. No. 0.046;
RESULT 682
ID AAG52602 standard; protein; 663 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66887.

PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   21.0%;   Score 86;   DB 3; Length 663;
  Best Local Similarity 32.8%; Pred. No. 0.055;
RESULT 683
ID AAG52601 standard; protein; 717 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66886.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   21.0%;   Score 86;   DB 3; Length 717;
  Best Local Similarity 32.8%; Pred. No. 0.06;
RESULT 684
ID AAG36124 standard; protein; 135 AA.
DE Zea mays protein fragment SEQ ID NO: 44225.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   20.6%;   Score 84.5; DB 3; Length 135;
  Best Local Similarity 30.5%; Pred. No. 0.014;
RESULT 685
ID AAG36123 standard; protein; 225 AA.
DE Zea mays protein fragment SEQ ID NO: 44224.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   20.6%;   Score 84.5; DB 3; Length 225;
  Best Local Similarity 30.5%; Pred. No. 0.025;
RESULT 686
ID AAG36122 standard; protein; 252 AA.
DE Zea mays protein fragment SEQ ID NO: 44223.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   20.6%;   Score 84.5; DB 3; Length 252;
  Best Local Similarity 30.5%; Pred. No. 0.028;
RESULT 687
ID AAG47038 standard; protein; 220 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59244.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   20.6%;   Score 84.5; DB 3; Length 220;
  Best Local Similarity 30.5%; Pred. No. 0.038;
RESULT 688
ID AAG47037 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59243.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   20.2%;   Score 83;   DB 3; Length 227;
  Best Local Similarity 30.9%; Pred. No. 0.039;
RESULT 689
ID AAG47036 standard; protein; 230 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59242.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   20.2%;   Score 83;   DB 3; Length 230;
  Best Local Similarity 30.9%; Pred. No. 0.04;
RESULT 690
ID ABM67329 standard; protein; 1175 AA.
DE Photorhabdus luminescens protein sequence #426.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
  Query Match   19.9%;   Score 81.5; DB 6; Length 1175;
  Best Local Similarity 31.6%; Pred. No. 0.39;
RESULT 691
ID ABU28937 standard; protein; 1158 AA.
DE Protein encoded by Prokaryotic essential gene #14464.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match   19.8%;   Score 81;   DB 6; Length 1158;
  Best Local Similarity 32.9%; Pred. No. 0.45;
RESULT 692
ID AAG30733 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36795.

PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   19.3%;   Score 79;   DB 3; Length 381;
  Best Local Similarity 27.3%; Pred. No. 0.23;
RESULT 693
ID AAG30732 standard; protein; 383 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36794.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   19.3%;   Score 79;   DB 3; Length 383;
  Best Local Similarity 27.3%; Pred. No. 0.23;
RESULT 694
ID AAG30731 standard; protein; 385 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36793.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match   19.3%;   Score 79;   DB 3; Length 385;
  Best Local Similarity 27.3%; Pred. No. 0.23;
RESULT 695
ID ABG30126 standard; protein; 1067 AA.
DE Novel human diagnostic protein #30117.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match   17.6%;   Score 72;   DB 4; Length 1067;
  Best Local Similarity 31.3%; Pred. No. 5.7;
RESULT 696
ID ABG29905 standard; protein; 1222 AA.
DE Novel human diagnostic protein #29896.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match   17.6%;   Score 72;   DB 4; Length 1222;
  Best Local Similarity 31.3%; Pred. No. 6.7;
RESULT 697
ID ABG15851 standard; protein; 1222 AA.
DE Novel human diagnostic protein #15842.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match   17.6%;   Score 72;   DB 4; Length 1222;
  Best Local Similarity 31.3%; Pred. No. 6.7;
RESULT 698
ID ABB68652 standard; protein; 1006 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32748.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
  Query Match   17.2%;   Score 70.5; DB 4; Length 1006;
  Best Local Similarity 29.2%; Pred. No. 8.3;
RESULT 699
ID AAU10558 standard; protein; 360 AA.
DE Human interleukin 8 receptor beta (IL8RB) variant polypeptide.
PN WO200179221-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISSANCE PHARM INC.
  Query Match   16.6%;   Score 68;   DB 5; Length 360;
  Best Local Similarity 22.6%; Pred. No. 5.4;
RESULT 700
ID ABO65182 standard; protein; 404 AA.
DE Klebsiella pneumoniae polypeptide seqid 11699.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   16.2%;   Score 66.5; DB 7; Length 404;
  Best Local Similarity 26.9%; Pred. No. 9.6;
RESULT 701
ID ABU31563 standard; protein; 263 AA.
DE Protein encoded by Prokaryotic essential gene #17090.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match   16.1%;   Score 66;   DB 6; Length 263;

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Best Local Similarity   37.5%;   Pred. No. 6.8;
RESULT 702
ID   ABO65873 standard; protein; 289 AA.
DE   Klebsiella pneumoniae polypeptide seqid 12390.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match      16.1%;   Score 66;   DB 7;   Length 289;
Best Local Similarity   37.5%;   Pred. No. 7.6;
RESULT 703
ID   AAB41282 standard; protein; 107 AA.
DE   Human ORFX ORF1046 polypeptide sequence SEQ ID NO:2092.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
Query Match      15.9%;   Score 65;   DB 3;   Length 107;
Best Local Similarity   28.8%;   Pred. No. 3.3;
RESULT 704
ID   ABU18961 standard; protein; 484 AA.
DE   Protein encoded by Prokaryotic essential gene #4488.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match      15.9%;   Score 65;   DB 6;   Length 484;
Best Local Similarity   33.3%;   Pred. No. 18;
RESULT 705
ID   ADF75261 standard; protein; 575 AA.
DE   Thale cress protein essential for plant growth and development SeqID78.
PN   WO2003074653-A2.
PD   12-SEP-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match      15.7%;   Score 64.5;   DB 7;   Length 575;
Best Local Similarity   26.0%;   Pred. No. 26;
RESULT 706
ID   AB059218 standard; protein; 278 AA.
DE   Human genome derived single exon protein #5452.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
Query Match      15.6%;   Score 64;   DB 8;   Length 278;
Best Local Similarity   22.1%;   Pred. No. 13;
RESULT 707
ID   ABO75371 standard; protein; 416 AA.
DE   Pseudomonas aeruginosa polypeptide #7546.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match      15.7%;   Score 64;   DB 7;   Length 416;
Best Local Similarity   26.0%;   Pred. No. 21;
RESULT 708
ID   ABG10021 standard; protein; 546 AA.
DE   Novel human diagnostic protein #10012.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match      15.6%;   Score 64;   DB 4;   Length 546;
Best Local Similarity   38.2%;   Pred. No. 28;
RESULT 709
ID   ADM87619 standard; protein; 546 AA.
DE   Human EST derived amino acid sequence SEQ ID NO:712.
PN   WO2004009834-A2.
PD   29-JAN-2004.
PA   (NUVE-) NUVELO INC.
Query Match      15.6%;   Score 64;   DB 8;   Length 546;
Best Local Similarity   22.1%;   Pred. No. 28;
RESULT 710
ID   ADG74252 standard; protein; 599 AA.
DE   Mouse frizzled protein, SEQ ID No 37.
PN   WO200292635-A2.
PD   21-NOV-2002.
PA   (REGC ) UNIV CALIFORNIA.

Query Match      15.6%;   Score 64;   DB 7;   Length 599;
Best Local Similarity   22.1%;   Pred. No. 31;
RESULT 711
ID   ADC12742 standard; protein; 619 AA.
DE   Human GPCR protein, SEQ ID NO 74.
PN   WO2003000893-A2.
PD   03-JAN-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match      15.6%;   Score 64;   DB 7;   Length 619;
Best Local Similarity   22.1%;   Pred. No. 32;
RESULT 712
ID   AAW31274 standard; protein; 685 AA.
DE   Mouse frizzled-8 protein Mfz8 (Wnt receptor).
PN   WO9739357-A1.
PD   23-OCT-1997.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (UYJO ) UNIV JOHNS HOPKINS.
Query Match      15.6%;   Score 64;   DB 2;   Length 685;
Best Local Similarity   22.1%;   Pred. No. 36;
RESULT 713
ID   ADG74272 standard; protein; 685 AA.
DE   Mouse frizzled protein, SEQ ID No 57.
PN   WO200292635-A2.
PD   21-NOV-2002.
PA   (REGC ) UNIV CALIFORNIA.
Query Match      15.6%;   Score 64;   DB 7;   Length 685;
Best Local Similarity   22.1%;   Pred. No. 36;
RESULT 714
ID   ADO29340 standard; protein; 685 AA.
DE   Mouse GPCR FZD8, SEQ ID NO:441.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
Query Match      15.6%;   Score 64;   DB 8;   Length 685;
Best Local Similarity   22.1%;   Pred. No. 36;
RESULT 715
ID   AAU74823 standard; protein; 694 AA.
DE   Human REPTR 6 protein.
PN   WO200198354-A2.
PD   27-DEC-2001.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match      15.6%;   Score 64;   DB 5;   Length 694;
Best Local Similarity   22.1%;   Pred. No. 37;
RESULT 716
ID   ABU55903 standard; protein; 694 AA.
DE   Human protein Frizzled-8.
PN   WO200277204-A2.
PD   03-OCT-2002.
PA   (AXOR-) AXORDIA LTD.
Query Match      15.6%;   Score 64;   DB 6;   Length 694;
Best Local Similarity   22.1%;   Pred. No. 37;
RESULT 717
ID   ADB75320 standard; protein; 694 AA.
DE   Prostate cancer marker protein.
PN   WO2003009814-A2.
PD   06-FEB-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match      15.6%;   Score 64;   DB 7;   Length 694;
Best Local Similarity   22.1%;   Pred. No. 37;
RESULT 718
ID   ADG74271 standard; protein; 694 AA.
DE   Human frizzled protein, SEQ ID No 56.
PN   WO200292635-A2.
PD   21-NOV-2002.
PA   (REGC ) UNIV CALIFORNIA.
Query Match      15.6%;   Score 64;   DB 7;   Length 694;
Best Local Similarity   22.1%;   Pred. No. 37;
RESULT 719
ID   ADN40026 standard; protein; 694 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C396.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
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Query Match          15.6%;   Score 64;   DB 7;   Length 694;
Best Local Similarity 22.1%;   Pred. No. 37;
RESULT 720
ID   ADM87157 standard; protein; 694 AA.
DE   Human protein SEQ ID NO:250.
PN   WO2004009834-A2.
PD   29-JAN-2004.
PA   (NUVE-) NUVELO INC.
RESULT 721
Query Match          15.6%;   Score 64;   DB 8;   Length 694;
Best Local Similarity 22.1%;   Pred. No. 37;
ID   ADO29339 standard; protein; 694 AA.
DE   Human GPCR FZD8, SEQ ID NO:440.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
RESULT 722
Query Match          15.6%;   Score 64;   DB 8;   Length 694;
Best Local Similarity 22.1%;   Pred. No. 37;
ID   ADO22266 standard; protein; 694 AA.
DE   Human FZD8 protein (homologue of Drosophila frizzled).
PN   WO2004042028-A2.
PD   21-MAY-2004.
PA   (REGC ) UNIV CALIFORNIA.
RESULT 723
Query Match          15.6%;   Score 64;   DB 8;   Length 694;
Best Local Similarity 22.1%;   Pred. No. 37;
ID   ADR46693 standard; protein; 694 AA.
DE   Cancer-associated protein, SEQ ID 106.
PN   WO2004073657-A2.
PD   02-SEP-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
RESULT 724
Query Match          15.6%;   Score 64;   DB 8;   Length 694;
Best Local Similarity 22.1%;   Pred. No. 37;
ID   ABG24617 standard; protein; 403 AA.
DE   Novel human diagnostic protein #24608.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 725
Query Match          15.5%;   Score 63.5;   DB 4;   Length 403;
Best Local Similarity 29.5%;   Pred. No. 23;
ID   AAU58372 standard; protein; 409 AA.
DE   Propionibacterium acnes immunogenic protein #19266.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
RESULT 726
Query Match          15.5%;   Score 63.5;   DB 4;   Length 409;
Best Local Similarity 33.3%;   Pred. No. 23;
ID   ABM54891 standard; protein; 409 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #19567.
PN   WO200303515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
RESULT 727
Query Match          15.5%;   Score 63.5;   DB 6;   Length 409;
Best Local Similarity 33.3%;   Pred. No. 23;
ID   ABP38658 standard; protein; 74 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3503.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
RESULT 728
Query Match          15.4%;   Score 63;   DB 5;   Length 74;
Best Local Similarity 36.5%;   Pred. No. 3.9;
ID   ADS05168 standard; protein; 74 AA.
DE   Staphylococcus epidermis polypeptide seqid 4463.
PN   US2004147734-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
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Query Match          15.4%;   Score 63;   DB 8;   Length 74;
Best Local Similarity 36.5%;   Pred. No. 3.9;
RESULT 729
ID   AAO02082 standard; protein; 71 AA.
DE   Human polypeptide SEQ ID NO 15974.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 730
Query Match          15.2%;   Score 62.5;   DB 4;   Length 71;
Best Local Similarity 25.0%;   Pred. No. 4.4;
ID   ABU45593 standard; protein; 412 AA.
DE   Protein encoded by Prokaryotic essential gene #31120.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 731
Query Match          15.2%;   Score 62.5;   DB 6;   Length 412;
Best Local Similarity 26.6%;   Pred. No. 32;
ID   ABU48248 standard; protein; 438 AA.
DE   Protein encoded by Prokaryotic essential gene #33775.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 732
Query Match          15.2%;   Score 62.5;   DB 6;   Length 438;
Best Local Similarity 26.6%;   Pred. No. 34;
ID   AAU07131 standard; protein; 2402 AA.
DE   Porcine reproductive and respiratory virus, PRRSV, ORF1a.
PN   WO200159077-A1.
PD   16-AUG-2001.
PA   (MINU ) UNIV MINNESOTA.
PA   (COLL/) COLLINS J E.
PA   (FAAB/) FAABERG K S.
PA   (ROSS/) ROSSOW K D.
RESULT 733
Query Match          15.2%;   Score 62.5;   DB 4;   Length 2402;
Best Local Similarity 30.1%;   Pred. No. 2.3e+02;
ID   ADC87597 standard; protein; 280 AA.
DE   Human GPCR protein SEQ ID NO:2050.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
RESULT 734
Query Match          15.1%;   Score 62;   DB 7;   Length 280;
Best Local Similarity 26.1%;   Pred. No. 24;
ID   AAW29662 standard; protein; 366 AA.
DE   Homo sapiens CN483_2 clone secreted protein.
PN   WO9830695-A2.
PD   16-JUL-1998.
PA   (GEMY ) GENETICS INST INC.
RESULT 735
Query Match          15.1%;   Score 62;   DB 2;   Length 366;
Best Local Similarity 24.2%;   Pred. No. 32;
ID   AAY02384 standard; protein; 551 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 974.
PN   WO200028876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 736
Query Match          15.1%;   Score 62;   DB 2;   Length 551;
Best Local Similarity 24.2%;   Pred. No. 51;
ID   ABP75790 standard; protein; 565 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 974.
PN   WO200028876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 737
Query Match          15.1%;   Score 62;   DB 6;   Length 565;
Best Local Similarity 24.2%;   Pred. No. 53;
ID   AAB18975 standard; protein; 578 AA.
DE   Amino acid sequence of a human transmembrane protein.
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PN   WO20056891-A2.
PD   28-SEP-2000.
PA   (INCY-) INCYTE PHARM INC.
     Query Match   15.1%;   Score 62;   DB 3;   Length 578;
     Best Local Similarity   24.2%;   Pred. No. 54;
RESULT 738
ID   AAE34057 standard; protein; 694 AA.
DE   FZD 8 protein.
PN   WO20290992-A2.
PD   14-NOV-2002.
PA   (AXOR-) AXORDIA LTD.
     Query Match   15.1%;   Score 62;   DB 6;   Length 694;
     Best Local Similarity   22.1%;   Pred. No. 66;
RESULT 739
ID   ABB17549 standard; protein; 92 AA.
DE   Human nervous system related polypeptide SEQ ID NO 6206.
PN   WO20159063-A2.
PD   16-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   15.0%;   Score 62;   DB 4;   Length 92;
     Best Local Similarity   35.3%;   Pred. No. 7.8;
RESULT 740
ID   AAG72963 standard; protein; 316 AA.
DE   Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2645.
PN   WO20127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   15.0%;   Score 61.5;   DB 4;   Length 316;
     Best Local Similarity   21.2%;   Pred. No. 32;
RESULT 741
ID   ABM67481 standard; protein; 320 AA.
DE   Photorhabdus luminescens protein sequence #578.
PN   WO20294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   15.0%;   Score 61.5;   DB 6;   Length 820;
     Best Local Similarity   27.0%;   Pred. No. 32;
RESULT 742
ID   ABO19498 standard; protein; 326 AA.
DE   Mouse GPCR MOR 3' Beta 1.
PN   US200412130-A1.
PD   24-JUN-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
PA   (CACA/) CACACE A.
PA   (BARB/) BARBER L.
PA   (KORN/) KORNACKER M G.
     Query Match   15.0%;   Score 61.5;   DB 6;   Length 326;
     Best Local Similarity   21.2%;   Pred. No. 33;
RESULT 743
ID   ADQ98156 standard; protein; 326 AA.
DE   Mouse olfactory receptor 3' beta 1.
PN   US2004121130-A1.
PD   30-JAN-2003.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G A.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
PA   (CACA/) CACACE A.
PA   (BARB/) BARBER L E.
PA   (KORN/) KORNACKER M G.
PA   (RYSE/) RYSECK R.
PA   (BENN/) BENNETT K L.
PA   (NELS/) NELSON T C.
     Query Match   15.0%;   Score 61.5;   DB 8;   Length 326;
     Best Local Similarity   21.2%;   Pred. No. 33;
RESULT 744
ID   AAG72618 standard; protein; 339 AA.
DE   Murine OR-like polypeptide query sequence, SEQ ID NO: 2299.

PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   15.0%;   Score 61.5;   DB 4;   Length 339;
     Best Local Similarity   21.2%;   Pred. No. 34;
RESULT 745
ID   ABU28157 standard; protein; 417 AA.
DE   Protein encoded by Prokaryotic essential gene #13684.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   15.0%;   Score 61.5;   DB 6;   Length 417;
     Best Local Similarity   34.5%;   Pred. No. 43;
RESULT 746
ID   ABB53979 standard; protein; 420 AA.
DE   Lactococcus lactis protein ftsW1.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   15.0%;   Score 61.5;   DB 5;   Length 420;
     Best Local Similarity   25.3%;   Pred. No. 44;
RESULT 747
ID   ABO76137 standard; protein; 464 AA.
DE   Pseudomonas aeruginosa polypeptide #8312.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   15.0%;   Score 61.5;   DB 7;   Length 464;
     Best Local Similarity   25.4%;   Pred. No. 49;
RESULT 748
ID   AAR29939 standard; protein; 2396 AA.
DE   Deduced from Lelystad Agent genome ORF 1A.
PN   WO9221375-A1.
PD   10-DEC-1992.
PA   (DIER-) STICHTING CENT DIERGENEESKUNDIG INST.
     Query Match   15.0%;   Score 61.5;   DB 2;   Length 2396;
     Best Local Similarity   30.1%;   Pred. No. 3.1e+02;
RESULT 749
ID   ADH74482 standard; protein; 3859 AA.
DE   Lelystad virus ORFlab protein.
PN   US2003219732-A1.
PD   27-NOV-2003.
PA   (VRIJ/) VAN RIJN P A.
PA   (MEUL/) MEULENBERG J J M.
     Query Match   15.0%;   Score 61.5;   DB 8;   Length 3859;
     Best Local Similarity   30.1%;   Pred. No. 5.3e+02;
RESULT 750
ID   ABP75625 standard; protein; 72 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 809.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   14.9%;   Score 61;   DB 6;   Length 72;
     Best Local Similarity   35.3%;   Pred. No. 6.9;
RESULT 751
ID   ABB81433 standard; protein; 118 AA.
DE   Human prostate specific protein (PSP) SEQ ID NO:205.
PN   WO20024299-A2.
PD   30-MAY-2002.
PA   (DIAD-) DIADEXUS INC.
     Query Match   14.9%;   Score 61;   DB 5;   Length 118;
     Best Local Similarity   34.0%;   Pred. No. 12;
RESULT 752
ID   ADC87275 standard; protein; 306 AA.
DE   Human GPCR protein SEQ ID NO:1728.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match   14.9%;   Score 61;   DB 7;   Length 306;
     Best Local Similarity   25.6%;   Pred. No. 35;
RESULT 753

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ID   ADC01153 standard; protein; 373 AA.
DE   Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1197.
PN   JP200235074-A.
PD   10-DEC-2002.
PA   (UYTS-) UNIV TSUKUBA.
     Query Match             14.9%;  Score 61; DB 7; Length 373;
     Best Local Similarity   29.4%;  Pred. No. 44;

RESULT 754
ID   ADN23301 standard; protein; 392 AA.
DE   Bacterial polypeptide #5954.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match             14.9%;  Score 61; DB 8; Length 392;
     Best Local Similarity   29.3%;  Pred. No. 47;

RESULT 755
ID   ABP41946 standard; protein; 584 AA.
DE   Human ovarian antigen HHEND31, SEQ ID NO:3078.
PN   WO200200677-A1.
PD   03-JAN-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             14.9%;  Score 61; DB 5; Length 584;
     Best Local Similarity   24.2%;  Pred. No. 73;

RESULT 756
ID   AAU14794 standard; protein; 2298 AA.
DE   Novel bone marrow polypeptide #193.
PN   WO200157187-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             14.9%;  Score 61; DB 4; Length 2298;
     Best Local Similarity   29.1%;  Pred. No. 3.4e+02;

RESULT 757
ID   AAU14720 standard; protein; 2301 AA.
DE   Novel bone marrow polypeptide #119.
PN   WO200157187-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             14.9%;  Score 61; DB 4; Length 2301;
     Best Local Similarity   29.1%;  Pred. No. 3.4e+02;

RESULT 758
ID   ABM73281 standard; protein; 339 AA.
DE   Staphylococcus aureus protein #2521.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             14.8%;  Score 60.5; DB 6; Length 339;
     Best Local Similarity   39.0%;  Pred. No. 46;

RESULT 759
ID   ABU32397 standard; protein; 436 AA.
DE   Protein encoded by Prokaryotic essential gene #17924.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             14.8%;  Score 60.5; DB 6; Length 436;
     Best Local Similarity   26.5%;  Pred. No. 61;

RESULT 760
ID   ABO63574 standard; protein; 441 AA.
DE   Klebsiella pneumoniae polypeptide seqid 10091.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             14.8%;  Score 60.5; DB 7; Length 441;
     Best Local Similarity   26.5%;  Pred. No. 62;

RESULT 761
ID   ABM67254 standard; protein; 444 AA.
DE   Photorhabdus luminescens protein sequence #351.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
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PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             14.8%;  Score 60.5; DB 6; Length 444;
     Best Local Similarity   32.6%;  Pred. No. 62;

RESULT 762
ID   ABG96496 standard; protein; 2396 AA.
DE   PRRS virus ORF1a protein sequence.
PN   WO200272802-A2.
PD   19-SEP-2002.
PA   (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
     Query Match             14.8%;  Score 60.5; DB 5; Length 2396;
     Best Local Similarity   30.1%;  Pred. No. 4.2e+02;

RESULT 763
ID   ADI21643 standard; protein; 137 AA.
DE   Novel human polypeptide #122.
PN   WO200325148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match             14.6%;  Score 60; DB 7; Length 137;
     Best Local Similarity   24.4%;  Pred. No. 19;

RESULT 764
ID   ADI95325 standard; protein; 221 AA.
DE   OSPF-related SARS coronavirus matrix protein.
PN   WO2004002415-A2.
PD   08-JAN-2004.
PA   (DAND ) DANA FARBER CANCER INST INC.
     Query Match             14.6%;  Score 60; DB 8; Length 221;
     Best Local Similarity   24.0%;  Pred. No. 33;

RESULT 765
ID   ADM20157 standard; protein; 248 AA.
DE   Protein encoded by novel human channel/transporter gene #268 clone 2.
PN   WO200154472-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             14.6%;  Score 60; DB 4; Length 248;
     Best Local Similarity   37.9%;  Pred. No. 37;

RESULT 766
ID   ABB83433 standard; protein; 387 AA.
DE   Human repeated protein 42.57.
PN   CN1339463-A.
PD   13-MAR-2002.
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
     Query Match             14.6%;  Score 60; DB 5; Length 387;
     Best Local Similarity   24.4%;  Pred. No. 62;

RESULT 767
ID   AAO26227 standard; protein; 387 AA.
DE   MDDT related human protein SEQ ID No 5.
PN   WO200296951-A1.
PD   05-DEC-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match             14.6%;  Score 60; DB 6; Length 387;
     Best Local Similarity   24.4%;  Pred. No. 62;

RESULT 768
ID   ADM04402 standard; protein; 387 AA.
DE   Human PRO polypeptide #690.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match             14.6%;  Score 60; DB 7; Length 387;
     Best Local Similarity   24.4%;  Pred. No. 62;

RESULT 769
ID   ADO20493 standard; protein; 387 AA.
DE   Human protein of the invention SEQ ID NO:3087.
PN   WO2004043351-A2.
PD   27-MAY-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match             14.6%;  Score 60; DB 8; Length 387;
     Best Local Similarity   24.4%;  Pred. No. 62;

RESULT 770
ID   ABB66583 standard; protein; 472 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 26541.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
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Query Match   14.6%; Score 60; DB 4; Length 472;
Best Local Similarity 33.3%; Pred. No. 77;
RESULT 771
ID ADG74253 standard; protein; 516 AA.
DE Human frizzled protein, SEQ ID No 38.
PN WO200292635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.

Query Match   14.6%; Score 60; DB 7; Length 516;
Best Local Similarity 23.1%; Pred. No. 85;
RESULT 772
ID ADQ07984 standard; protein; 526 AA.
DE Human hypothetical protein FLJ20371-encoding cDNA.
PN WO2004061123-A2.
PD 22-JUL-2004.
PA (EXEL-) EXELIXIS INC.

Query Match   14.6%; Score 60; DB 8; Length 526;
Best Local Similarity 26.4%; Pred. No. 87;
RESULT 773
ID ADP25065 standard; protein; 526 AA.
DE PRO polypeptide SEQ ID NO:2243.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match   14.6%; Score 60; DB 8; Length 526;
Best Local Similarity 26.4%; Pred. No. 87;
RESULT 774
ID AAW31271 standard; protein; 585 AA.
DE Human frizzled-5 protein Mfz5 (Wnt receptor).
PN WO9739357-A1.
PD 23-OCT-1997.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
    (UYJO) UNIV JOHNS HOPKINS.

Query Match   14.6%; Score 60; DB 2; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 775
ID ABU55900 standard; protein; 585 AA.
DE Human protein Frizzled-5.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.

Query Match   14.6%; Score 60; DB 6; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 776
ID AAE34054 standard; protein; 585 AA.
DE FZD5 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.

Query Match   14.6%; Score 60; DB 6; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 777
ID ABG75231 standard; protein; 585 AA.
DE Hair papilla cell growth promoter related human protein SEQ ID NO: 4.
PN WO2003086334-A1.
PD 23-OCT-2003.
PA (TAIS) TAISHO PHARM CO LTD.

Query Match   14.6%; Score 60; DB 7; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 778
ID ADG74266 standard; protein; 585 AA.
DE Human frizzled protein, SEQ ID No 51.
PN WO200292635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.

Query Match   14.6%; Score 60; DB 7; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 779
ID ADO29333 standard; protein; 585 AA.
DE Human GPCR FZD5, SEQ ID NO:434.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.

Query Match   14.6%; Score 60; DB 8; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 780
ID ADO22260 standard; protein; 585 AA.
DE Human FZD5 protein (homologue of Drosophila frizzled).
PN WO2004042028-A2.
PD 21-MAY-2004.
PA (REGC) UNIV CALIFORNIA.

Query Match   14.6%; Score 60; DB 8; Length 585;
Best Local Similarity 23.1%; Pred. No. 98;
RESULT 781
ID ADI21171 standard; protein; 601 AA.
DE Novel human protein #146.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.

Query Match   14.6%; Score 60; DB 7; Length 601;
Best Local Similarity 24.4%; Pred. No. 1e+02;
RESULT 782
ID ABG29043 standard; protein; 728 AA.
DE Novel human diagnostic protein #29034.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match   14.6%; Score 60; DB 4; Length 728;
Best Local Similarity 26.9%; Pred. No. 1.3e+02;
RESULT 783
ID AAO01208 standard; protein; 124 AA.
DE Human polypeptide SEQ ID NO 15100.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

Query Match   14.5%; Score 59.5; DB 4; Length 124;
Best Local Similarity 30.2%; Pred. No. 20;
RESULT 784
ID ADL04363 standard; protein; 134 AA.
DE M. catarrhalis protein #129.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match   14.5%; Score 59.5; DB 8; Length 134;
Best Local Similarity 30.8%; Pred. No. 22;
RESULT 785
ID AAR60133 standard; protein; 175 AA.
DE Human G-CSF.
PN WO9418236-A1.
PD 18-AUG-1994.
PA (AMRA-) AMRAD CORP LTD.

Query Match   14.5%; Score 59.5; DB 2; Length 175;
Best Local Similarity 29.1%; Pred. No. 29;
RESULT 786
ID AAY74779 standard; protein; 214 AA.
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1032.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
    (GENO-) INST GENOMIC RES.

Query Match   14.5%; Score 59.5; DB 3; Length 214;
Best Local Similarity 28.3%; Pred. No. 37;
RESULT 787
ID AAY74780 standard; protein; 217 AA.
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1034.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
    (GENO-) INST GENOMIC RES.

Query Match   14.5%; Score 59.5; DB 3; Length 217;
Best Local Similarity 28.3%; Pred. No. 37;
RESULT 788
ID AAY74783 standard; protein; 221 AA.
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1040.
PN WO9957280-A2.
PD 11-NOV-1999.

PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
     Query Match   14.5%;   Score 59.5;   DB 3;   Length 221;
     Best Local Similarity   28.3%;   Pred. No. 38;
RESULT 789
ID AAY74782 standard; protein; 221 AA.
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1038.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
     Query Match   14.5%;   Score 59.5;   DB 3;   Length 221;
     Best Local Similarity   28.3%;   Pred. No. 38;
RESULT 790
ID ABB63281 standard; protein; 351 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16635.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PKE) PE CORP NY.
     Query Match   14.5%;   Score 59.5;   DB 4;   Length 351;
     Best Local Similarity   32.1%;   Pred. No. 64;
RESULT 791
ID ABB63284 standard; protein; 351 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16644.
PN WO200171042-A2.
PD 27-SEP-2001
PA (PKE) PE CORP NY.
     Query Match   14.5%;   Score 59.5;   DB 4;   Length 351;
     Best Local Similarity   32.1%;   Pred. No. 64;
RESULT 792
ID AAE01035 standard; protein; 551 AA.
DE Human death domain-containing receptor (DDCR) protein from HODDX59 clone.
PN WO200129063-A2.
PD 26-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
     Query Match   14.5%;   Score 59.5;   DB 4;   Length 551;
     Best Local Similarity   31.7%;   Pred. No. 1.1e+02;
RESULT 793
ID AAG75604 standard; protein; 705 AA.
DE Human colon cancer antigen protein SEQ ID NO:6368.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
     Query Match   14.5%;   Score 59.5;   DB 4;   Length 705;
     Best Local Similarity   31.7%;   Pred. No. 1.4e+02;
RESULT 794
ID ADC06850 standard; protein; 1142 AA.
DE Kidins 220Pc-related protein Pc473.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   14.5%;   Score 59.5;   DB 7;   Length 1142;
     Best Local Similarity   31.7%;   Pred. No. 2.4e+02;
RESULT 795
ID ADC06846 standard; protein; 1184 AA.
DE Human Kidins220Pc protein XM_045362.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   14.5%;   Score 59.5;   DB 7;   Length 1184;
     Best Local Similarity   31.7%;   Pred. No. 2.5e+02;
RESULT 796
ID AAM39025 standard; protein; 1715 AA.
DE Human polypeptide SEQ ID NO 2170.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
     Query Match   14.5%;   Score 59.5;   DB 4;   Length 1715;
     Best Local Similarity   31.7%;   Pred. No. 3.8e+02;
RESULT 797
ID AAM38993 standard; protein; 1715 AA.
DE Human polypeptide SEQ ID NO 2138.
PN WO200153312-A1.

PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
     Query Match   14.5%;   Score 59.5;   DB 4;   Length 1715;
     Best Local Similarity   31.7%;   Pred. No. 3.8e+02;
RESULT 798
ID AAE25144 standard; protein; 1715 AA.
DE Human ARMS protein.
PN WO200250273-A2.
PD 27-JUN-2002.
PA (UYNY) UNIV NEW YORK STATE.
     Query Match   14.5%;   Score 59.5;   DB 5;   Length 1715;
     Best Local Similarity   31.7%;   Pred. No. 3.8e+02;
RESULT 799
ID AAU96840 standard; protein; 1715 AA.
DE Human kidins220 protein.
PN WO200220786-A2.
PD 14-MAR-2002.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
     Query Match   14.5%;   Score 59.5;   DB 5;   Length 1715;
     Best Local Similarity   31.7%;   Pred. No. 3.8e+02;
RESULT 800
ID AAE32128 standard; protein; 1715 AA.
DE Human cytoskeleton-associated protein, CSAP-26.
PN WO200279404-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
     Query Match   14.5%;   Score 59.5;   DB 6;   Length 1715;
     Best Local Similarity   31.7%;   Pred. No. 3.8e+02;
RESULT 801
ID ADA09988 standard; protein; 1753 AA.
DE Human receptor and membrane-associated protein REMAP-30, SEQ ID:30.
PN WO2003070902-A2.
PD 28-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
     Query Match   14.5%;   Score 59.5;   DB 6;   Length 1753;
     Best Local Similarity   31.7%;   Pred. No. 3.9e+02;
RESULT 802
ID ADC06847 standard; protein; 1771 AA.
DE Human kidins220Pc protein AB033076.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   14.5%;   Score 59.5;   DB 7;   Length 1771;
     Best Local Similarity   31.7%;   Pred. No. 4e+02;
RESULT 803
ID ADB08926 standard; protein; 155 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:2866.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
     Query Match   14.4%;   Score 59;   DB 6;   Length 155;
     Best Local Similarity   31.0%;   Pred. No. 29;
RESULT 804
ID AAG46085 standard; protein; 174 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57940.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   14.4%;   Score 59;   DB 3;   Length 174;
     Best Local Similarity   35.0%;   Pred. No. 34;
RESULT 805
ID AAW63009 standard; protein; 244 AA.
DE Mouse dectin-1.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
     Query Match   14.4%;   Score 59;   DB 2;   Length 244;
     Best Local Similarity   33.3%;   Pred. No. 49;
RESULT 806
ID ABB82844 standard; protein; 244 AA.
DE Mouse Dectin-1 polypeptide.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.

Query Match   14.4%; Score 59; DB 6; Length 244;
Best Local Similarity 33.3%; Pred. No. 49;
RESULT 807
ID   AAE21313 standard; protein; 300 AA.
DE   Mouse MrgA15 (mas-related gene) protein.
PN   WO200183555-A2.
PD   08-NOV-2001.
PA   (CALY) CALIFORNIA INST OF TECHNOLOGY.

Query Match   14.4%; Score 59; DB 5; Length 300;
Best Local Similarity 31.7%; Pred. No. 62;
RESULT 808
ID   ADH08569 standard; protein; 300 AA.
DE   MrgA15.
PN   WO2004003133-A1.
PD   08-JAN-2004.
PA   (CALY) CALIFORNIA INST OF TECHNOLOGY.

Query Match   14.4%; Score 59; DB 8; Length 300;
Best Local Similarity 31.7%; Pred. No. 62;
RESULT 809
ID   AAR91225 standard; protein; 328 AA.
DE   Human placenta G-protein coupled receptor protein.
PN   WO9605302-A1.
PD   22-FEB-1996.
PA   (TAKE) TAKEDA CHEM IND LTD.

Query Match   14.4%; Score 59; DB 2; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 810
ID   AAB04393 standard; protein; 328 AA.
DE   Human P2-purinergic receptor subtype, P2Y6.
PN   WO200146454-A1.
PD   28-JUN-2001.
PA   (CORT-) COR THERAPEUTICS INC.

Query Match   14.4%; Score 59; DB 4; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 811
ID   ABP81869 standard; protein; 328 AA.
DE   Human purinergic receptor P2Y6 protein SEQ ID NO:223.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.

Query Match   14.4%; Score 59; DB 6; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 812
ID   ADC37341 standard; protein; 328 AA.
DE   Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 174.
PN   WO2003048202-A2.
PD   12-JUN-2003.
PA   (ASAH) ASAHI KASEI KK.

Query Match   14.4%; Score 59; DB 7; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 813
ID   ADD45306 standard; protein; 328 AA.
DE   Human Protein Q15077, SEQ ID NO 10739.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.

Query Match   14.4%; Score 59; DB 7; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 814
ID   ADE38349 standard; protein; 328 AA.
DE   Human protein 2427 amino acid sequence.
PN   WO2003065006-A2.
PD   07-AUG-2003.
PA   (MILL-) MILLENNIUM PHARM INC.

Query Match   14.4%; Score 59; DB 7; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 815
ID   ADN39970 standard; protein; 328 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C340.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match   14.4%; Score 59; DB 7; Length 328;
Best Local Similarity 26.9%; Pred. No. 702.
RESULT 816
ID   ADO29600 standard; protein; 328 AA.
DE   Human GPCR P2RY6, SEQ ID NO:702.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

Query Match   14.4%; Score 59; DB 8; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 817
ID   ADP49195 standard; protein; 328 AA.
DE   Human P2Y6 purinergic receptor protein sequence for odour modulation.
PN   WO2004047749-A2.
PD   10-JUN-2004.
PA   (UTAH) UNIV UTAH RES FOUND.

Query Match   14.4%; Score 59; DB 8; Length 328;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 818
ID   ADR46666 standard; protein; 328 AA.
DE   Cancer-associated protein, SEQ ID 79.
PN   WO2004073557-A2.
PD   02-SEP-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.

Query Match   14.4%; Score 59; DB 8; Length 359;
Best Local Similarity 26.9%; Pred. No. 69;
RESULT 819
ID   ADO29525 standard; protein; 359 AA.
DE   Mouse GPCR IL8RB, SEQ ID NO:627.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

Query Match   14.4%; Score 59; DB 8; Length 369;
Best Local Similarity 23.1%; Pred. No. 76;
RESULT 820
ID   ABM85488 standard; protein; 369 AA.
DE   Mouse protein sequence mCP2823.
PN   WO2003107826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.

Query Match   14.4%; Score 59; DB 7; Length 369;
Best Local Similarity 23.1%; Pred. No. 78;
RESULT 821
ID   AAU03816 standard; protein; 376 AA.
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #15.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (PHAA) PHARMACIA & UPJOHN.

Query Match   14.4%; Score 59; DB 4; Length 376;
Best Local Similarity 25.7%; Pred. No. 80;
RESULT 822
ID   ABU50099 standard; protein; 386 AA.
DE   Protein encoded by Prokaryotic essential gene #35626.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

Query Match   14.4%; Score 59; DB 6; Length 386;
Best Local Similarity 37.5%; Pred. No. 82;
RESULT 823
ID   ADN24200 standard; protein; 399 AA.
DE   Bacterial polypeptide #6853.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

Query Match   14.4%; Score 59; DB 8; Length 399;
Best Local Similarity 25.7%; Pred. No. 86;
RESULT 824
ID   ABO74175 standard; protein; 473 AA.
DE   Pseudomonas aeruginosa polypeptide #6350.

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PN   US6651795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match      14.4%;  Score 59;    DB 7;  Length 473;
     Best Local Similarity 23.8%;  Pred. No. 1e+02;
RESULT 825
ID   AAG41250 standard; protein; 612 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 51299.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match      14.4%;  Score 59;    DB 3;  Length 612;
     Best Local Similarity 35.0%;  Pred. No. 1.4e+02;
RESULT 826
ID   AAG41249 standard; protein; 697 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 51298.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match      14.4%;  Score 59;    DB 3;  Length 697;
     Best Local Similarity 35.0%;  Pred. No. 1.6e+02;
RESULT 827
ID   AAG41248 standard; protein; 763 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 51297.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match      14.4%;  Score 59;    DB 3;  Length 763;
     Best Local Similarity 35.0%;  Pred. No. 1.8e+02;
RESULT 828
ID   AAM83543 standard; protein; 57 AA.
DE   Human immune/haematopoietic antigen SEQ ID NO:11136.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match      14.3%;  Score 58.5;  DB 4;  Length 57;
     Best Local Similarity 35.0%;  Pred. No. 11;
RESULT 829
ID   AAU0233 standard; protein; 246 AA.
DE   Novel human secreted protein #724.
PN   WO200179449-A2.
PD   25-OCT-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match      14.3%;  Score 58.5;  DB 4;  Length 246;
     Best Local Similarity 27.1%;  Pred. No. 57;
RESULT 830
ID   ADH09917 standard; protein; 282 AA.
DE   Human host factor protein, SEQ ID No 445.
PN   WO2003094847-A2.
PD   20-NOV-2003.
PA   (UYEM-) UNIV EMORY.
     Query Match      14.3%;  Score 58.5;  DB 8;  Length 282;
     Best Local Similarity 24.2%;  Pred. No. 67;
RESULT 831
ID   AAY30163 standard; protein; 322 AA.
DE   Human dorsal root receptor 5 hDRR5.
PN   WO9932519-A1.
PD   01-JUL-1999.
PA   (ASTR ) ASTRA PHARMA INC.
PA   (ASTR ) ASTRA AB.
     Query Match      14.3%;  Score 58.5;  DB 2;  Length 322;
     Best Local Similarity 30.6%;  Pred. No. 78;
RESULT 832
ID   ABU30868 standard; protein; 358 AA.
DE   Protein encoded by Prokaryotic essential gene #16395.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match      14.3%;  Score 58.5;  DB 6;  Length 358;
     Best Local Similarity 26.4%;  Pred. No. 88;
RESULT 833
ID   ABR42416 standard; protein; 499 AA.
DE   Human potassium channel Kv1.2.
PN   WO2003035690-A2.
PD   01-MAY-2003.
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

     Query Match      14.3%;  Score 58.5;  DB 6;  Length 499;
     Best Local Similarity 21.7%;  Pred. No. 1.3e+02;
RESULT 834
ID   ABO85019 standard; protein; 499 AA.
DE   Human cancer-associated protein (CAP) HP07-112.
PN   WO2004058146-A2.
PD   15-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match      14.3%;  Score 58.5;  DB 8;  Length 499;
     Best Local Similarity 21.7%;  Pred. No. 1.3e+02;
RESULT 835
ID   ABR43491 standard; protein; 661 AA.
DE   Mouse sweet taste receptor T1R2 protein SEQ ID NO:5.
PN   WO2003025137-A2.
PD   27-MAR-2003.
PA   (IRMI-) IRM LLC.
PA   (SCRI ) SCRIPPS RES INST.
     Query Match      14.3%;  Score 58.5;  DB 6;  Length 661;
     Best Local Similarity 30.1%;  Pred. No. 1.8e+02;
RESULT 836
ID   AAY77557 standard; protein; 843 AA.
DE   Mouse GPCR-B4 polypeptide.
PN   WO200006593-A1.
PD   10-FEB-2000.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match      14.3%;  Score 58.5;  DB 3;  Length 843;
     Best Local Similarity 30.1%;  Pred. No. 2.3e+02;
RESULT 837
ID   ADK90718 standard; protein; 843 AA.
DE   Mouse taste receptor T1R2 protein.
PN   WO2003004992-A2.
PD   16-JAN-2003.
PA   (REGC ) UNIV CALIFORNIA.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
     Query Match      14.3%;  Score 58.5;  DB 7;  Length 843;
     Best Local Similarity 30.1%;  Pred. No. 2.3e+02;
RESULT 838
ID   ADM42817 standard; protein; 843 AA.
DE   Murine taste receptor protein T1R2 SeqID 61.
PN   WO2003100057-A1.
PD   04-DEC-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
     Query Match      14.3%;  Score 58.5;  DB 8;  Length 843;
     Best Local Similarity 30.1%;  Pred. No. 2.3e+02;
RESULT 839
ID   ADP70073 standard; protein; 843 AA.
DE   Mouse T1R2 receptor protein.
PN   JP2004154029-A.
PD   03-JUN-2004.
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
     Query Match      14.3%;  Score 58.5;  DB 8;  Length 843;
     Best Local Similarity 30.1%;  Pred. No. 2.3e+02;
RESULT 840
ID   ABP63752 standard; protein; 67 AA.
DE   Human ORF122.
PN   US2002082206-A1.
PD   27-JUN-2002.
PA   (LEAC/) LEACH M D.
PA   (MEHR/) MEHRABAN F.
PA   (CONL/) CONLEY P B.
PA   (TOPP/) TOPPER J N.
PA   (LAWD/) LAW D.
     Query Match      14.1%;  Score 58;    DB 5;  Length 67;
     Best Local Similarity 28.4%;  Pred. No. 15;
RESULT 841
ID   ADK35554 standard; protein; 98 AA.
DE   Novel human polypeptide SeqID7636.
PN   WO200216439-A2.
PD   28-FEB-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match      14.1%;  Score 58;    DB 5;  Length 98;
     Best Local Similarity 41.7%;  Pred. No. 23;
RESULT 842
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ID   AAY74781 standard; protein; 169 AA.
DE   Neisseria gonorrhoeae ORF 259 protein sequence SEQ ID NO:1036.
PN   WO9957280-A2.
PD   11-NOV-1999.
PA   (CHIR ) CHIRON CORP.
PA   (GENO-) INST GENOMIC RES.
     Query Match            14.1%;  Score 58;  DB 3;  Length 169;
     Best Local Similarity  26.9%;  Pred. No. 43;
RESULT 843
ID   AAY74778 standard; protein; 216 AA.
DE   Neisseria gonorrhoeae ORF 259 protein sequence SEQ ID NO:1030.
PN   WO9957280-A2.
PD   11-NOV-1999.
PA   (CHIR ) CHIRON CORP.
PA   (GENO-) INST GENOMIC RES.
     Query Match            14.1%;  Score 58;  DB 3;  Length 216;
     Best Local Similarity  26.9%;  Pred. No. 57;
RESULT 844
ID   ABP80786 standard; protein; 216 AA.
DE   N. gonorrhoeae amino acid sequence SEQ ID 8102.
PN   WO200279243-A2.
PD   10-OCT-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match            14.1%;  Score 58;  DB 6;  Length 216;
     Best Local Similarity  26.9%;  Pred. No. 57;
RESULT 845
ID   AAB96791 standard; protein; 232 AA.
DE   Putative P. abyssi cobalamin-5-phosphate synthase.
PN   FR2792651-A1.
PD   27-OCT-2000.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
PA   (IPRE-) IFREMER INST FR RECH EXPL MER.
     Query Match            14.1%;  Score 58;  DB 4;  Length 232;
     Best Local Similarity  46.2%;  Pred. No. 62;
RESULT 846
ID   ADH87199 standard; protein; 234 AA.
DE   Enterococcus faecalis polypeptide #1679.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match            14.1%;  Score 58;  DB 7;  Length 234;
     Best Local Similarity  30.8%;  Pred. No. 63;
RESULT 847
ID   ABU39580 standard; protein; 293 AA.
DE   Protein encoded by Prokaryotic essential gene #25107.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match            14.1%;  Score 58;  DB 6;  Length 293;
     Best Local Similarity  35.7%;  Pred. No. 81;
RESULT 848
ID   ABM69224 standard; protein; 294 AA.
DE   Photorhabdus luminescens protein sequence #2321.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match            14.1%;  Score 58;  DB 6;  Length 294;
     Best Local Similarity  27.9%;  Pred. No. 81;
RESULT 849
ID   ABM67244 standard; protein; 305 AA.
DE   Photorhabdus luminescens protein sequence #341.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match            14.1%;  Score 58;  DB 6;  Length 305;
     Best Local Similarity  37.0%;  Pred. No. 85;
RESULT 850
ID   ABU39650 standard; protein; 335 AA.
DE   Protein encoded by Prokaryotic essential gene #25177.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match            14.1%;  Score 58;  DB 6;  Length 335;
     Best Local Similarity  36.6%;  Pred. No. 94;
RESULT 851
ID   AAU80490 standard; protein; 355 AA.
DE   Rhesus macaque CXCR2 receptor #2.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR ) PHARMACOPEIA INC.
     Query Match            14.1%;  Score 58;  DB 5;  Length 355;
     Best Local Similarity  22.6%;  Pred. No. 1e+02;
RESULT 852
ID   ADD48095 standard; protein; 359 AA.
DE   Rat Protein AAC52961, SEQ ID NO 13793.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match            14.1%;  Score 58;  DB 7;  Length 359;
     Best Local Similarity  23.1%;  Pred. No. 1e+02;
RESULT 853
ID   ABB62002 standard; protein; 417 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 12798.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match            14.1%;  Score 58;  DB 4;  Length 417;
     Best Local Similarity  31.9%;  Pred. No. 1.2e+02;
RESULT 854
ID   ABB66915 standard; protein; 417 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 27537.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match            14.1%;  Score 58;  DB 4;  Length 417;
     Best Local Similarity  31.9%;  Pred. No. 1.2e+02;
RESULT 855
ID   AAY42328 standard; protein; 498 AA.
DE   Staphylococcus aureus fmtB protein.
PN   WO9947662-A1.
PD   23-SEP-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match            14.1%;  Score 58;  DB 2;  Length 498;
     Best Local Similarity  25.4%;  Pred. No. 1.5e+02;
RESULT 856
ID   AAY31821 standard; protein; 498 AA.
DE   Staphylococcus aureus fmtB protein.
PN   WO9947639-A2.
PD   23-SEP-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
     Query Match            14.1%;  Score 58;  DB 2;  Length 498;
     Best Local Similarity  25.4%;  Pred. No. 1.5e+02;
RESULT 857
ID   ABM73394 standard; protein; 498 AA.
DE   Staphylococcus aureus protein #2634.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match            14.1%;  Score 58;  DB 6;  Length 498;
     Best Local Similarity  25.4%;  Pred. No. 1.5e+02;
RESULT 858
ID   ADF43550 standard; protein; 498 AA.
DE   Staphylococcus aureus fmtB.
PN   US2003153733-A1.
PD   14-AUG-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match            14.1%;  Score 58;  DB 7;  Length 498;
     Best Local Similarity  25.4%;  Pred. No. 1.5e+02;
RESULT 859
ID   ADP29710 standard; protein; 537 AA.
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DE Human secreted protein SEQ ID #477.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVB-) FIVE PRIME THERAPEUTICS INC.
Query Match   14.1%;   Score 58;   DB 8;   Length 537;
Best Local Similarity 19.6%;   Pred. No. 1.6e+02;
RESULT 860
ID ADG74255 standard; protein; 544 AA.
DE Rat frizzled protein, SEQ ID No 40.
PN WO20029635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match   14.1%;   Score 58;   DB 7;   Length 544;
Best Local Similarity 19.6%;   Pred. No. 1.6e+02;
RESULT 861
ID ABU55897 standard; protein; 565 AA.
DE Human protein Frizzled-2.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match   14.1%;   Score 58;   DB 6;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 862
ID AAB34051 standard; protein; 565 AA.
DE FZD2 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match   14.1%;   Score 58;   DB 6;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 863
ID ABP81948 standard; protein; 565 AA.
DE Human frizzled-2 protein SEQ ID NO:382.
PN WO20026l087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match   14.1%;   Score 58;   DB 6;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 864
ID ADF76959 standard; protein; 565 AA.
DE Novel human secreted and transmembrane protein SeqID 634.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   14.1%;   Score 58;   DB 7;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 865
ID ADG74261 standard; protein; 565 AA.
DE Human frizzled protein, SEQ ID No 46.
PN WO20029635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match   14.1%;   Score 58;   DB 7;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 866
ID ADH87897 standard; protein; 565 AA.
DE Human GPCR FZD2, SEQ ID NO:428.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match   14.1%;   Score 58;   DB 7;   Length 565;
Best Local Similarity 30.0%;   Pred. No. 1.7e+02;
RESULT 867
ID ADO29327 standard; protein; 565 AA.
DE Human GPCR FZD2, SEQ ID NO:428.
PN WO200040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match   14.1%;   Score 58;   DB 8;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 868
ID ADO22254 standard; protein; 565 AA.

DE Human FZD2 protein (homologue of Drosophila frizzled).
PN WO2004042028-A2.
PD 21-MAY-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match   14.1%;   Score 58;   DB 8;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 869
ID ADO28667 standard; protein; 565 AA.
DE Human frizzled 2 protein SEQ ID NO:96.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match   14.1%;   Score 58;   DB 8;   Length 565;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 870
ID ADO29328 standard; protein; 570 AA.
DE Mouse GPCR FZD2, SEQ ID NO:429.
PN WO200040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match   14.1%;   Score 58;   DB 8;   Length 570;
Best Local Similarity 19.6%;   Pred. No. 1.7e+02;
RESULT 871
ID ABB47273 standard; protein; 572 AA.
DE Enterococcus faecalis polypeptide Abcl1.
PN WO200179257-A2.
PD 25-OCT-2001.
PA (PHYI-) PHYTERA INC.
Query Match   14.1%;   Score 58;   DB 4;   Length 572;
Best Local Similarity 30.0%;   Pred. No. 1.7e+02;
RESULT 872
ID ADO29334 standard; protein; 577 AA.
DE Mouse GPCR FZD5, SEQ ID NO:435.
PN WO200040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match   14.1%;   Score 58;   DB 8;   Length 577;
Best Local Similarity 21.2%;   Pred. No. 1.7e+02;
RESULT 873
ID ADG74260 standard; protein; 626 AA.
DE Mouse frizzled protein, SEQ ID No 45.
PN WO20029635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match   14.1%;   Score 58;   DB 7;   Length 626;
Best Local Similarity 19.6%;   Pred. No. 1.9e+02;
RESULT 874
ID AAB12117 standard; protein; 647 AA.
DE Hydrophobic domain protein from clone HP02539 isolated from Saos-2 cells.
PN WO200029448-A2.
PD 25-MAY-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match   14.1%;   Score 58;   DB 3;   Length 647;
Best Local Similarity 19.6%;   Pred. No. 2e+02;
RESULT 875
ID ABU55896 standard; protein; 647 AA.
DE Human protein Frizzled-1.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match   14.1%;   Score 58;   DB 6;   Length 647;
Best Local Similarity 19.6%;   Pred. No. 2e+02;
RESULT 876
ID AAE34050 standard; protein; 647 AA.
DE FZD1 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match   14.1%;   Score 58;   DB 6;   Length 647;
Best Local Similarity 19.6%;   Pred. No. 2e+02;
RESULT 877
ID ADG74259 standard; protein; 647 AA.

DE   Human frizzled protein, SEQ ID No 44.
PN   WO200292635-A2.
PD   21-NOV-2002.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   14.1%; Score 58; DB 7; Length 647;
     Best Local Similarity 19.6%; Pred. No. 2e+02;

RESULT 878
ID   ADP65222 standard; protein; 647 AA.
DE   Human frizzled 1, frizzled (Drosophila) homologue 1.
PN   WO2003072827-A1.
PD   04-SEP-2003.
PA   (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
     Query Match   14.1%; Score 58; DB 7; Length 647;
     Best Local Similarity 19.6%; Pred. No. 2e+02;

RESULT 879
ID   ADO22252 standard; protein; 647 AA.
DE   Human FzD1 protein (homologue of Drosophila frizzled).
PN   WO2004042028-A2.
PD   21-MAY-2004.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   14.1%; Score 58; DB 8; Length 647;
     Best Local Similarity 19.6%; Pred. No. 2e+02;

RESULT 880
ID   ADQ29693 standard; protein; 648 AA.
DE   Human GPCR FZD1, SEQ ID NO:795.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   14.1%; Score 58; DB 8; Length 648;
     Best Local Similarity 19.6%; Pred. No. 2e+02;

RESULT 881
ID   ABU25395 standard; protein; 686 AA.
DE   Protein encoded by Prokaryotic essential gene #10922.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   14.1%; Score 58; DB 6; Length 686;
     Best Local Similarity 23.3%; Pred. No. 2.1e+02;

RESULT 882
ID   ABG24263 standard; protein; 1303 AA.
DE   Novel human diagnostic protein #24254.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   14.1%; Score 58; DB 4; Length 1303;
     Best Local Similarity 23.3%; Pred. No. 2.1e+02;

RESULT 883
ID   AAW67738 standard; protein; 2476 AA.
DE   Pig p105 zona pellucida-binding protein.
PN   US5851817-A.
PD   22-DEC-1998.
PA   (TEXA) UNIV TEXAS SYSTEM.
     Query Match   14.1%; Score 58; DB 2; Length 2476;
     Best Local Similarity 22.4%; Pred. No. 9e+02;

RESULT 884
ID   AAM24446 standard; protein; 63 AA.
DE   Human EST encoded protein SEQ ID NO: 1971.
PN   WO20015477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   14.1%; Score 57.5; DB 4; Length 63;
     Best Local Similarity 24.1%; Pred. No. 17;

RESULT 885
ID   AAB42727 standard; protein; 73 AA.
DE   Human ORFX ORF2491 polypeptide sequence SEQ ID NO:4982.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
     Query Match   14.0%; Score 57.5; DB 3; Length 73;
     Best Local Similarity 26.7%; Pred. No. 20;

RESULT 886
ID   ADH88922 standard; protein; 108 AA.
DE   Enterococcus faecalis polypeptide #3402.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match   14.0%; Score 57.5; DB 7; Length 108;
     Best Local Similarity 23.3%; Pred. No. 30;

RESULT 887
ID   ADL92433 standard; protein; 115 AA.
DE   Single domain antibody (dAb)-related TAR2h-5 protein.
PN   WO2004003019-A2.
PD   08-JAN-2004.
PA   (DOMA-) DOMANTIS LTD.
     Query Match   14.0%; Score 57.5; DB 8; Length 115;
     Best Local Similarity 32.7%; Pred. No. 33;

RESULT 888
ID   ADQ77040 standard; protein; 115 AA.
DE   TAR2-5 protein sequence.
PN   WO2004058821-A2.
PD   15-JUL-2004.
PA   (DOMA-) DOMANTIS LTD.
     Query Match   14.0%; Score 57.5; DB 8; Length 115;
     Best Local Similarity 32.7%; Pred. No. 33;

RESULT 889
ID   ADL92391 standard; protein; 116 AA.
DE   Single domain antibody (dAb)-related TAR2-5 protein.
PN   WO2004003019-A2.
PD   08-JAN-2004.
PA   (DOMA-) DOMANTIS LTD.
     Query Match   14.0%; Score 57.5; DB 8; Length 116;
     Best Local Similarity 32.7%; Pred. No. 33;

RESULT 890
ID   ADQ76999 standard; protein; 116 AA.
DE   TAR2-5 protein sequence.
PN   WO2004058821-A2.
PD   15-JUL-2004.
PA   (DOMA-) DOMANTIS LTD.
     Query Match   14.0%; Score 57.5; DB 8; Length 116;
     Best Local Similarity 32.7%; Pred. No. 33;

RESULT 891
ID   ADB11434 standard; protein; 125 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:5626.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP) WYETH HOLDINGS CORP.
     Query Match   14.0%; Score 57.5; DB 6; Length 125;
     Best Local Similarity 25.2%; Pred. No. 36;

RESULT 892
ID   ABB70366 standard; protein; 170 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 37890.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   14.0%; Score 57.5; DB 4; Length 170;
     Best Local Similarity 23.6%; Pred. No. 51;

RESULT 893
ID   ABB67475 standard; protein; 231 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 29217.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   14.0%; Score 57.5; DB 4; Length 231;
     Best Local Similarity 24.2%; Pred. No. 72;

RESULT 894
ID   ABB48370 standard; protein; 250 AA.
DE   Listeria monocytogenes protein #1074.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   14.0%; Score 57.5; DB 5; Length 250;
     Best Local Similarity 26.8%; Pred. No. 78;

RESULT 895
ID   ABG28657 standard; protein; 342 AA.
DE   Novel human diagnostic protein #28648.

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PN   WO20175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
       Query Match        14.0%;   Score 57.5;  DB 4;   Length 342;
       Best Local Similarity 25.0%;  Pred. No. 1.1e+02;
RESULT 896
ID   ADI28462 standard; protein; 349 AA.
DE   Mouse GPCR5D polypeptide.
PN   WO2004001060-A2.
PD   31-DEC-2003.
PA   (BRIM-) BRISTOL-MYERS SQUIBB CO.
       Query Match        14.0%;   Score 57.5;  DB 8;   Length 349;
       Best Local Similarity 33.3%;  Pred. No. 1.1e+02;
RESULT 897
ID   ADO29633 standard; protein; 356 AA.
DE   Mouse GPCR RAI3, SEQ ID NO:735.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
       Query Match        14.0%;   Score 57.5;  DB 8;   Length 356;
       Best Local Similarity 33.3%;  Pred. No. 1.2e+02;
RESULT 898
ID   ABU33917 standard; protein; 408 AA.
DE   Protein encoded by Prokaryotic essential gene #19444.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
       Query Match        14.0%;   Score 57.5;  DB 6;   Length 408;
       Best Local Similarity 34.6%;  Pred. No. 1.4e+02;
RESULT 899
ID   ADM87323 standard; protein; 436 AA.
DE   Human protein SEQ ID NO:416.
PN   WO2004009834-A2.
PD   29-JAN-2004.
PA   (NUVE-) NUVELO INC.
       Query Match        14.0%;   Score 57.5;  DB 8;   Length 436;
       Best Local Similarity 39.1%;  Pred. No. 1.5e+02;
RESULT 900
ID   ABG28672 standard; protein; 506 AA.
DE   Novel human diagnostic protein #28663.
PN   WO20175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
       Query Match        14.0%;   Score 57.5;  DB 4;   Length 506;
       Best Local Similarity 25.0%;  Pred. No. 1.7e+02;
RESULT 901
ID   ADA34879 standard; protein; 1062 AA.
DE   Acinetobacter baumannii protein #2040.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
       Query Match        14.0%;   Score 57.5;  DB 6;   Length 1062;
       Best Local Similarity 26.7%;  Pred. No. 4e+02;
RESULT 902
ID   ABU22339 standard; protein; 1077 AA.
DE   Protein encoded by Prokaryotic essential gene #7866.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
       Query Match        14.0%;   Score 57.5;  DB 6;   Length 1077;
       Best Local Similarity 30.0%;  Pred. No. 4.1e+02;
RESULT 903
ID   AAG72380 standard; protein; 145 AA.
DE   Human OR-like polypeptide query sequence, SEQ ID NO: 2061.
PN   WO20127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
       Query Match        13.9%;   Score 57;  DB 4;   Length 145;
       Best Local Similarity 27.0%;  Pred. No. 49;
RESULT 904
ID   AAW58880 standard; protein; 148 AA.
DE   Recombinant MPO protein fragment H11.

PN   WO9807848-A1.
PD   26-FEB-1998.
PA   (TEIK ) TEIKOKU HORMONE MFG CO LTD.
       Query Match        13.9%;   Score 57;  DB 2;   Length 148;
       Best Local Similarity 35.6%;  Pred. No. 50;
RESULT 905
ID   AAU60896 standard; protein; 172 AA.
DE   Propionibacterium acnes immunogenic protein #21792.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
       Query Match        13.9%;   Score 57;  DB 4;   Length 172;
       Best Local Similarity 33.3%;  Pred. No. 60;
RESULT 906
ID   ABM57415 standard; protein; 172 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #22091.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
       Query Match        13.9%;   Score 57;  DB 6;   Length 172;
       Best Local Similarity 33.3%;  Pred. No. 60;
RESULT 907
ID   AAW58879 standard; protein; 205 AA.
DE   Recombinant MPO protein fragment H6.
PN   WO9807848-A1.
PD   26-FEB-1998.
PA   (TEIK ) TEIKOKU HORMONE MFG CO LTD.
       Query Match        13.9%;   Score 57;  DB 2;   Length 205;
       Best Local Similarity 35.6%;  Pred. No. 73;
RESULT 908
ID   AAW58874 standard; protein; 234 AA.
DE   Recombinant MPO protein fragment H3.
PN   WO9807848-A1.
PD   26-FEB-1998.
PA   (TEIK ) TEIKOKU HORMONE MFG CO LTD.
       Query Match        13.9%;   Score 57;  DB 2;   Length 234;
       Best Local Similarity 35.6%;  Pred. No. 84;
RESULT 909
ID   AAR79060 standard; peptide; 242 AA.
DE   3 hydroxy-beta-ionone ring methylene to keto group converting peptide.
PN   WO9518220-A1.
PD   06-JUL-1995.
PA   (KIRI ) KIRIN BEER KK.
PA   (MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
       Query Match        13.9%;   Score 57;  DB 2;   Length 242;
       Best Local Similarity 26.0%;  Pred. No. 88;
RESULT 910
ID   AAW69538 standard; protein; 242 AA.
DE   Amino acid sequence of crtE W1-crt W12.
PN   JP1015497-A.
PD   16-JUN-1998.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
       Query Match        13.9%;   Score 57;  DB 2;   Length 242;
       Best Local Similarity 26.0%;  Pred. No. 88;
RESULT 911
ID   AAW87885 standard; protein; 242 AA.
DE   Protein encoded by the carotenoid biosynthesis gene crtW.
PN   JP10327865-A.
PD   15-DEC-1998.
PA   (KIRI ) KIRIN BREWERY KK.
PA   (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
       Query Match        13.9%;   Score 57;  DB 2;   Length 242;
       Best Local Similarity 26.0%;  Pred. No. 88;
RESULT 912
ID   ADO61159 standard; protein; 242 AA.
DE   Alcaligenes sp. ketolase.
PN   DE10238978-A1.
PD   04-MAR-2004.
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
       Query Match        13.9%;   Score 57;  DB 8;   Length 242;
       Best Local Similarity 26.0%;  Pred. No. 88;
RESULT 913
ID   ADO61076 standard; protein; 242 AA.
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DE   Alcaligenes sp. ketolase.
PN   DE10238980-A1.
PD   04-MAR-2004.
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
      Query Match   13.9%;   Score 57;   DB 8;   Length 242;
      Best Local Similarity   26.0%;   Pred. No. 88;
RESULT 914
ID   ADQ38245 standard; protein; 242 AA.
DE   Alcaligenes sp. Ketolase.
PN   DE10258971-A1.
PD   01-JUL-2004.
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
      Query Match   13.9%;   Score 57;   DB 8;   Length 242;
      Best Local Similarity   26.0%;   Pred. No. 88;
RESULT 915
ID   ADR03860 standard; protein; 242 AA.
DE   Alcaligenes sp ketolase SEQ ID NO: 18.
PN   WO200406359-A2.
PD   29-JUL-2004.
PA   (BADI) BASF AG.
      Query Match   13.9%;   Score 57;   DB 8;   Length 242;
      Best Local Similarity   26.0%;   Pred. No. 88;
RESULT 916
ID   ADR03940 standard; protein; 242 AA.
DE   Alcaligenes ketolase.
PN   WO200406358-A1.
PD   29-JUL-2004.
PA   (BADI) BASF AG.
      Query Match   13.9%;   Score 57;   DB 8;   Length 242;
      Best Local Similarity   26.0%;   Pred. No. 88;
RESULT 917
ID   ADH09916 standard; protein; 247 AA.
DE   Human host factor protein, SEQ ID No 444.
PN   WO2003094847-A2.
PD   20-NOV-2003.
PA   (UYEM-) UNIV EMORY.
      Query Match   13.9%;   Score 57;   DB 8;   Length 247;
      Best Local Similarity   26.6%;   Pred. No. 90;
RESULT 918
ID   ADN95988 standard; protein; 299 AA.
DE   Human NOVX polypeptide #21.
PN   US200406749-A1.
PD   08-APR-2004.
PA   (ZHON/) ZHONG M.
PA   (LILL/) LI L.
PA   (GORM/) GORMAN L.
PA   (SPYT/) SPYTEK K A.
PA   (KEKU/) KEKUDA R.
PA   (TAUP/) TAUPIER R J.
PA   (ANDE/) ANDERSON D W.
PA   (VERN/) VERNET C A M.
PA   (CATT/) CATTERTON E.
PA   (MILL/) MILLER C E.
PA   (SHEN/) SHENOY S G.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (TCHE/) TCHERNEV V T.
PA   (PADI/) PADIGARU M.
PA   (GUSE/) GUSEV V Y.
PA   (MALY/) MALIYANKAR U M.
PA   (BURG/) BURGESS C E.
PA   (GERL/) GERLACH V.
PA   (CASM/) CASMAN S J.
PA   (RIEG/) RIEGER D K.
PA   (GROS/) GROSSE W M.
PA   (SMIT/) SMITHSON G.
PA   (PEYM/) PEYMAN J A.
PA   (STAR/) STARLING G.
PA   (ROTH/) ROTHENBERG M E.
PA   (LARO/) LAROCHELLE W J.
PA   (SHIM/) SHIMKETS R A.
PA   (CRAB/) CRABTREE J.
PA   (RAST/) RASTELLI L.

PA   (VOSS/) VOSS E Z.
PA   (BOLD/) BOLDOG F L.
PA   (EDIN/) EDINGER S R.
PA   (MILL/) MILLET I.
PA   (MACD/) MACDOUGALL J R.
PA   (ELLE/) ELLERMAN K.
PA   (CHAP/) CHAPOVAL A.
      Query Match   13.9%;   Score 57;   DB 8;   Length 299;
      Best Local Similarity   26.5%;   Pred. No. 1.1e+02;
RESULT 919
ID   ABP25981 standard; protein; 300 AA.
DE   Streptococcus polypeptide SEQ ID NO 1138.
PN   WO200034771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO/) INST GENOMIC RES.
      Query Match   13.9%;   Score 57;   DB 5;   Length 300;
      Best Local Similarity   38.2%;   Pred. No. 1.1e+02;
RESULT 920
ID   ABB49251 standard; protein; 305 AA.
DE   Listeria monocytogenes protein #1955.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
      Query Match   13.9%;   Score 57;   DB 5;   Length 305;
      Best Local Similarity   24.1%;   Pred. No. 1.1e+02;
RESULT 921
ID   ADI16827 standard; protein; 315 AA.
DE   Murine NOVX protein homologue SeqID 363.
PN   WO20026864-A2.
PD   06-SEP-2002.
PA   (CURA-) CURAGEN CORP.
      Query Match   13.9%;   Score 57;   DB 5;   Length 315;
      Best Local Similarity   25.0%;   Pred. No. 1.2e+02;
RESULT 922
ID   ABW02144 standard; protein; 315 AA.
DE   Human GPCR related protein #6.
PN   US2003195335-A1.
PD   16-OCT-2003.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (CASM/) CASMAN S.
PA   (ALSO/) ALSOBROOK J P.
PA   (BURG/) BURGESS C E.
PA   (PADI/) PADIGARU M.
PA   (TAYL/) TAYLOR S.
PA   (TCHE/) TCHERNEV V T.
PA   (SPYT/) SPYTEK K A.
PA   (LILL/) LI L.
PA   (SHEN/) SHENOY S.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (STON/) STONE D J.
PA   (SMIT/) SMITHSON G.
PA   (MACD/) MACDOUGALL J R.
      Query Match   13.9%;   Score 57;   DB 7;   Length 315;
      Best Local Similarity   25.0%;   Pred. No. 1.2e+02;
RESULT 923
ID   ADM42847 standard; protein; 315 AA.
DE   Murine odourant receptor protein Olfr68 SeqID 91.
PN   WO200310057-A1.
PD   04-DEC-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
      Query Match   13.9%;   Score 57;   DB 8;   Length 315;
      Best Local Similarity   25.0%;   Pred. No. 1.2e+02;
RESULT 924
ID   ADI16828 standard; protein; 316 AA.
DE   Murine NOVX protein homologue SeqID 364.
PN   WO20026864-A2.
PD   06-SEP-2002.
PA   (CURA-) CURAGEN CORP.
      Query Match   13.9%;   Score 57;   DB 5;   Length 316;
      Best Local Similarity   25.0%;   Pred. No. 1.2e+02;

RESULT 925
ID   AB019500 standard; protein; 316 AA.
DE   Mouse GPCR MOR 3' Beta 3.
PN   US20030222237-A1.
PD   30-JAN-2003.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
PA   (CACA/) CACACE A.
PA   (BARB/) BARBER L.
PA   (KORN/) KORNACKER M G.
  Query Match   13.9%; Score 57; DB 6; Length 316;
  Best Local Similarity   25.0%; Pred. No. 1.2e+02;

RESULT 926
ID   ABW02145 standard; protein; 316 AA.
DE   Human GPCR related protein #7.
PN   US2003195335-A1.
PD   16-OCT-2003.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (CASM/) CASMAN S.
PA   (ALSO/) ALSOBROOK J P.
PA   (BURG/) BURGESS C E.
PA   (PADI/) PADIGARU M.
PA   (TAYL/) TAYLOR S.
PA   (TCHE/) TCHERNEV V T.
PA   (SPYT/) SPYTEK K A.
PA   (LILL/) LI L.
PA   (SHEN/) SHENOY S.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (STON/) STONE D J.
PA   (SMIT/) SMITHSON G.
PA   (MACD/) MACDOUGALL J R.
  Query Match   13.9%; Score 57; DB 7; Length 316;
  Best Local Similarity   25.0%; Pred. No. 1.2e+02;

RESULT 927
ID   ADQ98158 standard; protein; 316 AA.
DE   Mouse olfactory receptor 3' beta 3.
PN   US200412130-A1.
PD   24-JUN-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN G A.
PA   (HAWK/) HAWKEN D R.
PA   (CACA/) CACACE A.
PA   (BARB/) BARBER L E.
PA   (KORN/) KORNACKER M G.
PA   (RYSE/) RYSECK R.
PA   (BENN/) BENNETT K L.
PA   (NELS/) NELSON T C.
  Query Match   13.9%; Score 57; DB 8; Length 316;
  Best Local Similarity   25.0%; Pred. No. 1.2e+02;

RESULT 928
ID   ADC12684 standard; protein; 317 AA.
DE   Human GPCR protein, SEQ ID No 16.
PN   WO2003000893-A2.
PD   03-JAN-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match   13.9%; Score 57; DB 7; Length 317;
  Best Local Similarity   27.9%; Pred. No. 1.2e+02;

RESULT 929
ID   AAW09433 standard; protein; 328 AA.
DE   Human placenta purinergic P-2u receptor, PNR.
PN   WO9638558-A2.
PD   05-DEC-1996.
PA   (INCY-) INCYTE PHARM INC.
  Query Match   13.9%; Score 57; DB 2; Length 328;
  Best Local Similarity   26.9%; Pred. No. 1.2e+02;

RESULT 930
ID   AAG72619 standard; protein; 344 AA.
DE   Murine OR-like polypeptide query sequence, SEQ ID NO: 2300.
PN   WO20127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
  Query Match   13.9%; Score 57; DB 4; Length 344;
  Best Local Similarity   25.0%; Pred. No. 1.3e+02;

RESULT 931
ID   AAG72620 standard; protein; 347 AA.
DE   Murine OR-like polypeptide query sequence, SEQ ID NO: 2301.
PN   WO20127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
  Query Match   13.9%; Score 57; DB 4; Length 347;
  Best Local Similarity   25.0%; Pred. No. 1.3e+02;

RESULT 932
ID   AAU80492 standard; protein; 355 AA.
DE   Baboon CXCR2 receptor.
PN   WO20190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
  Query Match   13.9%; Score 57; DB 5; Length 355;
  Best Local Similarity   25.0%; Pred. No. 1.3e+02;

RESULT 933
ID   ADE08292 standard; protein; 375 AA.
DE   Novel protein (useful for identifying genetic disorders) #447.
PN   WO200305152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match   13.9%; Score 57; DB 7; Length 375;
  Best Local Similarity   22.5%; Pred. No. 1.4e+02;

RESULT 934
ID   AAW58872 standard; protein; 462 AA.
DE   Recombinant MPO protein fragment NP1.4.
PN   WO9807848-A1.
PD   26-FEB-1998.
PA   (TBIK) TEIKOKU HORMONE MFG CO LTD.
  Query Match   13.9%; Score 57; DB 2; Length 462;
  Best Local Similarity   35.6%; Pred. No. 1.8e+02;

RESULT 935
ID   AAY94518 standard; protein; 500 AA.
DE   Rice diacylglycerol acyltransferase protein #2.
PN   WO2000032756-A2.
PD   08-JUN-2000.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
  Query Match   13.9%; Score 57; DB 3; Length 500;
  Best Local Similarity   31.5%; Pred. No. 2e+02;

RESULT 936
ID   ABB65529 standard; protein; 631 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 23679.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
  Query Match   13.9%; Score 57; DB 4; Length 631;
  Best Local Similarity   26.3%; Pred. No. 2.6e+02;

RESULT 937
ID   ABO70421 standard; protein; 693 AA.
DE   Pseudomonas aeruginosa polypeptide #2596.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   13.9%; Score 57; DB 7; Length 693;
  Best Local Similarity   23.1%; Pred. No. 2.9e+02;

RESULT 938
ID   AAW17800 standard; protein; 745 AA.
DE   Myeloperoxidase.
PN   JP09047286-A.
PD   18-FEB-1997.
PA   (SRLS-) SRL KK.
  Query Match   13.9%; Score 57; DB 2; Length 745;
  Best Local Similarity   35.6%; Pred. No. 3.1e+02;

RESULT 939
ID   ADJ68744 standard; protein; 745 AA.

DE   Human heat mitochondrial protein as a therapeutic target SeqID550.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   13.9%; Score 57; DB 7; Length 745;
     Best Local Similarity   35.6%; Pred. No. 3.1e+02;
RESULT 940
ID   ADJ68203 standard; protein; 745 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID9.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   13.9%; Score 57; DB 7; Length 745;
     Best Local Similarity   35.6%; Pred. No. 3.1e+02;
RESULT 941
ID   ADM67178 standard; protein; 745 AA.
DE   Human adipocyte specific myeloperoxidase protein SeqID 531.
PN   WO2004011618-A2.
PD   05-FEB-2004.
PA   (HMGE-) HMGENE INC.
     Query Match   13.9%; Score 57; DB 8; Length 745;
     Best Local Similarity   35.6%; Pred. No. 3.1e+02;
RESULT 942
ID   ABM81909 standard; protein; 745 AA.
DE   Tumour-associated antigenic target (TAT) polypeptide PRO2839, SEQ:4904.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.9%; Score 57; DB 8; Length 745;
     Best Local Similarity   35.6%; Pred. No. 3.1e+02;
RESULT 943
ID   ADQ39805 standard; protein; 745 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1468.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   13.9%; Score 57; DB 8; Length 745;
     Best Local Similarity   35.6%; Pred. No. 3.1e+02;
RESULT 944
ID   ADQ39803 standard; protein; 777 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1466.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   13.9%; Score 57; DB 8; Length 777;
     Best Local Similarity   35.6%; Pred. No. 3.3e+02;
RESULT 945
ID   ADQ39802 standard; protein; 792 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1465.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   13.9%; Score 57; DB 8; Length 792;
     Best Local Similarity   35.6%; Pred. No. 3.3e+02;
RESULT 946
ID   ABP40237 standard; protein; 118 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5082.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.8%; Score 56.5; DB 5; Length 118;
     Best Local Similarity   23.4%; Pred. No. 45;
RESULT 947
ID   ABR48486 standard; protein; 170 AA.
DE   Human Benzodiazepine Receptor 2.
PN   WO200294864-A2.
PD   28-NOV-2002.
PA   (GEST) GENSET.
     Query Match   13.8%; Score 56.5; DB 6; Length 170;
     Best Local Similarity   34.6%; Pred. No. 68;
RESULT 948

ID   AAR15208 standard; protein; 174 AA.
DE   [Arg11,23,Ser17,27,60,65]huG-CSF.
PN   EP45630-A.
PD   04-DEC-1991.
PA   (ICIL) IMPERIAL CHEM IND PLC.
PA   (ZENE) ZENECA LTD.
     Query Match   13.8%; Score 56.5; DB 2; Length 174;
     Best Local Similarity   32.4%; Pred. No. 70;
RESULT 949
ID   AAR15204 standard; protein; 174 AA.
DE   [Arg11,Ser17,27,60,65]huG-CSF.
PN   EP45630-A.
PD   04-DEC-1991.
PA   (ICIL) IMPERIAL CHEM IND PLC.
PA   (ZENE) ZENECA LTD.
     Query Match   13.8%; Score 56.5; DB 2; Length 174;
     Best Local Similarity   32.4%; Pred. No. 70;
RESULT 950
ID   AAR15209 standard; protein; 174 AA.
DE   [Arg11,40,Ser17,27,60,65]huG-CSF.
PN   EP45630-A.
PD   04-DEC-1991.
PA   (ICIL) IMPERIAL CHEM IND PLC.
PA   (ZENE) ZENECA LTD.
     Query Match   13.8%; Score 56.5; DB 2; Length 174;
     Best Local Similarity   32.4%; Pred. No. 70;
RESULT 951
ID   ABO58635 standard; protein; 201 AA.
DE   Human genome derived single exon protein #4869.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
     Query Match   13.8%; Score 56.5; DB 8; Length 201;
     Best Local Similarity   36.5%; Pred. No. 82;
RESULT 952
ID   ABU05715 standard; protein; 229 AA.
DE   M. tuberculosis and M. leprae marker protein #366.
PN   WO200274903-A2.
PD   26-SEP-2002.
PA   (INSP) INST PASTEUR.
     Query Match   13.8%; Score 56.5; DB 5; Length 229;
     Best Local Similarity   23.7%; Pred. No. 95;
RESULT 953
ID   ADC94492 standard; protein; 246 AA.
DE   E. faecium protein sequence SEQ ID 4119.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.8%; Score 56.5; DB 7; Length 246;
     Best Local Similarity   25.7%; Pred. No. 1e+02;
RESULT 954
ID   AAW88334 standard; protein; 339 AA.
DE   Salmonella enterica O antigen wbaP gene protein product.
PN   WO9850531-A1.
PD   12-NOV-1998.
PA   (UNSY) UNIV SYDNEY.
     Query Match   13.8%; Score 56.5; DB 2; Length 339;
     Best Local Similarity   25.0%; Pred. No. 1.5e+02;
RESULT 955
ID   AAU02946 standard; protein; 452 AA.
DE   Angiotensin converting enzyme (ACEV) splice variant protein #46.
PN   WO200136632-A2.
PD   25-MAY-2001.
PA   (COMP-) COMPUGEN LTD.
     Query Match   13.8%; Score 56.5; DB 4; Length 452;
     Best Local Similarity   22.6%; Pred. No. 2.1e+02;
RESULT 956
ID   AAU02945 standard; protein; 455 AA.
DE   Angiotensin converting enzyme (ACEV) splice variant protein #45.
PN   WO200136632-A2.
PD   25-MAY-2001.

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PA    (COMP-) COMPUGEN LTD.
      Query Match         13.8%;    Score 56.5;   DB 4;    Length 455;
      Best Local Similarity 22.6%;  Pred. No. 2.1e+02;
RESULT 957
ID    ADM72385 standard; protein; 465 AA.
DE    Maize CDPK polypeptide.
PN    WO200402922-A2.
PD    08-APR-2004.
PA    (PION-) PIONEER HI-BRED INT INC.
      Query Match         13.8%;    Score 56.5;   DB 8;    Length 465;
      Best Local Similarity 31.3%;  Pred. No. 2.1e+02;
RESULT 958
ID    ABB82659 standard; protein; 475 AA.
DE    Anabaena PCC7120 protein.
PN    WO200281622-A2.
PD    17-OCT-2002.
PA    (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
      Query Match         13.8%;    Score 56.5;   DB 6;    Length 475;
      Best Local Similarity 30.0%;  Pred. No. 2.2e+02;
RESULT 959
ID    ADC64555 standard; protein; 475 AA.
DE    Anabaena sp. all5073 protein.
PN    US2003192076-A1.
PD    09-OCT-2003.
PA    (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
      Query Match         13.8%;    Score 56.5;   DB 7;    Length 475;
      Best Local Similarity 30.0%;  Pred. No. 2.2e+02;
RESULT 960
ID    ADQ07356 standard; protein; 475 AA.
DE    Anabaena IctB-homologue protein.
PN    US2004128720-A1.
PD    01-JUL-2004.
PA    (KAPL/) KAPLAN A.
PA    (LIEM/) LIEMAN-HURWITZ J.
PA    (SCHA/) SCHATZ D.
PA    (MITT/) MITTLER R.
PA    (RACH/) RACHMILEVITCH S.
      Query Match         13.8%;    Score 56.5;   DB 8;    Length 475;
      Best Local Similarity 30.0%;  Pred. No. 2.2e+02;
RESULT 961
ID    AAY44568 standard; protein; 506 AA.
DE    Mouse Voltage-gated Potassium channel monomer, Kv6.2 variant #3.
PN    WO200001811-A1.
PD    13-JAN-2000.
PA    (ICAG-) ICAGEN INC.
      Query Match         13.8%;    Score 56.5;   DB 8;    Length 475;
      Best Local Similarity 30.0%;  Pred. No. 2.2e+02;
RESULT 962
ID    AAY44566 standard; protein; 506 AA.
DE    Mouse Voltage-gated Potassium channel monomer, Kv6.2 variant #1.
PN    WO200001811-A1.
PD    13-JAN-2000.
PA    (ICAG-) ICAGEN INC.
      Query Match         13.8%;    Score 56.5;   DB 3;    Length 506;
      Best Local Similarity 25.9%;  Pred. No. 2.3e+02;
RESULT 963
ID    AAY44564 standard; protein; 506 AA.
DE    Mouse Voltage-gated Potassium channel monomer, Kv6.2 polypeptide.
PN    WO200001811-A1.
PD    13-JAN-2000.
PA    (ICAG-) ICAGEN INC.
      Query Match         13.8%;    Score 56.5;   DB 3;    Length 506;
      Best Local Similarity 25.9%;  Pred. No. 2.3e+02;
RESULT 964
ID    AAY44567 standard; protein; 506 AA.
DE    Mouse Voltage-gated Potassium channel monomer, Kv6.2 variant #2.
PN    WO200001811-A1.
PD    13-JAN-2000.
PA    (ICAG-) ICAGEN INC.
      Query Match         13.8%;    Score 56.5;   DB 3;    Length 506;
      Best Local Similarity 25.9%;  Pred. No. 2.3e+02;
RESULT 965
ID    ABM83196 standard; protein; 517 AA.

DE    Human diagnostic and therapeutic pprotein SEQ ID NO:3445.
PN    WO2004023973-A2.
PD    25-MAR-2004.
PA    (INCY-) INCYTE CORP.
      Query Match         13.8%;    Score 56.5;   DB 8;    Length 517;
      Best Local Similarity 22.6%;  Pred. No. 2.4e+02;
RESULT 966
ID    ABB63658 standard; protein; 519 AA.
DE    Drosophila melanogaster polypeptide SEQ ID NO 17766.
PN    WO200171042-A2.
PD    27-SEP-2001.
PA    (PEKE ) PE CORP NY.
      Query Match         13.8%;    Score 56.5;   DB 4;    Length 519;
      Best Local Similarity 20.7%;  Pred. No. 2.4e+02;
RESULT 967
ID    ABB80692 standard; protein; 541 AA.
DE    Human GLUT 10 glucose transporter protein.
PN    WO200218621-A2.
PD    07-MAR-2002.
PA    (UYWA-) UNIV WAKE FOREST.
      Query Match         13.8%;    Score 56.5;   DB 5;    Length 541;
      Best Local Similarity 36.5%;  Pred. No. 2.5e+02;
RESULT 968
ID    ABB08251 standard; protein; 541 AA.
DE    Human glucose transporting protein.
PN    WO200202586-A1.
PD    10-JAN-2002.
PA    (UYDU-) UNIV DUKE.
      Query Match         13.8%;    Score 56.5;   DB 5;    Length 541;
      Best Local Similarity 36.5%;  Pred. No. 2.5e+02;
RESULT 969
ID    ABP97191 standard; protein; 541 AA.
DE    Tumour-associated antigenic target protein TAT198 SEQ ID NO:73.
PN    WO2003024392-A2.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match         13.8%;    Score 56.5;   DB 6;    Length 541;
      Best Local Similarity 36.5%;  Pred. No. 2.5e+02;
RESULT 970
ID    ADD22916 standard; protein; 562 AA.
DE    Human sugar transporter, 8105, protein.
PN    US200313841-A1.
PD    19-JUN-2003.
PA    (CURT/) CURTIS R A J.
PA    (GUWW/) GU W.
      Query Match         13.8%;    Score 56.5;   DB 7;    Length 562;
      Best Local Similarity 36.5%;  Pred. No. 2.6e+02;
RESULT 971
ID    ADQ81765 standard; protein; 565 AA.
DE    A deliciosa multifunctional germacrene-D synthase.
PN    WO200458814-A1.
PD    15-JUL-2004.
PA    (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
      Query Match         13.8%;    Score 56.5;   DB 8;    Length 565;
      Best Local Similarity 32.4%;  Pred. No. 2.6e+02;
RESULT 972
ID    AAO14209 standard; protein; 614 AA.
DE    Human transporter and ion channel TRICH-26.
PN    WO200204520-A2.
PD    17-JAN-2002.
PA    (INCY-) INCYTE GENOMICS INC.
      Query Match         13.8%;    Score 56.5;   DB 5;    Length 614;
      Best Local Similarity 36.5%;  Pred. No. 2.9e+02;
RESULT 973
ID    ABG26622 standard; protein; 639 AA.
DE    Novel human diagnostic protein #26613.
PN    WO200175067-A2.
PD    11-OCT-2001.
PA    (HYSE-) HYSEQ INC.
      Query Match         13.8%;    Score 56.5;   DB 4;    Length 639;
      Best Local Similarity 36.5%;  Pred. No. 3e+02;
RESULT 974
ID    ABR42418 standard; protein; 653 AA.
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DE   Human potassium channel Kv1.4.
PN   WO200035690-A2.
PD   01-MAY-2003.
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
     Query Match   13.8%;   Score 56.5;   DB 6;   Length 653;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 975
ID   ADA83742 standard; protein; 653 AA.
DE   Human KCNA4 protein.
PN   WO200210028-A2.
PD   27-DEC-2002.
PA   (BIOM-) BIOMEDICAL CENT
     Query Match   13.8%;   Score 56.5;   DB 6;   Length 653;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 976
ID   ADE57786 standard; protein; 653 AA.
DE   Human Protein P22459, SEQ ID NO 3651.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   13.8%;   Score 56.5;   DB 7;   Length 653;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 977
ID   ADE63497 standard; protein; 653 AA.
DE   Human Protein P22459, SEQ ID NO 9441.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   13.8%;   Score 56.5;   DB 7;   Length 653;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 978
ID   ABO59441 standard; protein; 653 AA.
DE   Human genome derived single exon protein #5675.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
     Query Match   13.8%;   Score 56.5;   DB 7;   Length 653;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 979
ID   ADE63495 standard; protein; 655 AA.
DE   Rat Protein CAA34133, SEQ ID NO 9439.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   13.8%;   Score 56.5;   DB 7;   Length 655;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 980
ID   ADB57784 standard; protein; 655 AA.
DE   Rat Protein P15385, SEQ ID NO 3649.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   13.8%;   Score 56.5;   DB 7;   Length 655;
     Best Local Similarity   22.0%;   Pred. No. 3.1e+02;
RESULT 981
ID   ADN22745 standard; protein; 658 AA.
DE   Bacterial polypeptide #5398.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   13.8%;   Score 56.5;   DB 8;   Length 658;
     Best Local Similarity   26.7%;   Pred. No. 3.1e+02;
RESULT 982

ID   ABP80763 standard; protein; 717 AA.
DE   N. gonorrhoeae amino acid sequence SEQ ID 8056.
PN   WO200279243-A2.
PD   10-OCT-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   13.8%;   Score 56.5;   DB 6;   Length 717;
     Best Local Similarity   27.8%;   Pred. No. 3.5e+02;
RESULT 983
ID   ABU40365 standard; protein; 971 AA.
DE   Protein encoded by Prokaryotic essential gene #25892.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   13.8%;   Score 56.5;   DB 6;   Length 971;
     Best Local Similarity   33.3%;   Pred. No. 4.9e+02;
RESULT 984
ID   AAY21815 standard; protein; 1308 AA.
DE   A. nidulans atrC polypeptide.
PN   WO9932505-A1.
PD   01-JUL-1999.
PA   (ELIL) LILLY & CO ELI.
PA   (UYWA-) UNIV WAGENINGEN AGRIC.
     Query Match   13.8%;   Score 56.5;   DB 2;   Length 1308;
     Best Local Similarity   20.0%;   Pred. No. 6.8e+02;
RESULT 985
ID   AAM37179 standard; protein; 60 AA.
DE   Peptide #11216 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE/) MOLECULAR DYNAMICS INC.
     Query Match   13.7%;   Score 56;   DB 4;   Length 60;
     Best Local Similarity   28.6%;   Pred. No. 24;
RESULT 986
ID   ABG28619 standard; protein; 117 AA.
DE   Novel human diagnostic protein #28610.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   13.7%;   Score 56;   DB 4;   Length 117;
     Best Local Similarity   32.1%;   Pred. No. 52;
RESULT 987
ID   AAG27278 standard; protein; 144 AA.
DE   Zea mays protein fragment SEQ ID NO: 32051.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   13.7%;   Score 56;   DB 3;   Length 144;
     Best Local Similarity   28.6%;   Pred. No. 65;
RESULT 988
ID   AAG27277 standard; protein; 145 AA.
DE   Zea mays protein fragment SEQ ID NO: 32050.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   13.7%;   Score 56;   DB 3;   Length 145;
     Best Local Similarity   30.2%;   Pred. No. 66;
RESULT 989
ID   ABU44223 standard; protein; 198 AA.
DE   Protein encoded by Prokaryotic essential gene #29750.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   13.7%;   Score 56;   DB 6;   Length 198;
     Best Local Similarity   35.5%;   Pred. No. 94;
RESULT 990
ID   ABB89782 standard; protein; 228 AA.
DE   Human polypeptide SEQ ID NO 2158.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   13.7%;   Score 56;   DB 5;   Length 228;
     Best Local Similarity   28.6%;   Pred. No. 1.1e+02;
RESULT 991
ID   ABP70453 standard; peptide; 242 AA.
DE   Partial amino acid sequence of fish taste receptor T1RA.

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PN   WO200301876-A2.
PD   09-JAN-2003.
PA   (SENO-) SENOMYX INC.
     Query Match     13.7%;    Score 56;    DB 6;    Length 242;
     Best Local Similarity    34.1%;    Pred. No. 1.2e+02;
RESULT 992
ID   ADG73587 standard; protein; 242 AA.
DE   Puffer fish T1RA #2.
PN   US200232407-A1.
PD   18-DEC-2003.
PA   (SENO-) SENOMYX INC.
     Query Match     13.7%;    Score 56;    DB 8;    Length 242;
     Best Local Similarity    34.1%;    Pred. No. 1.2e+02;
RESULT 993
ID   ADR29266 standard; protein; 242 AA.
DE   Taste receptor modulation-related tetraodon T1RA part protein SeqID205.
PN   WO2004069191-A2.
PD   19-AUG-2004.
PA   (SENO-) SENOMYX INC.
     Query Match     13.7%;    Score 56;    DB 8;    Length 242;
     Best Local Similarity    34.1%;    Pred. No. 1.2e+02;
RESULT 994
ID   ABP25982 standard; protein; 300 AA.
DE   Streptococcus polypeptide SEQ ID NO 1140.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match     13.7%;    Score 56;    DB 5;    Length 300;
     Best Local Similarity    35.3%;    Pred. No. 1.5e+02;
RESULT 995
ID   AAB87760 standard; protein; 319 AA.
DE   Human T2R30 amino acid sequence SEQ ID NO:51.
PN   WO200118050-A2.
PD   15-MAR-2001.
PA   (REGC ) UNIV CALIFORNIA.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
     Query Match     13.7%;    Score 56;    DB 4;    Length 319;
     Best Local Similarity    24.7%;    Pred. No. 1.6e+02;
RESULT 996
ID   ADR29112 standard; protein; 319 AA.
DE   Taste receptor modulation-related human T2R30 protein sequence SeqID51.
PN   WO2004069191-A2.
PD   19-AUG-2004.
PA   (SENO-) SENOMYX INC.
     Query Match     13.7%;    Score 56;    DB 8;    Length 319;
     Best Local Similarity    24.7%;    Pred. No. 1.6e+02;
RESULT 997
ID   AAU80489 standard; protein; 355 AA.
DE   Rhesus macaque CXCR2 receptor #1.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match     13.7%;    Score 56;    DB 5;    Length 355;
     Best Local Similarity    25.0%;    Pred. No. 1.8e+02;
RESULT 998
ID   AAU80491 standard; protein; 355 AA.
DE   Vervet monkey CXCR2 receptor #1.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match     13.7%;    Score 56;    DB 5;    Length 355;
     Best Local Similarity    25.0%;    Pred. No. 1.8e+02;
RESULT 999
ID   AB081142 standard; protein; 356 AA.
DE   Pseudomonas aeruginosa polypeptide #13317.
PN   US651795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match     13.7%;    Score 56;    DB 7;    Length 356;
     Best Local Similarity    26.0%;    Pred. No. 1.8e+02;
RESULT 1000
ID   AAW98234 standard; protein; 389 AA.

DE   H. pylori GHPO 558 protein.
PN   WO9843478-A1.
PD   08-OCT-1998.
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     13.7%;    Score 56;    DB 2;    Length 389;
     Best Local Similarity    36.5%;    Pred. No. 2e+02;
RESULT 1001
ID   ABU49219 standard; protein; 393 AA.
DE   Protein encoded by Prokaryotic essential gene #34746.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match     13.7%;    Score 56;    DB 6;    Length 393;
     Best Local Similarity    26.5%;    Pred. No. 2e+02;
RESULT 1002
ID   ADS23341 standard; protein; 417 AA.
DE   Bacterial polypeptide #12374.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match     13.7%;    Score 56;    DB 8;    Length 417;
     Best Local Similarity    28.1%;    Pred. No. 2.2e+02;
RESULT 1003
ID   ABU30937 standard; protein; 429 AA.
DE   Protein encoded by Prokaryotic essential gene #16464.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match     13.7%;    Score 56;    DB 6;    Length 429;
     Best Local Similarity    36.5%;    Pred. No. 2.2e+02;
RESULT 1004
ID   ADN22966 standard; protein; 645 AA.
DE   Bacterial polypeptide #5619.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match     13.7%;    Score 56;    DB 8;    Length 645;
     Best Local Similarity    28.6%;    Pred. No. 3.6e+02;
RESULT 1005
ID   AAW94919 standard; protein; 667 AA.
DE   Rat pheromone receptor Go-VN3.
PN   WO9900422-A1.
PD   07-JAN-1999.
PA   (HARD ) HARVARD COLLEGE.
     Query Match     13.7%;    Score 56;    DB 2;    Length 667;
     Best Local Similarity    26.3%;    Pred. No. 3.7e+02;
RESULT 1006
ID   ABB71797 standard; protein; 694 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 42183.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match     13.7%;    Score 56;    DB 4;    Length 694;
     Best Local Similarity    21.2%;    Pred. No. 3.9e+02;
RESULT 1007
ID   ABG26663 standard; protein; 789 AA.
DE   Novel human diagnostic protein #26654.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match     13.7%;    Score 56;    DB 4;    Length 789;
     Best Local Similarity    24.7%;    Pred. No. 4.5e+02;
RESULT 1008
ID   ABB66062 standard; protein; 1035 AA.
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DE   Drosophila melanogaster polypeptide SEQ ID NO 24978.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
   Query Match             13.7%;  Score 56;   DB 4;  Length 1035;
   Best Local Similarity   38.5%;  Pred. No. 6.1e+02;
RESULT 1009
ID   ADR10240 standard; protein; 1300 AA.
DE   Human protein useful for treating neurological disease Seq 3746.
PN   EP1447413-A2.
PD   18-AUG-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
   Query Match             13.7%;  Score 56;   DB 8;  Length 1300;
   Best Local Similarity   26.9%;  Pred. No. 7.8e+02;
RESULT 1010
ID   AAU19518 standard; protein; 1603 AA.
DE   Human diagnostic and therapeutic polypeptide (DITHP) #104.
PN   WO200162927-A2.
PD   30-AUG-2001.
PA   (INCY-) INCYTE GENOMICS INC.
   Query Match             13.7%;  Score 56;   DB 4;  Length 1603;
   Best Local Similarity   27.0%;  Pred. No. 9.9e+02;
RESULT 1011
ID   ADB60401 standard; protein; 1682 AA.
DE   Human Protein Q01118, SEQ ID NO 6310.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
   Query Match             13.7%;  Score 56;   DB 7;  Length 1682;
   Best Local Similarity   23.4%;  Pred. No. 1e+03;
RESULT 1012
ID   AAB82242 standard; protein; 2015 AA.
DE   Human Nav1.5 sodium channel mutant delF1617.
PN   US2003157600-A1.
PD   21-AUG-2003.
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (MAKI/) MAKIELSKI J C.
PA   (YEBB/) YE B.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2015;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1013
ID   ADF56441 standard; protein; 2015 AA.
DE   Human SCN5A variant 4 protein SEQ ID NO:8.
PN   WO2004012668-A2.
PD   12-FEB-2004.
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
   Query Match             13.7%;  Score 56;   DB 7;  Length 2015;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1014
ID   ADM34001 standard; protein; 2015 AA.
DE   Human SCN5A variant 3 protein SEQ ID NO:6.
PN   WO2004012668-A2.
PD   12-FEB-2004.
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
   Query Match             13.7%;  Score 56;   DB 8;  Length 2015;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1015
ID   ADM33999 standard; protein; 2016 AA.
DE   Human hH1 sodium channel protein.
PN   WO9802040-A1.
PD   22-JAN-1998.
PA   (MEDT/) MEDTRONIC INC.
   Query Match             13.7%;  Score 56;   DB 8;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1016
ID   AAW23994 standard; protein; 2016 AA.
DE   Human hH1 sodium channel protein.
PN   WO9802040-A1.
PD   22-JAN-1998.
PA   (MEDT ) MEDTRONIC INC.
   Query Match             13.7%;  Score 56;   DB 2;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1017


ID   AAB82239 standard; protein; 2016 AA.
DE   Human SCN5A protein.
PN   WO200124681-A2.
PD   12-APR-2001.
PA   (UTAH ) UNIV UTAH RES FOUND.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1018
ID   AAB82240 standard; protein; 2016 AA.
DE   Human SCN5A mutant D1114N.
PN   WO200124681-A2.
PD   12-APR-2001.
PA   (UTAH ) UNIV UTAH RES FOUND.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1019
ID   AAB82245 standard; protein; 2016 AA.
DE   Human SCN5A mutant S1787N.
PN   WO200124681-A2.
PD   12-APR-2001.
PA   (UTAH ) UNIV UTAH RES FOUND.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1020
ID   AAB82243 standard; protein; 2016 AA.
DE   Human SCN5A mutant R1623L.
PN   WO200124681-A2.
PD   12-APR-2001.
PA   (UTAH ) UNIV UTAH RES FOUND.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1021
ID   AAB82244 standard; protein; 2016 AA.
DE   Human SCN5A mutant E1784K.
PN   WO200124681-A2.
PD   12-APR-2001.
PA   (UTAH ) UNIV UTAH RES FOUND.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1022
ID   AAB82241 standard; protein; 2016 AA.
DE   Human SCN5A mutant L1501V.
PN   WO200124681-A2.
PD   12-APR-2001.
PA   (UTAH ) UNIV UTAH RES FOUND.
   Query Match             13.7%;  Score 56;   DB 4;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1023
ID   ADD44756 standard; protein; 2016 AA.
DE   Human Protein Q14524, SEQ ID NO 10185.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
   Query Match             13.7%;  Score 56;   DB 7;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1024
ID   ADE55106 standard; protein; 2016 AA.
DE   Human Protein NP_000326, SEQ ID NO 911.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
   Query Match             13.7%;  Score 56;   DB 7;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
RESULT 1025
ID   ADM33997 standard; protein; 2016 AA.
DE   Human SCN5A variant 2 protein SEQ ID NO:4.
PN   WO2004012668-A2.
PD   12-FEB-2004.
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
   Query Match             13.7%;  Score 56;   DB 8;  Length 2016;
   Best Local Similarity   27.0%;  Pred. No. 1.3e+03;
```

RESULT 1026
ID   ADM33995 standard; protein; 2016 AA.
DE   Human SCN5A variant 1 protein SEQ ID NO:2.
PN   WO2004012668-A2.
PD   12-FEB-2004.
PA   (WISC) WISCONSIN ALUMNI RES FOUND.
     Query Match   13.7%; Score 56; DB 8; Length 2016;
     Best Local Similarity   27.0%; Pred. No. 1.3e+03;

RESULT 1027
ID   AAR67913 standard; protein; 2019 AA.
DE   Cardiac sodium channel protein.
PN   US5380836-A.
PD   10-JAN-1995.
PA   (ARCH-) ARCH DEV CORP.
     Query Match   13.7%; Score 56; DB 2; Length 2019;
     Best Local Similarity   27.0%; Pred. No. 1.3e+03;

RESULT 1028
ID   AAR06584 standard; protein; 2020 AA.
DE   Cardiac sodium channel.
PN   WO9009391-A.
PD   23-AUG-1990.
PA   (ARCH-) ARCH DEV CORP.
     Query Match   13.7%; Score 56; DB 2; Length 2020;
     Best Local Similarity   27.0%; Pred. No. 1.3e+03;

RESULT 1029
ID   ABP00874 standard; protein; 54 AA.
DE   Human ORFX protein sequence SEQ ID NO:1730.
PN   WO200192523-A2.
PD   06-DEC-2001.
PA   (CURA-) CURAGEN CORP.
     Query Match   13.5%; Score 55.5; DB 5; Length 54;
     Best Local Similarity   36.6%; Pred. No. 25;

RESULT 1030
ID   ABB50756 standard; protein; 86 AA.
DE   Human secreted protein encoded by gene 62 SEQ ID NO:708.
PN   WO200162891-A2.
PD   30-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   13.5%; Score 55.5; DB 4; Length 86;
     Best Local Similarity   25.0%; Pred. No. 42;

RESULT 1031
ID   ABO45013 standard; protein; 86 AA.
DE   Novel human secreted protein #62 fragment #1.
PN   US200306S160-A1.
PD   03-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   13.5%; Score 55.5; DB 7; Length 86;
     Best Local Similarity   25.0%; Pred. No. 42;

RESULT 1032
ID   ABO26493 standard; protein; 86 AA.
DE   Protein associated with novel secreted protein gene 62 #1.
PN   US6525174-B1.
PD   25-FEB-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   13.5%; Score 55.5; DB 6; Length 86;
     Best Local Similarity   25.0%; Pred. No. 42;

RESULT 1033
ID   AAO00339 standard; protein; 103 AA.
DE   Human.polypeptide SEQ ID NO 14231.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   13.5%; Score 55.5; DB 4; Length 103;
     Best Local Similarity   25.0%; Pred. No. 42;

RESULT 1034
ID   ABO63309 standard; protein; 122 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9826.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.5%; Score 55.5; DB 7; Length 122;
     Best Local Similarity   20.2%; Pred. No. 63;

RESULT 1035
ID   AAY41225 standard; protein; 168 AA.
DE   M. polymorpha YM16-MARPO protein.
PN   WO9951753-A1.
PD   14-OCT-1999.
PA   (UYAL-) UNIV ALBERTA.
     Query Match   13.5%; Score 55.5; DB 2; Length 168;
     Best Local Similarity   29.1%; Pred. No. 90;

RESULT 1036
ID   AAR15206 standard; protein; 174 AA.
DE   [Arg11,Glu15,Ser17,27,60,65,Ala26,28,Lys30]huG-CSF.
PN   EP455630-A.
PD   04-DEC-1991.
PA   (ICIL) IMPERIAL CHEM IND PLC.
PA   (ZENE) ZENECA LTD.
     Query Match   13.5%; Score 55.5; DB 2; Length 174;
     Best Local Similarity   32.4%; Pred. No. 94;

RESULT 1037
ID   AAB65780 standard; protein; 174 AA.
DE   Cysteine protease #21.
PN   WO20007S331-A1.
PD   14-DEC-2000.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
PA   (FLET-) FLETCHER CHALLENGE FORESTS LTD.
     Query Match   13.5%; Score 55.5; DB 4; Length 174;
     Best Local Similarity   40.0%; Pred. No. 94;

RESULT 1038
ID   ABG74380 standard; protein; 174 AA.
DE   Partial human granulocyte colony stimulating factor T38A mutant.
PN   US2002151488-A1.
PD   17-OCT-2002.
PA   (SARK/) SARKAR C A.
PA   (LAUF/) LAUFFENBURGER D A.
     Query Match   13.5%; Score 55.5; DB 7; Length 174;
     Best Local Similarity   31.0%; Pred. No. 94;

RESULT 1039
ID   ADB94799 standard; protein; 174 AA.
DE   Programmed cell death pathway cysteine protease #21.
PN   US2003082724-A1.
PD   01-MAY-2003.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   13.5%; Score 55.5; DB 7; Length 174;
     Best Local Similarity   40.0%; Pred. No. 94;

RESULT 1040
ID   AAU97123 standard; protein; 175 AA.
DE   Human G-CSF mutant, Thr38Ala.
PN   WO200220767-A2.
PD   14-MAR-2002.
PA   (AMGE-) AMGEN INC.
     Query Match   13.5%; Score 55.5; DB 5; Length 175;
     Best Local Similarity   31.0%; Pred. No. 94;

RESULT 1041
ID   ABB15590 standard; protein; 177 AA.
DE   Human nervous system related polypeptide SEQ ID NO 4247.
PN   WO200159063-A2.
PD   16-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   13.5%; Score 55.5; DB 4; Length 177;
     Best Local Similarity   34.0%; Pred. No. 96;

RESULT 1042
ID   ABP30450 standard; protein; 266 AA.
DE   Streptococcus polypeptide SEQ ID NO 10076.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match   13.5%; Score 55.5; DB 5; Length 266;
     Best Local Similarity   30.2%; Pred. No. 1.5e+02;

RESULT 1043
ID   ADC87335 standard; protein; 286 AA.
DE   Human GPCR protein SEQ ID NO:1788.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match   13.5%;   Score 55.5;   DB 7;   Length 286;
    Best Local Similarity   27.5%;   Pred. No. 1.6e+02;
RESULT 1044
ID AAB68530 standard; protein; 292 AA.
DE Human GTP-binding associated protein #30.
PN WO200105970-A2.
PD 25-JAN-2001.
PA (INCY-) INCYTE GENOMICS INC.
    Query Match   13.5%;   Score 55.5;   DB 4;   Length 292;
    Best Local Similarity   34.0%;   Pred. No. 1.7e+02;
RESULT 1045
ID AAU79300 standard; protein; 292 AA.
DE Accessory factor TIP30-32.12 polypeptide.
PN CN1311116-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
    Query Match   13.5%;   Score 55.5;   DB 5;   Length 292;
    Best Local Similarity   34.0%;   Pred. No. 1.7e+02;
RESULT 1046
ID ADC79326 standard; protein; 292 AA.
DE Human G protein coupled receptor X (GPCRX) cDNA seq id 12.
PN US20030083463-A1.
PD 01-MAY-2003.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (COLM/) COLMAN S D.
PA (SPYT/) SPYTEK K A.
PA (BALL/) BALLINGER R A.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S G.
PA (CASM/) CASMAN S J.
PA (GUSE/) GUSEV V Y.
    Query Match   13.5%;   Score 55.5;   DB 7;   Length 292;
    Best Local Similarity   24.2%;   Pred. No. 1.7e+02;
RESULT 1047
ID ABP29833 standard; protein; 310 AA.
DE Streptococcus polypeptide SEQ ID NO 8842.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
    Query Match   13.5%;   Score 55.5;   DB 5;   Length 310;
    Best Local Similarity   30.2%;   Pred. No. 1.8e+02;
RESULT 1048
ID ABP27806 standard; protein; 310 AA.
DE Streptococcus polypeptide SEQ ID NO 4788.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
    Query Match   13.5%;   Score 55.5;   DB 5;   Length 310;
    Best Local Similarity   30.2%;   Pred. No. 1.8e+02;
RESULT 1049
ID AAG71553 standard; protein; 313 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1234.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
    Query Match   13.5%;   Score 55.5;   DB 4;   Length 313;
    Best Local Similarity   24.2%;   Pred. No. 1.8e+02;
RESULT 1050
ID ABP61134 standard; protein; 313 AA.
DE Human GPCRX protein #6.
PN WO200255557-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
    Query Match   13.5%;   Score 55.5;   DB 5;   Length 313;
    Best Local Similarity   24.2%;   Pred. No. 1.8e+02;
RESULT 1051
ID ADC86365 standard; protein; 313 AA.

DE Human GPCR protein SEQ ID NO:818.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match   13.5%;   Score 55.5;   DB 7;   Length 313;
    Best Local Similarity   24.2%;   Pred. No. 1.8e+02;
RESULT 1052
ID AAU36197 standard; protein; 322 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #187.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   13.5%;   Score 55.5;   DB 4;   Length 322;
    Best Local Similarity   50.0%;   Pred. No. 1.9e+02;
RESULT 1053
ID ABU38266 standard; protein; 322 AA.
DE Protein encoded by Prokaryotic essential gene #23793.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   13.5%;   Score 55.5;   DB 6;   Length 322;
    Best Local Similarity   50.0%;   Pred. No. 1.9e+02;
RESULT 1054
ID ADF06388 standard; protein; 326 AA.
DE Bacterial polypeptide #2501.
PN US665709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   13.5%;   Score 55.5;   DB 7;   Length 326;
    Best Local Similarity   27.7%;   Pred. No. 1.9e+02;
RESULT 1055
ID ABP69626 standard; protein; 328 AA.
DE Human polypeptide SEQ ID NO 1673.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
    Query Match   13.5%;   Score 55.5;   DB 5;   Length 328;
    Best Local Similarity   34.0%;   Pred. No. 1.9e+02;
RESULT 1056
ID AAG90308 standard; protein; 345 AA.
DE C glutamicum protein fragment SEQ ID NO: 4062.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
    Query Match   13.5%;   Score 55.5;   DB 4;   Length 345;
    Best Local Similarity   41.9%;   Pred. No. 2e+02;
RESULT 1057
ID ABU41969 standard; protein; 349 AA.
DE Protein encoded by Prokaryotic essential gene #27496.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   13.5%;   Score 55.5;   DB 6;   Length 349;
    Best Local Similarity   24.4%;   Pred. No. 2.1e+02;
RESULT 1058
ID AAU80487 standard; protein; 355 AA.
DE Orangutan CXCR2 receptor #1.
PN WO200190134-A1.
PD 29-NOV-2001.
PA (PHAR-) PHARMACOPEIA INC.
    Query Match   13.5%;   Score 55.5;   DB 5;   Length 355;
    Best Local Similarity   19.0%;   Pred. No. 2.1e+02;
RESULT 1059
ID AAB34521 standard; protein; 360 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 139.
PN WO200056767-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   13.5%;   Score 55.5;   DB 3;   Length 360;
    Best Local Similarity   37.0%;   Pred. No. 2.1e+02;
RESULT 1060
ID ADD44831 standard; protein; 360 AA.

DE   Rat Protein CAA68971, SEQ ID NO 10262.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 360;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1061
ID   ADD44835 standard; protein; 360 AA.
DE   Rat Protein CAA68971, SEQ ID NO 10266.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 360;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1062
ID   ADD44839 standard; protein; 360 AA.
DE   Rat Protein CAA68971, SEQ ID NO 10270.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 360;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1063
ID   ADD46478 standard; protein; 360 AA.
DE   Rat Protein CAA68971, SEQ ID NO 12159.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 360;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1064
ID   ADD44843 standard; protein; 360 AA.
DE   Rat Protein CAA68971, SEQ ID NO 10274.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 360;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1065
ID   ADJ76258 standard; protein; 362 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1510.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
     Query Match   13.5%;   Score 55.5;   DB 8;   Length 362;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1066
ID   ADJ76153 standard; protein; 362 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1405.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
     Query Match   13.5%;   Score 55.5;   DB 8;   Length 362;
     Best Local Similarity 37.0%;   Pred. No. 2.1e+02;
RESULT 1067
ID   ABP95656 standard; protein; 365 AA.
DE   Human GPCR polypeptide SEQ ID NO 122.
PN   WO200215548-A2.
PD   28-FEB-2002.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
     Query Match   13.5%;   Score 55.5;   DB 5;   Length 365;
     Best Local Similarity 24.2%;   Pred. No. 2.2e+02;
RESULT 1068
ID   AAU95698 standard; protein; 365 AA.
DE   Human olfactory and pheromone G protein-coupled receptor #185.
PN   WO200224726-A2.
PD   28-MAR-2002.
PA   (CHEM-) CHEMCOM SA.

     Query Match   13.5%;   Score 55.5;   DB 5;   Length 365;
     Best Local Similarity 24.2%;   Pred. No. 2.2e+02;
RESULT 1069
ID   ADC95364 standard; protein; 370 AA.
DE   E. faecium protein sequence SEQ ID 4991.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 370;
     Best Local Similarity 22.1%;   Pred. No. 2.2e+02;
RESULT 1070
ID   AB071130 standard; protein; 373 AA.
DE   Pseudomonas aeruginosa polypeptide #3305.
PN   US6551795-B1.
PD   22-APR-2001.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 373;
     Best Local Similarity 50.0%;   Pred. No. 2.2e+02;
RESULT 1071
ID   AB061721 standard; protein; 374 AA.
DE   Klebsiella pneumoniae polypeptide seqid 8238.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.5%;   Score 55.5;   DB 7;   Length 374;
     Best Local Similarity 35.1%;   Pred. No. 2.2e+02;
RESULT 1072
ID   AAU24559 standard; protein; 384 AA.
DE   Human olfactory receptor AOLFR46.
PN   WO200168805-A2.
PD   20-SEP-2001.
PA   (SENO-) SENOMYX INC.
     Query Match   13.5%;   Score 55.5;   DB 4;   Length 384;
     Best Local Similarity 24.2%;   Pred. No. 2.3e+02;
RESULT 1073
ID   AAU85179 standard; protein; 384 AA.
DE   G-coupled olfactory receptor #40.
PN   WO200198526-A2.
PD   27-DEC-2001.
PA   (SENO-) SENOMYX INC.
     Query Match   13.5%;   Score 55.5;   DB 4;   Length 384;
     Best Local Similarity 24.2%;   Pred. No. 2.3e+02;
RESULT 1074
ID   ABB67596 standard; protein; 423 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 29580.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   13.5%;   Score 55.5;   DB 4;   Length 423;
     Best Local Similarity 26.2%;   Pred. No. 2.6e+02;
RESULT 1075
ID   ABP74050 standard; protein; 453 AA.
DE   Candida albicans essential protein SEQ ID NO 7887.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   13.5%;   Score 55.5;   DB 5;   Length 453;
     Best Local Similarity 22.9%;   Pred. No. 2.8e+02;
RESULT 1076
ID   AAW88350 standard; protein; 476 AA.
DE   Salmonella enterica O antigen pathway galactosyl transferase.
PN   WO9805361-A1.
PD   12-NOV-1998.
PA   (UNSY) UNIV SYDNEY.
     Query Match   13.5%;   Score 55.5;   DB 2;   Length 476;
     Best Local Similarity 25.0%;   Pred. No. 2.9e+02;
RESULT 1077
ID   ABG21153 standard; protein; 498 AA.
DE   Novel human diagnostic protein #21144.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   13.5%;   Score 55.5;   DB 4;   Length 498;

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     Best Local Similarity  25.8%;  Pred. No. 3.1e+02;
RESULT 1078
ID   ABG61660 standard; protein; 506 AA.
DE   Klebsiella pneumoniae polypeptide seqid 8177.
PN   US5610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match  13.5%;  Score 55.5;  DB 7;  Length 506;
     Best Local Similarity  25.8%;  Pred. No. 3.1e+02;
RESULT 1079
ID   ADN26658 standard; protein; 702 AA.
DE   Bacterial polypeptide #9311.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match  13.5%;  Score 55.5;  DB 8;  Length 702;
     Best Local Similarity  28.2%;  Pred. No. 4.5e+02;
RESULT 1080
ID   ADS28704 standard; protein; 720 AA.
DE   Bacterial polypeptide #17737.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match  13.5%;  Score 55.5;  DB 8;  Length 720;
     Best Local Similarity  28.2%;  Pred. No. 4.7e+02;
RESULT 1081
ID   AAY77556 standard; protein; 843 AA.
DE   Rat GPCR-B4 polypeptide.
PN   WO200006593-A1.
PD   10-FEB-2000.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match  13.5%;  Score 55.5;  DB 3;  Length 843;
     Best Local Similarity  26.8%;  Pred. No. 5.6e+02;
RESULT 1082
ID   ABR13494 standard; protein; 843 AA.
DE   Rat sweet taste receptor T1R2 protein SEQ ID NO:6.
PN   WO2003025137-A2.
PD   27-MAR-2003.
PA   (IRMI-) IRM LLC.
PA   (SCRI ) SCRIPPS RES INST.
     Query Match  13.5%;  Score 55.5;  DB 6;  Length 843;
     Best Local Similarity  26.8%;  Pred. No. 5.6e+02;
RESULT 1083
ID   ADK90717 standard; protein; 843 AA.
DE   Rat taste receptor T1R2 protein.
PN   WO200304992-A2.
PD   16-JAN-2003.
PA   (REGC ) UNIV CALIFORNIA.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
     Query Match  13.5%;  Score 55.5;  DB 7;  Length 843;
     Best Local Similarity  26.8%;  Pred. No. 5.6e+02;
RESULT 1084
ID   ADI41010 standard; protein; 843 AA.
DE   Rat taste receptor TR2 #2.
PN   US2004018976-A1.
PD   29-JAN-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
     Query Match  13.5%;  Score 55.5;  DB 8;  Length 843;
     Best Local Similarity  26.8%;  Pred. No. 5.6e+02;
RESULT 1085
ID   ADI40978 standard; protein; 843 AA.
DE   Rat taste receptor TR2.
PN   US2004018976-A1.

PD   29-JAN-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
     Query Match  13.5%;  Score 55.5;  DB 8;  Length 843;
     Best Local Similarity  26.8%;  Pred. No. 5.6e+02;
RESULT 1086
ID   ADF06662 standard; protein; 883 AA.
DE   Bacterial polypeptide #2775.
PN   US665709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match  13.5%;  Score 55.5;  DB 7;  Length 883;
     Best Local Similarity  31.7%;  Pred. No. 5.9e+02;
RESULT 1087
ID   ABU41831 standard; protein; 930 AA.
DE   Protein encoded by Prokaryotic essential gene #27358.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match  13.5%;  Score 55.5;  DB 6;  Length 930;
     Best Local Similarity  31.2%;  Pred. No. 6.2e+02;
RESULT 1088
ID   ABG25961 standard; protein; 1212 AA.
DE   Novel human diagnostic protein #25952.
PN   WO20017067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match  13.5%;  Score 55.5;  DB 4;  Length 1212;
     Best Local Similarity  20.8%;  Pred. No. 8.4e+02;
RESULT 1089
ID   ABP07353 standard; protein; 51 AA.
DE   Human ORFX protein sequence SEQ ID NO:14688.
PN   WO200192523-A2.
PD   06-DEC-2001.
PA   (CURA-) CURAGEN CORP.
     Query Match  13.4%;  Score 55;  DB 5;  Length 51;
     Best Local Similarity  48.1%;  Pred. No. 27;
RESULT 1090
ID   ADF59396 standard; protein; 58 AA.
DE   Human polypeptide sequence SEQ ID NO:1804.
PN   WO2003080795-A2.
PD   02-OCT-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match  13.4%;  Score 55;  DB 7;  Length 58;
     Best Local Similarity  33.3%;  Pred. No. 31;
RESULT 1091
ID   ABB11090 standard; peptide; 116 AA.
DE   Human hydrophobic domain protein homologue, SEQ ID NO:1460.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match  13.4%;  Score 55;  DB 4;  Length 116;
     Best Local Similarity  25.0%;  Pred. No. 69;
RESULT 1092
ID   ABP70452 standard; peptide; 137 AA.
DE   Partial amino acid sequence of fish taste receptor T1RA.
PN   WO200301876-A2.
PD   09-JAN-2003.
PA   (SENO-) SENOMYX INC.
     Query Match  13.4%;  Score 55;  DB 6;  Length 137;
     Best Local Similarity  34.1%;  Pred. No. 83;
RESULT 1093
ID   ADG73586 standard; protein; 137 AA.
DE   Puffer fish T1RA #1.
PN   US2003232407-A1.
PD   18-DEC-2003.
PA   (SENO-) SENOMYX INC.
     Query Match  13.4%;  Score 55;  DB 8;  Length 137;
     Best Local Similarity  34.1%;  Pred. No. 83;
RESULT 1094
ID   ADR29265 standard; protein; 137 AA.
DE   Taste receptor modulation-related fugu T1RA partial protein SeqID204.
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PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
  Query Match   13.4%; Score 55; DB 8; Length 137;
  Best Local Similarity   34.1%; Pred. No. 83;
RESULT 1095
ID AAM06762 standard; protein; 155 AA.
DE Human foetal protein, SEQ ID NO: 970.
PN WO200155339-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
  Query Match   13.4%; Score 55; DB 4; Length 155;
  Best Local Similarity   31.7%; Pred. No. 95;
RESULT 1096
ID AAW29673 standard; protein; 189 AA.
DE Homo sapiens clone CO851_1 secreted protein.
PN WO9832853-A2.
PD 30-JUL-1998.
PA (GBMY) GENETICS INST INC.
  Query Match   13.4%; Score 55; DB 2; Length 189;
  Best Local Similarity   27.6%; Pred. No. 1.2e+02;
RESULT 1097
ID ADS93517 standard; protein; 224 AA.
DE Apple tree alpha-farnesene synthase partial protein SeqID 7.
PN WO2004035791-A1.
PD 29-APR-2004.
PA (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
  Query Match   13.4%; Score 55; DB 8; Length 224;
  Best Local Similarity   30.8%; Pred. No. 1.4e+02;
RESULT 1098
ID AAW82260 standard; protein; 242 AA.
DE C. utilis crtW protein.
PN JP10248575-A.
PD 22-SEP-1998.
PA (KIRI) KIRIN BREWERY KK.
  Query Match   13.4%; Score 55; DB 2; Length 242;
  Best Local Similarity   27.3%; Pred. No. 1.6e+02;
RESULT 1099
ID ADO61157 standard; protein; 242 AA.
DE A. aurantiacum ketolase.
PN DE10238978-A1.
PD 04-MAR-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
  Query Match   13.4%; Score 55; DB 8; Length 242;
  Best Local Similarity   27.3%; Pred. No. 1.6e+02;
RESULT 1100
ID ADO61074 standard; protein; 242 AA.
DE A. aurantiacum ketolase.
PN DE10238980-A1.
PD 04-MAR-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
  Query Match   13.4%; Score 55; DB 8; Length 242;
  Best Local Similarity   27.3%; Pred. No. 1.6e+02;
RESULT 1101
ID ADQ38243 standard; protein; 242 AA.
DE Agrobacterium aurantiacum ketolase.
PN DE10258971-A1.
PD 01-JUL-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
  Query Match   13.4%; Score 55; DB 8; Length 242;
  Best Local Similarity   27.3%; Pred. No. 1.6e+02;
RESULT 1102
ID ADR03858 standard; protein; 242 AA.
DE Agrobacterium aurantiacum ketolase SEQ ID NO: 16.
PN WO2004063359-A2.
PD 29-JUL-2004.
PA (BADI) BASF AG.
  Query Match   13.4%; Score 55; DB 8; Length 242;
  Best Local Similarity   27.3%; Pred. No. 1.6e+02;
RESULT 1103
ID ADR03938 standard; protein; 242 AA.
DE A aurantiacum ketolase.
PN WO2004063358-A1.

PD 29-JUL-2004.
PA (BADI) BASF AG.
  Query Match   13.4%; Score 55; DB 8; Length 242;
  Best Local Similarity   27.3%; Pred. No. 1.6e+02;
RESULT 1104
ID ABU29533 standard; protein; 249 AA.
DE Protein encoded by Prokaryotic essential gene #15060.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match   13.4%; Score 55; DB 6; Length 249;
  Best Local Similarity   31.7%; Pred. No. 1.6e+02;
RESULT 1105
ID ADS29715 standard; protein; 249 AA.
DE Bacterial polypeptide #18748.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
  Query Match   13.4%; Score 55; DB 8; Length 249;
  Best Local Similarity   35.5%; Pred. No. 1.6e+02;
RESULT 1106
ID ABP38072 standard; protein; 289 AA.
DE Staphylococcus epidermis ORF amino acid sequence SEQ ID NO:2917.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   13.4%; Score 55; DB 5; Length 289;
  Best Local Similarity   20.8%; Pred. No. 1.9e+02;
RESULT 1107
ID ADS07459 standard; protein; 289 AA.
DE Staphylococcus epidermis polypeptide seqid 6754.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
  Query Match   13.4%; Score 55; DB 8; Length 289;
  Best Local Similarity   20.8%; Pred. No. 1.9e+02;
RESULT 1108
ID ABG71364 standard; protein; 294 AA.
DE Potato starch degrading enzyme CSD23.
PN WO200286112-A2.
PD 31-OCT-2002.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match   13.4%; Score 55; DB 6; Length 294;
  Best Local Similarity   29.9%; Pred. No. 2e+02;
RESULT 1109
ID ADC94895 standard; protein; 327 AA.
DE E. faecium protein sequence SEQ ID 4522.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   13.4%; Score 55; DB 7; Length 327;
  Best Local Similarity   31.7%; Pred. No. 2.2e+02;
RESULT 1110
ID ADO29264 standard; protein; 347 AA.
DE Mouse GPCR CNR2, SEQ ID NO:365.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
  Query Match   13.4%; Score 55; DB 8; Length 347;
  Best Local Similarity   27.8%; Pred. No. 2.4e+02;
RESULT 1111
ID ABB57956 standard; protein; 351 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 660.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
  Query Match   13.4%; Score 55; DB 4; Length 351;
  Best Local Similarity   33.3%; Pred. No. 2.4e+02;

RESULT 1112
ID   AAR53932 standard; protein; 354 AA.
DE   Interleukin 8 (IL-8) receptor.
PN   JP06100595-A.
PD   12-APR-1994.
PA   (UYBO-) UNIV BOSTON.
     Query Match   13.4%; Score 55; DB 2; Length 354;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1113
ID   ADH61817 standard; protein; 354 AA.
DE   Human interleukin-8 receptor beta protein sequence.
PN   US2003224426-A1.
PD   04-DEC-2003.
PA   (LIYY/) LI Y.
     Query Match   13.4%; Score 55; DB 8; Length 354;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1114
ID   AAR28272 standard; protein; 355 AA.
DE   Sequence in a high affinity recombinant rabbit interleukin-8 (IL-8)
DE   receptor polypeptide in F3R.
PN   WO9218641-A1.
PD   29-OCT-1992.
PA   (UYBO-) UNIV BOSTON.
PA   (REPK) REPLIGEN CORP.
     Query Match   13.4%; Score 55; DB 2; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1115
ID   AAR33420 standard; protein; 355 AA.
DE   Human IL-8 receptor from clone p2.
PN   WO9306229-A1.
PD   01-APR-1993.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICE.
     Query Match   13.4%; Score 55; DB 2; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1116
ID   AAR80950 standard; protein; 355 AA.
DE   Recombinant high affinity interleukin-8 receptor subtype A.
PN   WO9525126-A1.
PD   21-SEP-1995.
PA   (REPK) REPLIGEN CORP.
PA   (UYBO-) UNIV BOSTON.
     Query Match   13.4%; Score 55; DB 2; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1117
ID   AAB09990 standard; protein; 355 AA.
DE   Human IL-8 receptor protein hIL8RB.
PN   JP08103276-A.
PD   23-APR-1996.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   13.4%; Score 55; DB 2; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1118
ID   AAU80483 standard; protein; 355 AA.
DE   Chimpanzee CXCR2 receptor #1.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match   13.4%; Score 55; DB 5; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1119
ID   AAU80485 standard; protein; 355 AA.
DE   Gorilla CXCR2 receptor #1.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match   13.4%; Score 55; DB 5; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1120
ID   AAU80488 standard; protein; 355 AA.
DE   Orangutan CXCR2 receptor #2.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.

     Query Match   13.4%; Score 55; DB 5; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1121
ID   AAU80482 standard; protein; 355 AA.
DE   Human CXCR2 receptor #1.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match   13.4%; Score 55; DB 5; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1122
ID   AAU80484 standard; protein; 355 AA.
DE   Chimpanzee CXCR2 receptor #2.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match   13.4%; Score 55; DB 5; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1123
ID   AAU80486 standard; protein; 355 AA.
DE   Gorilla CXCR2 receptor #2.
PN   WO200190134-A1.
PD   29-NOV-2001.
PA   (PHAR-) PHARMACOPEIA INC.
     Query Match   13.4%; Score 55; DB 5; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1124
ID   ABU79168 standard; protein; 355 AA.
DE   Rabbit interleukin 8A (IL8A) receptor.
PN   US2002197706-A1.
PD   26-DEC-2002.
PA   (CADU-) CADUS PHARM CORP.
     Query Match   13.4%; Score 55; DB 6; Length 355;
     Best Local Similarity   20.8%; Pred. No. 2.4e+02;
RESULT 1125
ID   AAR28273 standard; protein; 360 AA.
DE   Sequence in a low affinity recombinant human interleukin-8 (IL-8)
DE   receptor polypeptide in 4AB.
PN   WO9218641-A1.
PD   29-OCT-1992.
PA   (UYBO-) UNIV BOSTON.
PA   (REPK) REPLIGEN CORP.
     Query Match   13.4%; Score 55; DB 2; Length 360;
     Best Local Similarity   20.8%; Pred. No. 2.5e+02;
RESULT 1126
ID   AAR80953 standard; protein; 360 AA.
DE   Recombinant high affinity interleukin-8 receptor subtype B.
PN   WO9525126-A1.
PD   21-SEP-1995.
PA   (REPK) REPLIGEN CORP.
PA   (UYBO-) UNIV BOSTON.
     Query Match   13.4%; Score 55; DB 2; Length 360;
     Best Local Similarity   20.8%; Pred. No. 2.5e+02;
RESULT 1127
ID   AAR80758 standard; protein; 360 AA.
DE   Interleukin 8 receptor B.
PN   US5440021-A.
PD   08-AUG-1995.
PA   (HEBE/) HEBERT C.
PA   (CHUN/) CHUNTHARAPAI A.
PA   (KIMK/) KIM K J.
PA   (LEEJ/) LEE J.
     Query Match   13.4%; Score 55; DB 2; Length 360;
     Best Local Similarity   20.8%; Pred. No. 2.5e+02;
RESULT 1128
ID   AAG80121 standard; protein; 360 AA.
DE   Human CXCR2 protein.
PN   WO200172830-A2.
PD   04-OCT-2001.
PA   (IPFP-) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
     Query Match   13.4%; Score 55; DB 4; Length 360;
     Best Local Similarity   20.8%; Pred. No. 2.5e+02;

RESULT 1129
ID   AAU10557 standard; protein; 360 AA.
DE   Human interleukin 8 receptor beta (IL8RB) polypeptide.
PN   WO200179221-A2.
PD   25-OCT-2001.
PA   (GENA-) GENAISSANCE PHARM INC.
     Query Match   13.4%; Score 55; DB 5; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1130
ID   ABP54802 standard; protein; 360 AA.
DE   Human COPD-related immunoglobulin-derived protein.
PN   WO200272788-A2.
PD   19-SEP-2002.
PA   (CENZ) CENTOCOR INC.
     Query Match   13.4%; Score 55; DB 5; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1131
ID   ABP81950 standard; protein; 360 AA.
DE   Human interleukin-8 receptor B protein SEQ ID NO:386.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   13.4%; Score 55; DB 6; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1132
ID   ADD48097 standard; protein; 360 AA.
DE   Human Protein NP_001548, SEQ ID NO 13795.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   13.4%; Score 55; DB 6; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1133
ID   ABM85489 standard; protein; 360 AA.
DE   Antipsoriatic protein sequence #332.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
     Query Match   13.4%; Score 55; DB 7; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1134
ID   ADN04275 standard; protein; 360 AA.
DE   Human protein sequence hCP35582.
PN   WO2004028479-A2.
PD   08-APR-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   13.4%; Score 55; DB 7; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1135
ID   ADQ29524 standard; protein; 360 AA.
DE   Human GPCR IL8RB, SEQ ID NO:626.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.4%; Score 55; DB 8; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1136
ID   ADO19582 standard; protein; 360 AA.
DE   Human PRO polypeptide #256.
PN   WO2004043361-A2.
PD   27-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.4%; Score 55; DB 8; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1137
ID   ADP24006 standard; protein; 360 AA.
DE   PRO polypeptide SEQ ID NO:1184.
PN   WO2004041170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.4%; Score 55; DB 8; Length 360;
     Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1138
ID   ABG72361 standard; protein; 363 AA.
DE   Rabbit orphan G-protein coupled receptor HM74A.
PN   WO200284298-A2.
PD   24-OCT-2002.
PA   (GLAX) GLAXO GROUP LTD.
     Query Match   13.4%; Score 55; DB 6; Length 363;
     Best Local Similarity 26.8%; Pred. No. 2.5e+02;

RESULT 1139
ID   ADQ97953 standard; protein; 363 AA.
DE   Mouse cancer associated sequence MP11-028, SEQ ID 930.
PN   WO2004060304-A2.
PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match   13.4%; Score 55; DB 8; Length 363;
     Best Local Similarity 27.8%; Pred. No. 2.5e+02;

RESULT 1140
ID   AAB96070 standard; protein; 375 AA.
DE   Putative glutathione-dependent Na/H antiporter transmembrane domain #1.
PN   FR2792651-A1.
PD   27-OCT-2000.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     (IFRB-) IFREMER INST FR RECH EXPL MER.
     Query Match   13.4%; Score 55; DB 4; Length 375;
     Best Local Similarity 29.3%; Pred. No. 2.6e+02;

RESULT 1141
ID   ABB12024 standard; peptide; 399 AA.
DE   Human IL-8R B homologue, SEQ ID NO:2394.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   13.4%; Score 55; DB 4; Length 399;
     Best Local Similarity 20.8%; Pred. No. 2.8e+02;

RESULT 1142
ID   ABG13609 standard; protein; 399 AA.
DE   Novel human diagnostic protein #13600.
PN   WO2003057841-A2.
PD   17-JUL-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   13.4%; Score 55; DB 4; Length 399;
     Best Local Similarity 20.8%; Pred. No. 2.8e+02;

RESULT 1143
ID   ADK40900 standard; protein; 399 AA.
DE   Novel human kinase protein #7.
PN   WO2003075067-A2.
PD   11-SEP-2003.
PA   (GRIG/) GRIGORIEV I V.
     (SUDA/) SUDARSANAM S.
     Query Match   13.4%; Score 55; DB 4; Length 399;
     Best Local Similarity 20.8%; Pred. No. 2.8e+02;

RESULT 1144
ID   ADR15624 standard; protein; 399 AA.
DE   Kinase 35582 hCT7327, SEQ ID 17.
PN   WO2004069154-A2.
PD   19-AUG-2004.
PA   (GRIG/) GRIGORIEV I V.
     (SUDA/) SUDARSANAM S.
     Query Match   13.4%; Score 55; DB 7; Length 399;
     Best Local Similarity 20.8%; Pred. No. 2.8e+02;

RESULT 1145
ID   AAG07601 standard; protein; 428 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 4817.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   13.4%; Score 55; DB 3; Length 428;
     Best Local Similarity 24.5%; Pred. No. 3e+02;

RESULT 1146
ID   AAU34470 standard; protein; 439 AA.
DE   E. coli cellular proliferation protein #51.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   13.4%; Score 55; DB 4; Length 439;

Best Local Similarity 24.6%; Pred. No. 3.1e+02;
RESULT 1147
ID ABU28522 standard; protein; 439 AA.
DE Protein encoded by Prokaryotic essential gene #14049.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.4%; Score 55; DB 6; Length 439;
Best Local Similarity 24.6%; Pred. No. 3.1e+02;
RESULT 1148
ID ABU28316 standard; protein; 443 AA.
DE Protein encoded by Prokaryotic essential gene #13843.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.4%; Score 55; DB 6; Length 443;
Best Local Similarity 35.8%; Pred. No. 3.1e+02;
RESULT 1149
ID AAG07600 standard; protein; 467 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4816.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (PEKE) PE CORP NY.
Query Match 13.4%; Score 55; DB 3; Length 467;
Best Local Similarity 24.5%; Pred. No. 3.3e+02;
RESULT 1150
ID ABB67349 standard; protein; 526 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28839.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.4%; Score 55; DB 4; Length 526;
Best Local Similarity 34.9%; Pred. No. 3.8e+02;
RESULT 1151
ID ADG74258 standard; protein; 570 AA.
DE Fruit fly frizzled protein, SEQ ID No 43.
PN WO200292635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 13.4%; Score 55; DB 7; Length 570;
Best Local Similarity 21.2%; Pred. No. 4.1e+02;
RESULT 1152
ID ABB68074 standard; protein; 581 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31014.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.4%; Score 55; DB 4; Length 581;
Best Local Similarity 34.9%; Pred. No. 4.2e+02;
RESULT 1153
ID AAW31267 standard; protein; 694 AA.
DE Drosophila frizzled-2 protein (Wnt receptor).
PN WO9739357-A1.
PD 23-OCT-1997.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 13.4%; Score 55; DB 2; Length 694;
Best Local Similarity 21.2%; Pred. No. 5.2e+02;
RESULT 1154
ID ABB58605 standard; protein; 995 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2607.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.4%; Score 55; DB 4; Length 995;
Best Local Similarity 24.6%; Pred. No. 7.8e+02;
RESULT 1155
ID AAR70124 standard; protein; 1064 AA.
DE IL8-R type 2-GBP 130 fusion protein.
PN WO9506737-A1.
PD 09-MAR-1995.
PA (PREN/) PRENDERGAST K F.
Query Match 13.4%; Score 55; DB 2; Length 1064;
Best Local Similarity 20.8%; Pred. No. 8.4e+02;

RESULT 1156
ID ABU50193 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #35720.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.4%; Score 55; DB 6; Length 1139;
Best Local Similarity 23.7%; Pred. No. 9.1e+02;
RESULT 1157
ID ADF59164 standard; protein; 58 AA.
DE Human polypeptide sequence SEQ ID NO:1572.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.3%; Score 54.5; DB 7; Length 58;
Best Local Similarity 30.4%; Pred. No. 36;
RESULT 1158
ID ABJ03718 standard; protein; 84 AA.
DE Human ovary specific protein SEQ ID NO: 160.
PN WO200240720-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 13.3%; Score 54.5; DB 5; Length 84;
Best Local Similarity 27.4%; Pred. No. 55;
RESULT 1159
ID ADF04506 standard; protein; 100 AA.
DE Bacterial polypeptide #619.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.3%; Score 54.5; DB 7; Length 100;
Best Local Similarity 28.2%; Pred. No. 67;
RESULT 1160
ID ABO67299 standard; protein; 109 AA.
DE Klebsiella pneumoniae polypeptide seqid 13816.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.3%; Score 54.5; DB 7; Length 109;
Best Local Similarity 35.5%; Pred. No. 74;
RESULT 1161
ID ADS88808 standard; protein; 152 AA.
DE Amino acid sequence of a truncated GPR54 receptor.
PN EP1464652-A1.
PD 06-OCT-2004.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYPA-) UNIV PARIS SUD.
PA (UYPA-) UNIV PARIS DESCARTES.
Query Match 13.3%; Score 54.5; DB 8; Length 152;
Best Local Similarity 27.3%; Pred. No. 1.1e+02;
RESULT 1162
ID AAB14852 standard; protein; 175 AA.
DE Granulopoietic activity protein bndry4_2.
PN WO200040728-A1.
PD 13-JUL-2000.
PA (XENC-) XENCOR INC.
Query Match 13.3%; Score 54.5; DB 3; Length 175;
Best Local Similarity 26.7%; Pred. No. 1.3e+02;
RESULT 1163
ID ADM47962 standard; protein; 244 AA.
DE Polypeptide sequence #12 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 13.3%; Score 54.5; DB 8; Length 244;
Best Local Similarity 28.8%; Pred. No. 1.8e+02;
RESULT 1164
ID AAW61620 standard; protein; 245 AA.
DE Clone HSBBF02 of TM4SF superfamily.
PN WO981799-A2.
PD 23-JUL-1998.

PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   13.3%; Score 54.5; DB 2; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1165
ID   AAY28677 standard; protein; 245 AA.
DE   Human bx141_2 secreted protein.
PN   WO9935165-A1.
PD   15-JUL-1999.
PA   (GEMY) GENETICS INST INC.
RESULT 1166
ID   AAY99340 standard; protein; 245 AA.
DE   Human PRO1560 (UNQ767) amino acid sequence SEQ ID NO:4.
PN   WO200012708-A2.
PD   09-MAR-2000.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 2; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1167
ID   AAM93505 standard; protein; 245 AA.
DE   Human polypeptide, SEQ ID NO: 3217.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match   13.3%; Score 54.5; DB 3; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1168
ID   AAU39033 standard; protein; 245 AA.
DE   Human secreted protein bx141_2.
PN   WO200175068-A2.
PD   11-OCT-2001.
PA   (GEMY) GENETICS INST INC.
Query Match   13.3%; Score 54.5; DB 4; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1169
ID   AAB66089 standard; protein; 245 AA.
DE   Protein of the invention #1.
PN   WO200078961-A1.
PD   28-DEC-2000.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 4; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1170
ID   AAB85032 standard; protein; 245 AA.
DE   Pain regulated protein sequence 27.
PN   WO200212338-A2.
PD   14-FEB-2002.
PA   (CHEF) GRUENENTHAL GMBH.
Query Match   13.3%; Score 54.5; DB 5; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1171
ID   ABP61468 standard; protein; 245 AA.
DE   Human NF-kB activating protein SEQ ID NO 89.
PN   WO200253737-A1.
PD   11-JUL-2002.
PA   (ASAH) ASAHI KASEI KOGYO KK.
Query Match   13.3%; Score 54.5; DB 5; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1172
ID   ABG34031 standard; protein; 245 AA.
DE   Human Pro peptide #2.
PN   WO20024888-A2.
PD   28-MAR-2002.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 5; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1173
ID   ABB55742 standard; protein; 245 AA.
DE   Human polypeptide SEQ ID NO 90.
PN   US2001039335-A1.
PD   08-NOV-2001.
PA   (JACO/) JACOBS K.

PA   (MCCO/) MCCOY J M.
PA   (LAVA/) LAVALLIE E R.
PA   (COLL/) COLLINS-RACIE L A.
PA   (EVAN/) EVANS C.
PA   (MERB/) MERBERG D.
PA   (TREA/) TREACY M.
PA   (AGOS/) AGOSTINO M J.
PA   (STEI/) STEININGER R J.
PA   (SPAU/) SPAULDING V.
PA   (WONG/) WONG G G.
PA   (CLAR/) CLARK H.
PA   (FECH/) FECHTEL K.
Query Match   13.3%; Score 54.5; DB 5; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1174
ID   ADA01272 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003068779-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 6; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1175
ID   ABO35582 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003073130-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 6; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1176
ID   ADA43701 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003064474-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 6; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1177
ID   ADA43469 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003073196-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 6; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1178
ID   ADA01144 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003068782-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 6; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1179
ID   ADA01028 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003068780-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 7; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1180
ID   ABO44435 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003044841-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.3%; Score 54.5; DB 7; Length 245;
Best Local Similarity 25.3%; Pred. No. 1.8e+02;
RESULT 1181
ID   ADA43585 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.

PN   US2003073190-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1182
ID   ABO33459 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003073129-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1183
ID   ADA06847 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003068781-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1184
ID   ADA08335 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003068783-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1185
ID   ADB99628 standard; protein; 245 AA.
DE   Human PRO polypeptide SEQ ID 4.
PN   US2003082728-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1186
ID   ADB86911 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003082726-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1187
ID   ADB66066 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003082729-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1188
ID   ADB99744 standard; protein; 245 AA.
DE   Human PRO polypeptide SEQ ID 4.
PN   US2003073192-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1189
ID   ADB99399 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003082731-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1190
ID   ADB65950 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003082732-A1.

PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1191
ID   ADC17873 standard; protein; 245 AA.
DE   Human PRO polypeptide #1.
PN   US2003064925-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1192
ID   ADC23348 standard; protein; 245 AA.
DE   Human transmembrane PRO polypeptide (SeqID 4).
PN   US2003073193-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1193
ID   ADC26041 standard; protein; 245 AA.
DE   Human PRO1560 protein.
PN   US2003073194-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1194
ID   ABW01502 standard; protein; 245 AA.
DE   Human receptor protein from clone HSBBF02.
PN   US2003129696-A1.
PD   10-JUL-2003.
PA   (NIJU/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (GENT/) GENTZ R.
RESULT 1195
ID   ADD70519 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003099625-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1196
ID   ADD39596 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003083462-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1197
ID   ADD70042 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003054406-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1198
ID   ADD38163 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003096955-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 7; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1199
ID   ADD39119 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.

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PN  US2003096954-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1200
ID  ADD38642 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003092061-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1201
ID  ADD40073 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003082627-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1202
ID  ADE04868 standard; protein; 245 AA.
DE  Human PRO polypeptide #2.
PN  US2003068778-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1203
ID  ADE50294 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003069179-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1204
ID  ADE11174 standard; protein; 245 AA.
DE  Human PRO polypeptide #2.
PN  US2003073191-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1205
ID  ADE19906 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003092883-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1206
ID  ADD88105 standard; protein; 245 AA.
DE  Human PRO polypeptide #2.
PN  US2003082733-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1207
ID  ADD95400 standard; protein; 245 AA.
DE  Human secreted/transmembrane polypeptide PRO1560.
PN  US2003064473-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1208
ID  ADE06330 standard; protein; 245 AA.
DE  Human PRO polypeptide #2.
PN  US2003073195-A1.

PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1209
ID  ADE38105 standard; protein; 245 AA.
DE  Human PRO polypeptide #2.
PN  US2003119120-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1210
ID  ADE49817 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003082626-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1211
ID  ADE21375 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003082628-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1212
ID  ADD88221 standard; protein; 245 AA.
DE  Human PRO polypeptide #2.
PN  US2003073189-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1213
ID  ADD89032 standard; protein; 245 AA.
DE  TAT273.
PN  WO2003057160-A2.
PD  17-JUL-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1214
ID  ADD90802 standard; protein; 245 AA.
DE  Human secreted/transmembrane polypeptide PRO1560.
PN  US2003073188-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1215
ID  ADF29800 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003204053-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1216
ID  ADF55693 standard; protein; 245 AA.
DE  Human secreted/transmembrane protein PRO1560.
PN  US2003204054-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             13.3%;    Score 54.5;    DB 7;     Length 245;
    Best Local Similarity   25.3%;    Pred. No. 1.8e+02;
RESULT 1217
ID  ADF99357 standard; protein; 245 AA.
DE  Human secreted/transmembrane polypeptide PRO1560.
PN  US2003078401-A1.
PD  24-APR-2003.
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PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 7;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1218
ID   ADG06450 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003077742-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 7;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1219
ID   ADG05401 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003077741-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 7;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1220
ID   ADG82402 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003077744-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 7;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1221
ID   ADH99197 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003065142-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 7;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1222
ID   ADE51655 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104560-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1223
ID   ADE51771 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104561-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1224
ID   ADE37629 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104564-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1225
ID   ADE37513 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104565-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1226
ID   ADD95284 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003138901-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.

Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1227
ID   ADE37984 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1228
ID   ADE76073 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003124665-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1229
ID   ADE39396 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119117-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1230
ID   ADB04200 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003096364-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1231
ID   ADE39797 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003138896-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1232
ID   ADE19662 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003138903-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1233
ID   ADE77240 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003124666-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1234
ID   ADE65348 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119116-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
Best Local Similarity      25.3%;  Pred. No. 1.8e+02;
RESULT 1235
ID   ADE75957 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003124663-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                13.3%;  Score 54.5;  DB 8;  Length 245;
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     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1236
ID   ADE37868 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119119-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1237
ID   ADE64478 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119114-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1238
ID   ADE38813 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003096363-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1239
ID   ADE51887 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104562-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1240
ID   ADD90918 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003138902-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1241
ID   ADE38697 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003108996-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1242
ID   ADE37397 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104563-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1243
ID   ADE06214 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003138898-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1244
ID   ADD90073 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003138904-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;

RESULT 1245
ID   ADE38581 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119086-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1246
ID   ADE39512 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119118-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1247
ID   ADD89117 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003138897-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1248
ID   ADD88884 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003138899-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1249
ID   ADE19778 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003138900-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1250
ID   ADE77356 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003124667-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1251
ID   ADE65232 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119113-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1252
ID   ADE39280 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119115-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1253
ID   ADE38465 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003104559-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           13.3%;   Score 54.5;   DB 8;   Length 245;
     Best Local Similarity   25.3%;   Pred. No. 1.8e+02;
RESULT 1254
```

ID   ADB96377 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003195347-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1255
ID   ADF25688 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003199675-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1256
ID   ADF24587 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003198993-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1257
ID   ADF29323 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003203401-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1258
ID   ADB96854 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003195334-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1259
ID   ADG11018 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003170809-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1260
ID   ADG10902 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003077743-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1261
ID   ADH31430 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119139-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1262
ID   ADH38678 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003119140-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1263
ID   ADH02892 standard; protein; 245 AA.

DE   Human secreted/transmembrane protein PRO1560.
PN   US2003216562-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1264
ID   ADH03846 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003220471-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1265
ID   ADH03369 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003224478-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1266
ID   ADH29313 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003119137-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1267
ID   ADH23616 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003119143-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1268
ID   ADH26946 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2003119135-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1269
ID   ADH38214 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119124-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1270
ID   ADH26830 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003119134-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1271
ID   ADH38098 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119123-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1272
ID   ADH38794 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.

PN   US2003119141-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1273
ID   ADH23732 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003119142-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1274
ID   ADH40108 standard; protein; 245 AA.
DE   Human PRO1560 protein.
PN   US2003119132-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1275
ID   ADH39992 standard; protein; 245 AA.
DE   Human PRO1560 protein.
PN   US2003119133-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1276
ID   ADH31314 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003119138-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1277
ID   ADH29192 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003119136-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1278
ID   ADH49407 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119127-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1279
ID   ADH51871 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119125-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1280
ID   ADH49726 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119128-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1281
ID   ADH52327 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119130-A1.

PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1282
ID   ADH52443 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119129-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1283
ID   ADH58440 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119121-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1284
ID   ADH51755 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119126-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1285
ID   ADH58816 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119122-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1286
ID   ADH04323 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2004005626-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1287
ID   ADI13513 standard; protein; 245 AA.
DE   Novel human secreted and transmembrane protein PRO1560.
PN   US2003119131-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1288
ID   ADH61324 standard; protein; 245 AA.
DE   Human secreted/transmembrane protein PRO1560.
PN   US2004014130-A1.
PD   22-JAN-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1289
ID   ADK00769 standard; protein; 245 AA.
DE   Human PRO polypeptide #2.
PN   US2003186373-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%; Score 54.5; DB 8; Length 245;
     Best Local Similarity   25.3%; Pred. No. 1.8e+02;
RESULT 1290
ID   ADL08510 standard; protein; 245 AA.
DE   Human secreted/transmembrane polypeptide PRO1560.
PN   US2003186372-A1.
PD   02-OCT-2003.

PA (GETH) GENENTECH INC.
    Query Match 13.3%;   Score 54.5;   DB 8;   Length 245;
    Best Local Similarity 25.3%;   Pred. No. 1.8e+02;
RESULT 1291
ID ADL31184 standard; protein; 245 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3217.
PN EP1196541-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
    Query Match 13.3%;   Score 54.5;   DB 8;   Length 245;
    Best Local Similarity 25.3%;   Pred. No. 1.8e+02;
RESULT 1292
ID ADL94523 standard; protein; 245 AA.
DE Human secreted/transmembrane protein PRO1560.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
    Query Match 13.3%;   Score 54.5;   DB 8;   Length 245;
    Best Local Similarity 25.3%;   Pred. No. 1.8e+02;
RESULT 1293
ID ADC79358 standard; protein; 272 AA.
DE Human G protein coupled receptor X (GPCRX) cDNA seq id 44.
PN US2003083463-A1.
PD 01-MAY-2003.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (COLM/) COLMAN S D.
PA (SPYT/) SPYTEK K A.
PA (BALL/) BALLINGER R A.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S G.
PA (CASM/) CASMAN S J.
PA (GUSE/) GUSEV V Y.
    Query Match 13.3%;   Score 54.5;   DB 7;   Length 272;
    Best Local Similarity 25.3%;   Pred. No. 2.1e+02;
RESULT 1294
ID ADC87479 standard; protein; 279 AA.
DE Human GPCR protein SEQ ID NO:1932.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match 13.3%;   Score 54.5;   DB 7;   Length 279;
    Best Local Similarity 22.2%;   Pred. No. 2.1e+02;
RESULT 1295
ID AAG75531 standard; protein; 284 AA.
DE Human colon cancer antigen protein SEQ ID NO:6295.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match 13.3%;   Score 54.5;   DB 4;   Length 284;
    Best Local Similarity 22.2%;   Pred. No. 2.2e+02;
RESULT 1296
ID ABB47532 standard; protein; 287 AA.
DE Listeria monocytogenes protein #236.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
    Query Match 13.3%;   Score 54.5;   DB 5;   Length 287;
    Best Local Similarity 25.3%;   Pred. No. 2.2e+02;
RESULT 1297
ID ABU32938 standard; protein; 287 AA.
DE Protein encoded by Prokaryotic essential gene #18465.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match 13.3%;   Score 54.5;   DB 6;   Length 287;
    Best Local Similarity 26.2%;   Pred. No. 2.2e+02;
RESULT 1298
ID ABP61150 standard; protein; 293 AA.
DE Human GPCRX protein #22.
PN WO200255557-A2.

PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
    Query Match 13.3%;   Score 54.5;   DB 5;   Length 293;
    Best Local Similarity 25.3%;   Pred. No. 2.3e+02;
RESULT 1299
ID ADC12690 standard; protein; 316 AA.
DE Human GPCR protein, SEQ ID No 22.
PN WO203000893-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
    Query Match 13.3%;   Score 54.5;   DB 7;   Length 316;
    Best Local Similarity 34.8%;   Pred. No. 2.5e+02;
RESULT 1300
ID AAG71540 standard; protein; 318 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1221.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
    Query Match 13.3%;   Score 54.5;   DB 4;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1301
ID AAG72395 standard; protein; 318 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2076.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
    Query Match 13.3%;   Score 54.5;   DB 4;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1302
ID ABP95657 standard; protein; 318 AA.
DE Human GPCR polypeptide SEQ ID NO 124.
PN WO200016548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
    Query Match 13.3%;   Score 54.5;   DB 5;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1303
ID AAU95699 standard; protein; 318 AA.
DE Human olfactory and pheromone G protein-coupled receptor #186.
PN WO200224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
    Query Match 13.3%;   Score 54.5;   DB 5;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1304
ID AAB71168 standard; protein; 318 AA.
DE Human GPCRX protein SEQ ID 12.
PN WO200250275-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
    Query Match 13.3%;   Score 54.5;   DB 5;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1305
ID ABU11220 standard; protein; 318 AA.
DE Human G-protein coupled receptor GCREC-73.
PN WO200279448-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
    Query Match 13.3%;   Score 54.5;   DB 6;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1306
ID ADC86371 standard; protein; 318 AA.
DE Human GPCR protein SEQ ID NO:824.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match 13.3%;   Score 54.5;   DB 7;   Length 318;
    Best Local Similarity 22.4%;   Pred. No. 2.5e+02;
RESULT 1307
ID ADD12737 standard; protein; 318 AA.

DE Novel human olfactory receptor (OR) seq id 7.
PN US2003109692-A1.
PD 12-JUN-2003.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (LILL/) LI L.
PA (BALL/) BALLINGER R A.
PA (CASM/) CASMAN S J.
PA (SPYT/) SPYTEK K A.
PA (BAUM/) BAUMGARTNER J C.
PA (BURG/) BURGESS C E.
    Query Match   13.3%;   Score 54.5; DB 7;   Length 318;
    Best Local Similarity 22.4%; Pred. No. 2.5e+02;
RESULT 1308
ID ADC12678 standard; protein; 323 AA.
DE Human GPCR protein, SEQ ID No 10.
PN WO2003000893-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
    Query Match   13.3%;   Score 54.5; DB 7;   Length 323;
    Best Local Similarity 27.3%; Pred. No. 2.5e+02;
RESULT 1309
ID ABU48609 standard; protein; 362 AA.
DE Protein encoded by Prokaryotic essential gene #34136.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   13.3%;   Score 54.5; DB 6;   Length 362;
    Best Local Similarity 33.3%; Pred. No. 2.9e+02;
RESULT 1310
ID ABU19559 standard; protein; 368 AA.
DE Protein encoded by Prokaryotic essential gene #5086.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   13.3%;   Score 54.5; DB 6;   Length 368;
    Best Local Similarity 23.7%; Pred. No. 2.9e+02;
RESULT 1311
ID AAB75200 standard; protein; 374 AA.
DE Drosophila gustatory receptor GR23A.1b protein sequence.
PN WO200077208-A2.
PD 21-DEC-2000.
PA (UYYA) UNIV YALE.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 374;
    Best Local Similarity 35.4%; Pred. No. 3e+02;
RESULT 1312
ID AAE30507 standard; protein; 374 AA.
DE Fruit fly gustatory receptor protein, Gr23A1b.
PN WO200142486-A1.
PD 14-JUN-2001.
PA (UYCO) UNIV COLUMBIA NEW YORK.
    Query Match   13.3%;   Score 54.5; DB 5;   Length 374;
    Best Local Similarity 35.4%; Pred. No. 3e+02;
RESULT 1313
ID AAE03545 standard; protein; 397 AA.
DE Human G-protein coupled receptor, AXOR12 related protein.
PN WO200142486-A1.
PD 14-JUN-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 397;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1314
ID ADC87413 standard; protein; 397 AA.
DE Human GPCR protein SEQ ID NO:1866.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match   13.3%;   Score 54.5; DB 7;   Length 397;
    Best Local Similarity 28.6%; Pred. No. 3.2e+02;
RESULT 1315
ID AAY91094 standard; protein; 398 AA.

DE Human G protein-coupled receptor protein hOT7T175.
PN WO200024890-A1.
PD 04-MAY-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
    Query Match   13.3%;   Score 54.5; DB 3;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1316
ID AAB08540 standard; protein; 398 AA.
DE A human G protein-coupled receptor designated GPR54.
PN WO200050563-A2.
PD 31-AUG-2000.
PA (MERI) MERCK & CO INC.
PA (MERI) MERCK FROSST CANADA & CO.
PA (UTOR) UNIV TORONTO.
    Query Match   13.3%;   Score 54.5; DB 3;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1317
ID AAU08997 standard; protein; 398 AA.
DE Human G-protein-coupled receptor, GPCR, 52872.
PN WO200164882-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1318
ID AAE03544 standard; protein; 398 AA.
DE Human G-protein coupled receptor, AXOR12.
PN WO200142486-A1.
PD 14-JUN-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1319
ID AAG64300 standard; protein; 398 AA.
DE Human GTP-binding protein-coupled receptor GPRv78.
PN WO200148189-A1.
PD 05-JUL-2001.
PA (HELI-) HELIX RES INST.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1320
ID AAM51415 standard; protein; 398 AA.
DE Human OT7T175 SEQ ID NO 7.
PN WO200175104-A1.
PD 11-OCT-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1321
ID AAE04550 standard; protein; 398 AA.
DE Human G-protein coupled receptor-6 (GCREC-6) protein.
PN WO200142288-A2.
PD 14-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
    Query Match   13.3%;   Score 54.5; DB 4;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1322
ID ABB79864 standard; protein; 398 AA.
DE Human G-protein coupled receptor GPR54.
PN WO200259344-A2.
PD 01-AUG-2002.
PA (MERI) MERCK & CO INC.
    Query Match   13.3%;   Score 54.5; DB 5;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;
RESULT 1323
ID ABP97222 standard; protein; 398 AA.
DE Tumour-associated antigenic target protein TAT184 SEQ ID NO:104.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   13.3%;   Score 54.5; DB 6;   Length 398;
    Best Local Similarity 27.3%; Pred. No. 3.2e+02;

RESULT 1324
ID   ABU09340 standard; protein; 398 AA.
DE   Human SNORF11 receptor.
PN   US2003022839-A1.
PD   30-JAN-2003.
PA   (BORO/) BOROWSKY B E.
PA   (QUAN/) QUAN Y.
PA   (SMIT/) SMITH K E.
     Query Match   13.3%;   Score 54.5;   DB 6;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1325
ID   ABP81995 standard; protein; 398 AA.
DE   Human G protein-coupled receptor GPR54 protein SEQ ID NO:477.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   13.3%;   Score 54.5;   DB 6;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1326
ID   ABU61629 standard; protein; 398 AA.
DE   Human G protein-coupled receptor SNORF11.
PN   US2002077469-A1.
PD   20-JUN-2002.
PA   (BORO/) BOROWSKY B E.
PA   (QUAN/) QUAN Y.
PA   (SMIT/) SMITH K E.
     Query Match   13.3%;   Score 54.5;   DB 7;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1327
ID   ADN39505 standard; protein; 398 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A105.
PN   WO200304 2661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   13.3%;   Score 54.5;   DB 7;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1328
ID   ADN39430 standard; protein; 398 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A30.
PN   WO200304 2661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   13.3%;   Score 54.5;   DB 7;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1329
ID   ADG19755 standard; protein; 398 AA.
DE   Human G protein coupled receptor (GPCR) 52872.
PN   US2003215860-A1.
PD   20-NOV-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1330
ID   ADL91585 standard; protein; 398 AA.
DE   Human immune-related polypeptide PRO47351, SEQ ID NO:100.
PN   WO200404072-A2.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1331
ID   ADO29412 standard; protein; 398 AA.
DE   Human GPCR GPR54, SEQ ID NO:514.
PN   WO200404 0000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1332
ID   ADQ89080 standard; protein; 398 AA.
DE   Human urological disorder related protein 52872 SEQ:32.
PN   WO200406 5576-A2.
PD   05-AUG-2004.

RESULT 1333
ID   ADR21325 standard; protein; 398 AA.
DE   Human metastin-related protein OT7T175, SEQ ID 9.
PN   WO200406 3221-A1.
PD   29-JUL-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1334
ID   ADS88809 standard; protein; 398 AA.
DE   Amino acid sequence of a mutant GPR54 receptor.
PN   EP1464652-A1.
PD   06-OCT-2004.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYPA-) UNIV PARIS SUD.
PA   (UYPA-) UNIV PARIS DESCARTES.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1335
ID   ADS88807 standard; protein; 398 AA.
DE   Amino acid sequence of GPR54 receptor.
PN   EP1464652-A1.
PD   06-OCT-2004.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYPA-) UNIV PARIS SUD.
PA   (UYPA-) UNIV PARIS DESCARTES.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1336
ID   ADT05941 standard; protein; 398 AA.
DE   Human OT7T175 polypeptide.
PN   WO200408 0479-A1.
PD   23-SEP-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   13.3%;   Score 54.5;   DB 8;   Length 398;
     Best Local Similarity 27.3%;   Pred. No. 3.2e+02;

RESULT 1337
ID   AAY32141 standard; protein; 403 AA.
DE   Human G-protein coupled receptor AXOR3.
PN   WO952944-A1.
PD   21-OCT-1999.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
     Query Match   13.3%;   Score 54.5;   DB 2;   Length 403;
     Best Local Similarity 26.4%;   Pred. No. 3.2e+02;

RESULT 1338
ID   AAY57287 standard; protein; 403 AA.
DE   Human GPCR protein (HGPRP) sequence (clone ID 2705201).
PN   WO200015793-A2.
PD   23-MAR-2000.
PA   (INCY-) INCYTE PHARM INC.
     Query Match   13.3%;   Score 54.5;   DB 3;   Length 403;
     Best Local Similarity 26.4%;   Pred. No. 3.2e+02;

RESULT 1339
ID   AAB43085 standard; protein; 403 AA.
DE   Human ORFX ORF2849 polypeptide sequence SEQ ID NO:5698.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
     Query Match   13.3%;   Score 54.5;   DB 3;   Length 403;
     Best Local Similarity 26.4%;   Pred. No. 3.2e+02;

RESULT 1340
ID   AAM93548 standard; protein; 403 AA.
DE   Human polypeptide, SEQ ID NO: 3306.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
     Query Match   13.3%;   Score 54.5;   DB 4;   Length 403;
     Best Local Similarity 26.4%;   Pred. No. 3.2e+02;

RESULT 1341
ID   AAM78615 standard; protein; 403 AA.

DE Human protein SEQ ID NO 1277.
PN WO20015719O-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match   13.3%;   Score 54.5; DB 4;   Length 403
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1342
ID ABG96333 standard; protein; 403 AA.
DE Human ovarian cancer marker M446.
PN WO20027192B-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match   13.3%;   Score 54.5; DB 5;   Length 403
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1343
ID ABU54869 standard; protein; 403 AA.
DE Human G-protein coupled receptor #5, Incyte clone 2705201CD1.
PN US2002106655-A1.
PD 08-AUG-2002.
PA (BAND/) BANDMAN O.
PA (LALP/) LAL P G.
PA (TANG/) TANG Y T.
PA (BAUG/) BAUGHN M R.
Query Match   13.3%;   Score 54.5; DB 5;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1344
ID ABB81627 standard; protein; 403 AA.
DE Human GPRC5B-like protein SEQ ID NO:2.
PN WO20025293I-A2.
PD 11-JUL-2002.
PA (DELT-) DELTAGEN INC.
Query Match   13.3%;   Score 54.5; DB 5;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1345
ID ABP81712 standard; protein; 403 AA.
DE Human G protein-coupled receptor GPRC5B protein SEQ ID NO:599.
PN WO20026108T-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match   13.3%;   Score 54.5; DB 6;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1346
ID ADN95281 standard; protein; 403 AA.
DE Human BEC/LEC-related protein sequence SeqID203.
PN WO20030B640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match   13.3%;   Score 54.5; DB 7;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1347
ID ADJ31962 standard; protein; 403 AA.
DE Human orphan GPCR5B protein.
PN US200323591Z-A1.
PD 25-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match   13.3%;   Score 54.5; DB 8;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1348
ID ADI28533 standard; protein; 403 AA.
DE Mouse GPCR5B polypeptide.
PN WO20040O106O-A2.
PD 31-DEC-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match   13.3%;   Score 54.5; DB 8;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1349
ID ADL31273 standard; protein; 403 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3306.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match   13.3%;   Score 54.5; DB 8;   Length 403;

Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1350
ID ADO29462 standard; protein; 403 AA.
DE Human GPCR GPRC5B, SEQ ID NO:564.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match   13.3%;   Score 54.5; DB 8;   Length 403;
Best Local Similarity   26.4%;   Pred. No. 3.2e+02;
RESULT 1351
ID AAW98252 standard; protein; 413 AA.
DE H. pylori GHPO 1312 protein.
PN WO984347B-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA) HUMAN GENOME SCI INC.
Query Match   13.3%;   Score 54.5; DB 2;   Length 413;
Best Local Similarity   25.0%;   Pred. No. 3.3e+02;
RESULT 1352
ID ABU30707 standard; protein; 413 AA.
DE Protein encoded by Prokaryotic essential gene #16234.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   13.3%;   Score 54.5; DB 6;   Length 413;
Best Local Similarity   25.0%;   Pred. No. 3.3e+02;
RESULT 1353
ID AAY32142 standard; protein; 427 AA.
DE Human G-protein coupled receptor AXOR3-related polypeptide.
PN WO9952944-A1.
PD 21-OCT-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match   13.3%;   Score 54.5; DB 2;   Length 427;
Best Local Similarity   26.4%;   Pred. No. 3.5e+02;
RESULT 1354
ID ABU15404 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #931.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   13.3%;   Score 54.5; DB 6;   Length 438;
Best Local Similarity   25.7%;   Pred. No. 3.6e+02;
RESULT 1355
ID ADK62370 standard; protein; 442 AA.
DE Disease treating protein complex-derived protein #311.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match   13.3%;   Score 54.5; DB 7;   Length 442;
Best Local Similarity   30.0%;   Pred. No. 3.6e+02;
RESULT 1356
ID ADO08029 standard; protein; 481 AA.
DE Mouse polypeptide #36.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match   13.3%;   Score 54.5; DB 8;   Length 481;
Best Local Similarity   27.7%;   Pred. No. 4e+02;
RESULT 1357
ID AAW49911 standard; protein; 482 AA.
DE Mouse CLK serine/threonine kinase mCLK1.
PN WO74B723-A2.
PD 24-DEC-1997.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match   13.3%;   Score 54.5; DB 2;   Length 482;
Best Local Similarity   28.3%;   Pred. No. 4e+02;
RESULT 1358
ID ADO08030 standard; protein; 483 AA.
DE Mouse polypeptide #37.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match   13.3%;   Score 54.5; DB 8;   Length 483;

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     Best Local Similarity   28.3%;  Pred. No. 4e+02;
RESULT 1359
ID   ABO85018 standard; protein; 499 AA.
DE   Murine cancer-associated protein (CAP) MP07-112.
PN   WO2004058146-A2.
PD   15-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match             13.3%;  Score 54.5;  DB 8;  Length 499;
     Best Local Similarity   20.7%;  Pred. No. 4.1e+02;
RESULT 1360
ID   ADA34498 standard; protein; 509 AA.
DE   Acinetobacter baumannii protein #1659.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             13.3%;  Score 54.5;  DB 6;  Length 509;
     Best Local Similarity   32.4%;  Pred. No. 4.2e+02;
RESULT 1361
ID   AAU10966 standard; protein; 510 AA.
DE   Xylella fastidiosa protein XfGUMJ.
PN   WO200185905-A2.
PD   15-NOV-2001.
PA   (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
     Query Match             13.3%;  Score 54.5;  DB 5;  Length 510;
     Best Local Similarity   34.0%;  Pred. No. 4.2e+02;
RESULT 1362
ID   AAU49463 standard; protein; 518 AA.
DE   Propionibacterium acnes immunogenic protein #10359.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
     Query Match             13.3%;  Score 54.5;  DB 4;  Length 518;
     Best Local Similarity   18.5%;  Pred. No. 4.3e+02;
RESULT 1363
ID   ABM45982 standard; protein; 518 AA.
DE   Propionibacterium acnes membrane-related polypeptide #10658.
PN   WO200303515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
     Query Match             13.3%;  Score 54.5;  DB 6;  Length 518;
     Best Local Similarity   18.5%;  Pred. No. 4.3e+02;
RESULT 1364
ID   ABB58577 standard; protein; 560 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2523.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             13.3%;  Score 54.5;  DB 4;  Length 560;
     Best Local Similarity   26.3%;  Pred. No. 4.7e+02;
RESULT 1365
ID   ABB67283 standard; protein; 576 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 28641.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             13.3%;  Score 54.5;  DB 4;  Length 576;
     Best Local Similarity   26.3%;  Pred. No. 4.9e+02;
RESULT 1366
ID   ABR53821 standard; protein; 616 AA.
DE   Protein sequence #SEQ ID 2507.
PN   EP1258494-A1.
PD   20-NOV-2002.
PA   (CELL-) CELLZOME AG.
     Query Match             13.3%;  Score 54.5;  DB 6;  Length 616;
     Best Local Similarity   32.8%;  Pred. No. 5.2e+02;
RESULT 1367
ID   ADK65000 standard; protein; 616 AA.
DE   Disease treating protein complex-derived protein #1516.
PN   EP1338608-A2.
PD   27-AUG-2003.
PA   (CELL-) CELLZOME AG.
     Query Match             13.3%;  Score 54.5;  DB 7;  Length 616;
     Best Local Similarity   32.8%;  Pred. No. 5.2e+02;

RESULT 1368
ID   ADF70413 standard; protein; 641 AA.
DE   Orphan receptor ligand-related human protein SeqID36.
PN   WO2003071272-A1.
PD   28-AUG-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             13.3%;  Score 54.5;  DB 7;  Length 641;
     Best Local Similarity   26.4%;  Pred. No. 5.5e+02;
RESULT 1369
ID   ABB63136 standard; protein; 747 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 16200.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             13.3%;  Score 54.5;  DB 4;  Length 747;
     Best Local Similarity   32.0%;  Pred. No. 6.5e+02;
RESULT 1370
ID   ADI41001 standard; protein; 931 AA.
DE   Mouse EMR1 hormone receptor.
PN   US2004018976-A1.
PD   29-JAN-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
     Query Match             13.3%;  Score 54.5;  DB 8;  Length 931;
     Best Local Similarity   34.1%;  Pred. No. 8.4e+02;
RESULT 1371
ID   ADO29306 standard; protein; 931 AA.
DE   Mouse GPCR EMRI, SEQ ID NO:407.
PN   WO204040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match             13.3%;  Score 54.5;  DB 8;  Length 931;
     Best Local Similarity   34.1%;  Pred. No. 8.4e+02;
RESULT 1372
ID   ABR41799 standard; protein; 1653 AA.
DE   Human DITHP growth/development-associated protein.
PN   WO200297031-A2.
PD   05-DEC-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match             13.3%;  Score 54.5;  DB 6;  Length 1653;
     Best Local Similarity   27.3%;  Pred. No. 1.6e+03;
RESULT 1373
ID   ABU11522 standard; protein; 1653 AA.
DE   Human MDDT polypeptide SEQ ID 469.
PN   WO200279449-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match             13.3%;  Score 54.5;  DB 6;  Length 1653;
     Best Local Similarity   27.3%;  Pred. No. 1.6e+03;
RESULT 1374
ID   ABG13667 standard; protein; 1682 AA.
DE   Novel human diagnostic protein #13658.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             13.3%;  Score 54.5;  DB 4;  Length 1682;
     Best Local Similarity   27.3%;  Pred. No. 1.6e+03;
RESULT 1375
ID   ABG07239 standard; protein; 1682 AA.
DE   Novel human diagnostic protein #7230.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             13.3%;  Score 54.5;  DB 4;  Length 1682;
     Best Local Similarity   27.3%;  Pred. No. 1.6e+03;
RESULT 1376
ID   AAW10344 standard; protein; 2763 AA.
DE   Maize dwarf mosaic virus polyprotein.
PN   WO9702352-A1.
PD   23-JAN-1997.
PA   (CIBA ) CIBA GEIGY AG.
     Query Match             13.3%;  Score 54.5;  DB 2;  Length 2763;
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        Best Local Similarity  30.4%;  Pred. No. 2.9e+03;
RESULT 1377
ID   AAR22268 standard; protein; 2818 AA.
DE   NF1 gene product.
PN   WO920387-A.
PD   09-JAN-1992.
PA   (UNMI ) UNIV MICHIGAN.
        Query Match       13.3%;  Score 54.5;  DB 2;  Length 2818;
        Best Local Similarity  27.3%;  Pred. No. 2.9e+03;
RESULT 1378
ID   AAW13280 standard; protein; 2818 AA.
DE   Human neurofibromin.
PN   US5605799-A.
PD   25-FEB-1997.
PA   (UTAH ) UNIV UTAH RES FOUND.
        Query Match       13.3%;  Score 54.5;  DB 2;  Length 2818;
        Best Local Similarity  27.3%;  Pred. No. 2.9e+03;
RESULT 1379
ID   AAE05486 standard; protein; 2818 AA.
DE   Human neurofibromatosis type 1 (NF1) protein.
PN   US6261761-B1.
PD   17-JUL-2001.
PA   (COLD-) COLD SPRING HARBOR LAB.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2818;
        Best Local Similarity  27.3%;  Pred. No. 2.9e+03;
RESULT 1380
ID   ABB08078 standard; protein; 2818 AA.
DE   Human neurofibromatosis 1 (NF1) protein.
PN   US6365126-B1.
PD   02-APR-2002.
PA   (COLD-) COLD SPRING HARBOR LAB.
        Query Match       13.3%;  Score 54.5;  DB 5;  Length 2818;
        Best Local Similarity  27.3%;  Pred. No. 2.9e+03;
RESULT 1381
ID   ABG13665 standard; protein; 2871 AA.
DE   Novel human diagnostic protein #13656.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2871;
        Best Local Similarity  27.3%;  Pred. No. 3e+03;
RESULT 1382
ID   ABG13555 standard; protein; 2871 AA.
DE   Novel human diagnostic protein #13546.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2871;
        Best Local Similarity  27.3%;  Pred. No. 3e+03;
RESULT 1383
ID   ABG07243 standard; protein; 2871 AA.
DE   Novel human diagnostic protein #7234.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2871;
        Best Local Similarity  27.3%;  Pred. No. 3e+03;
RESULT 1384
ID   ABG13666 standard; protein; 2891 AA.
DE   Novel human diagnostic protein #13657.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2891;
        Best Local Similarity  27.3%;  Pred. No. 3e+03;
RESULT 1385
ID   ABG07240 standard; protein; 2891 AA.
DE   Novel human diagnostic protein #7231.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2891;
        Best Local Similarity  27.3%;  Pred. No. 3e+03;

RESULT 1386
ID   ABG13556 standard; protein; 2891 AA.
DE   Novel human diagnostic protein #13547.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.3%;  Score 54.5;  DB 4;  Length 2891;
        Best Local Similarity  27.3%;  Pred. No. 3e+03;
RESULT 1387
ID   AAM91185 standard; protein; 77 AA.
DE   Human immune/haematopoietic antigen SEQ ID NO:18778.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match       13.2%;  Score 54;  DB 4;  Length 77;
        Best Local Similarity  31.0%;  Pred. No. 58;
RESULT 1388
ID   AAO23284 standard; protein; 81 AA.
DE   Glyceraldehyde-3-phosphate protein 8_91.
PN   CN1386850-A.
PD   25-DEC-2002.
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
        Query Match       13.2%;  Score 54;  DB 6;  Length 81;
        Best Local Similarity  34.3%;  Pred. No. 61;
RESULT 1389
ID   AAM24134 standard; protein; 89 AA.
DE   Human EST encoded protein SEQ ID NO: 1659.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.2%;  Score 54;  DB 4;  Length 89;
        Best Local Similarity  24.0%;  Pred. No. 68;
RESULT 1390
ID   ADL05626 standard; protein; 98 AA.
DE   M. catarrhalis protein #1392.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
        Query Match       13.2%;  Score 54;  DB 8;  Length 98;
        Best Local Similarity  30.4%;  Pred. No. 76;
RESULT 1391
ID   AAO06448 standard; protein; 133 AA.
DE   Human polypeptide SEQ ID NO 20340.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
        Query Match       13.2%;  Score 54;  DB 4;  Length 133;
        Best Local Similarity  36.4%;  Pred. No. 1.1e+02;
RESULT 1392
ID   ADC94829 standard; protein; 182 AA.
DE   E. faecium protein sequence SEQ ID 4456.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
        Query Match       13.2%;  Score 54;  DB 7;  Length 182;
        Best Local Similarity  26.5%;  Pred. No. 1.5e+02;
RESULT 1393
ID   ADA55585 standard; protein; 188 AA.
DE   Human protein, SEQ ID 3153.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
        Query Match       13.2%;  Score 54;  DB 6;  Length 188;
        Best Local Similarity  22.6%;  Pred. No. 1.6e+02;
RESULT 1394
ID   AAW69535 standard; protein; 242 AA.
DE   crtW2396 gene product beta-carotene beta-oxygenase.
PN   JP10155497-A.
PD   16-JUN-1998.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
        Query Match       13.2%;  Score 54;  DB 2;  Length 242;
        Best Local Similarity  25.5%;  Pred. No. 2.1e+02;
```

RESULT 1395
ID   ABU97244 standard; protein; 242 AA.
DE   Enzyme polypeptide #10.
PN   WO200299095-A2.
PD   12-DEC-2002.
PA   (HOFF) ROCHE VITAMINS AG.
     Query Match   13.2%; Score 54; DB 6; Length 242;
     Best Local Similarity   25.5%; Pred. No. 2.1e+02;

RESULT 1396
ID   ADO61161 standard; protein; 242 AA.
DE   P. marcusii ketolase.
PN   DE10238978-A1.
PD   04-MAR-2004.
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
     Query Match   13.2%; Score 54; DB 8; Length 242;
     Best Local Similarity   25.5%; Pred. No. 2.1e+02;

RESULT 1397
ID   ADO61078 standard; protein; 242 AA.
DE   P. marcusii ketolase.
PN   DE10238980-A1.
PD   04-MAR-2004.
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
     Query Match   13.2%; Score 54; DB 8; Length 242;
     Best Local Similarity   25.5%; Pred. No. 2.1e+02;

RESULT 1398
ID   ADQ38247 standard; protein; 242 AA.
DE   Paracoccus marcusii ketolase.
PN   DE10258971-A1.
PD   01-JUL-2004.
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
     Query Match   13.2%; Score 54; DB 8; Length 242;
     Best Local Similarity   25.5%; Pred. No. 2.1e+02;

RESULT 1399
ID   ADR03862 standard; protein; 242 AA.
DE   Paracoccus marcusii ketolase SEQ ID NO: 20.
PN   WO200406359-A2.
PD   29-JUL-2004.
PA   (BADI) BASF AG.
     Query Match   13.2%; Score 54; DB 8; Length 242;
     Best Local Similarity   25.5%; Pred. No. 2.1e+02;

RESULT 1400
ID   ADR03942 standard; protein; 242 AA.
DE   P marcussi ketolase.
PN   WO200406358-A1.
PD   29-JUL-2004.
PA   (BADI) BASF AG.
     Query Match   13.2%; Score 54; DB 8; Length 242;
     Best Local Similarity   25.5%; Pred. No. 2.1e+02;

RESULT 1401
ID   ABM85551 standard; protein; 294 AA.
DE   Human protein sequence hCP34831.
PN   WO200307826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
     Query Match   13.2%; Score 54; DB 7; Length 294;
     Best Local Similarity   19.6%; Pred. No. 2.6e+02;

RESULT 1402
ID   ADG76719 standard; protein; 331 AA.
DE   Phospholipase amino acid sequence SEQ ID NO:102.
PN   WO200308962O-A2.
PD   30-OCT-2003.
PA   (DIVE-) DIVERSA CORP.
     Query Match   13.2%; Score 54; DB 8; Length 331;
     Best Local Similarity   57.1%; Pred. No. 3e+02;

RESULT 1403
ID   ABU38629 standard; protein; 347 AA.
DE   Protein encoded by Prokaryotic essential gene #24156.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   13.2%; Score 54; DB 6; Length 347;
     Best Local Similarity   40.5%; Pred. No. 3.2e+02;

RESULT 1404

RESULT 1395
ID   AAR80952 standard; protein; 358 AA.
DE   Recombinant high affinity interleukin-8 receptor subtype B.
PN   WO9525126-A1.
PD   21-SEP-1995.
PA   (REPK) REPLIGEN CORP.
PA   (UYBO-) UNIV BOSTON.
     Query Match   13.2%; Score 54; DB 2; Length 358;
     Best Local Similarity   24.5%; Pred. No. 3.3e+02;

RESULT 1405
ID   AAW97788 standard; protein; 360 AA.
DE   Pig-tailed macaque HIV/SIV receptor protein Bob.
PN   WO903888-A1.
PD   28-JAN-1999.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   13.2%; Score 54; DB 2; Length 360;
     Best Local Similarity   26.4%; Pred. No. 3.3e+02;

RESULT 1406
ID   AAU04037 standard; protein; 360 AA.
DE   Pigtailed macaque SIV translocation agent, BOB.
PN   US6251582-B1.
PD   26-JUN-2001.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   13.2%; Score 54; DB 4; Length 360;
     Best Local Similarity   26.4%; Pred. No. 3.3e+02;

RESULT 1407
ID   ABB79748 standard; protein; 360 AA.
DE   Pig-tailed macaque G-protein coupled receptor BOB.
PN   US2002076594-A1.
PD   20-JUN-2002.
PA   (LITT/) LITTMAN D R.
PA   (DENG) DENG H.
PA   (UNUT/) UNUTMAZ D.
PA   (KEWA/) KEWALRAMANI V N.
     Query Match   13.2%; Score 54; DB 5; Length 360;
     Best Local Similarity   26.4%; Pred. No. 3.3e+02;

RESULT 1408
ID   ABU41907 standard; protein; 378 AA.
DE   Protein encoded by Prokaryotic essential gene #27434.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   13.2%; Score 54; DB 6; Length 378;
     Best Local Similarity   34.2%; Pred. No. 3.5e+02;

RESULT 1409
ID   ABO78765 standard; protein; 384 AA.
DE   Pseudomonas aeruginosa polypeptide #10940.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.2%; Score 54; DB 7; Length 384;
     Best Local Similarity   34.5%; Pred. No. 3.6e+02;

RESULT 1410
ID   ABO74075 standard; protein; 400 AA.
DE   Pseudomonas aeruginosa polypeptide #6250.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   13.2%; Score 54; DB 7; Length 400;
     Best Local Similarity   40.5%; Pred. No. 3.7e+02;

RESULT 1411
ID   ADC87419 standard; protein; 412 AA.
DE   Human GPCR protein SEQ ID NO:1872.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match   13.2%; Score 54; DB 7; Length 412;
     Best Local Similarity   28.6%; Pred. No. 3.9e+02;

RESULT 1412
ID   ADF06869 standard; protein; 434 AA.
DE   Bacterial polypeptide #2982.
PN   US6605709-B1.
PD   12-AUG-2003.

PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   13.2%;   Score 54;   DB 7;   Length 434;
Best Local Similarity   41.4%;   Pred. No. 4.1e+02;
RESULT 1413
ID   ABU18049 standard; protein; 483 AA.
DE   Protein encoded by Prokaryotic essential gene #3576.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   13.2%;   Score 54;   DB 6;   Length 483;
Best Local Similarity   31.5%;   Pred. No. 4.6e+02;
RESULT 1414
ID   ABB66372 standard; protein; 504 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 25908.
PN   WO20171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   13.2%;   Score 54;   DB 4;   Length 504;
Best Local Similarity   29.2%;   Pred. No. 4.8e+02;
RESULT 1415
ID   ADG74270 standard; protein; 512 AA.
DE   Mouse frizzled protein, SEQ ID No 55.
PN   WO20029635-A2.
PD   21-NOV-2002.
PA   (REGC) UNIV CALIFORNIA.
Query Match   13.2%;   Score 54;   DB 7;   Length 512;
Best Local Similarity   19.6%;   Pred. No. 4.9e+02;
RESULT 1416
ID   ABB68395 standard; protein; 527 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 31977.
PN   WO20171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   13.2%;   Score 54;   DB 4;   Length 527;
Best Local Similarity   34.0%;   Pred. No. 5.1e+02;
RESULT 1417
ID   ADG74256 standard; protein; 529 AA.
DE   Rat frizzled protein, SEQ ID No 41.
PN   WO20029635-A2.
PD   21-NOV-2002.
PA   (REGC) UNIV CALIFORNIA.
Query Match   13.2%;   Score 54;   DB 7;   Length 529;
Best Local Similarity   19.6%;   Pred. No. 5.1e+02;
RESULT 1418
ID   ABB65176 standard; protein; 540 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 22320.
PN   WO20171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   13.2%;   Score 54;   DB 4;   Length 540;
Best Local Similarity   34.0%;   Pred. No. 5.2e+02;
RESULT 1419
ID   AAU38962 standard; protein; 540 AA.
DE   Drosophila G-protein coupled receptor, GCPR #40.
PN   WO20170980-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   13.2%;   Score 54;   DB 4;   Length 540;
Best Local Similarity   40.0%;   Pred. No. 5.2e+02;
RESULT 1420
ID   AAB86952 standard; protein; 540 AA.
DE   D. melanogaster peptide receptor SEQ ID 2.
PN   DE10013618-A1.
PD   20-SEP-2001.
PA   (FARB) BAYER AG.
Query Match   13.2%;   Score 54;   DB 4;   Length 540;
Best Local Similarity   40.0%;   Pred. No. 5.2e+02;
RESULT 1421
ID   ADC35868 standard; protein; 540 AA.
DE   Drosophila G protein coupled receptor seq id 42.
PN   US2003092124-A1.
PD   15-MAY-2003.
PA   (APPL-) APPLERA CORP.

Query Match   13.2%;   Score 54;   DB 7;   Length 540;
Best Local Similarity   40.0%;   Pred. No. 5.2e+02;
RESULT 1422
ID   AAU03213 standard; protein; 542 AA.
DE   Fruit fly G protein coupled receptor, DmGPCR7.
PN   WO20013105-A2.
PD   03-MAY-2001.
PA   (PHAA) PHARMACIA & UPJOHN CO.
Query Match   13.2%;   Score 54;   DB 4;   Length 542;
Best Local Similarity   40.0%;   Pred. No. 5.3e+02;
RESULT 1423
ID   AAE38178 standard; protein; 542 AA.
DE   Fruit fly G protein-coupled receptor (GPCR) protein #27.
PN   WO2003052078-A2.
PD   26-JUN-2003.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match   13.2%;   Score 54;   DB 7;   Length 542;
Best Local Similarity   40.0%;   Pred. No. 5.3e+02;
RESULT 1424
ID   ADL83388 standard; protein; 542 AA.
DE   Drosophila G protein coupled receptor 7 (DmGPCR7).
PN   US2003162223-A1.
PD   28-AUG-2003.
PA   (LOWE/) LOWERY D E.
PA   (SMIT/) SMITH V G.
PA   (KUBI/) KUBIAK T M.
PA   (LARS/) LARSEN M J.
Query Match   13.2%;   Score 54;   DB 7;   Length 542;
Best Local Similarity   40.0%;   Pred. No. 5.3e+02;
RESULT 1425
ID   ADR03108 standard; protein; 542 AA.
DE   Drosophila G-protein coupled receptor DmGPCR7.
PN   US2004121956-A1.
PD   24-JUN-2004.
PA   (LOWE/) LOWERY D E.
PA   (SMIT/) SMITH V G.
PA   (KUBI/) KUBIAK T M.
PA   (LARS/) LARSEN M J.
Query Match   13.2%;   Score 54;   DB 8;   Length 542;
Best Local Similarity   40.0%;   Pred. No. 5.3e+02;
RESULT 1426
ID   ABB75749 standard; protein; 543 AA.
DE   Mentha spicata limonene synthase.
PN   WO200220815-A2.
PD   14-MAR-2002.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match   13.2%;   Score 54;   DB 5;   Length 543;
Best Local Similarity   26.3%;   Pred. No. 5.3e+02;
RESULT 1427
ID   ABG75232 standard; protein; 570 AA.
DE   Hair papilla cell growth promoter related rat protein SEQ ID NO: 6.
PN   WO2003086334-A1.
PD   23-OCT-2003.
PA   (TAIS) TAISHO PHARM CO LTD.
Query Match   13.2%;   Score 54;   DB 7;   Length 570;
Best Local Similarity   19.6%;   Pred. No. 5.6e+02;
RESULT 1428
ID   AAW31273 standard; protein; 572 AA.
DE   Mouse frizzled-7 protein Mfz7 (Wnt receptor).
PN   WO9739357-A1.
PD   23-OCT-1997.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
PA   (UYJO) UNIV JOHNS HOPKINS.
Query Match   13.2%;   Score 54;   DB 2;   Length 572;
Best Local Similarity   19.6%;   Pred. No. 5.6e+02;
RESULT 1429
ID   ADO29338 standard; protein; 572 AA.
DE   Mouse GPCR FZD7, SEQ ID NO:439.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
Query Match   13.2%;   Score 54;   DB 8;   Length 572;
Best Local Similarity   19.6%;   Pred. No. 5.6e+02;

RESULT 1430
ID   ABU55902 standard; protein; 574 AA.
DE   Human protein Frizzled-7.
PN   WO200277204-A2.
PA   (AXOR-) AXORDIA LTD.
PD   03-OCT-2002.
  Query Match   13.2%; Score 54; DB 6; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1431
ID   AAB34056 standard; protein; 574 AA.
DE   F2D7 protein.
PN   WO200290992-A2.
PD   14-NOV-2002.
PA   (AXOR-) AXORDIA LTD.
  Query Match   13.2%; Score 54; DB 6; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1432
ID   ADG74269 standard; protein; 574 AA.
DE   Human frizzled protein, SEQ ID NO 54.
PN   WO200292635-A2.
PD   21-NOV-2002.
PA   (REGC) UNIV CALIFORNIA.
  Query Match   13.2%; Score 54; DB 7; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1433
ID   ADN03982 standard; protein; 574 AA.
DE   Antipsoriatic protein sequence #186.
PN   WO200428479-A2.
PD   08-APR-2004.
PA   (GETH) GENENTECH INC.
  Query Match   13.2%; Score 54; DB 8; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1434
ID   ADO29337 standard; protein; 574 AA.
DE   Human GPCR F2D7, SEQ ID NO:438.
PN   WO200440000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
  Query Match   13.2%; Score 54; DB 8; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1435
ID   ADO22264 standard; protein; 574 AA.
DE   Human FZD7 protein (homologue of Drosophila frizzled).
PN   WO200442028-A2.
PD   21-MAY-2004.
PA   (REGC) UNIV CALIFORNIA.
  Query Match   13.2%; Score 54; DB 8; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1436
ID   ADQ18261 standard; protein; 574 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 1079.
PN   WO200448938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match   13.2%; Score 54; DB 8; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1437
ID   ADS92964 standard; protein; 574 AA.
DE   Frizzled homologue 7.
PN   WO2004037990-A2.
PD   06-MAY-2004.
PA   (EXEL-) EXELIXIS INC.
  Query Match   13.2%; Score 54; DB 8; Length 574;
  Best Local Similarity   19.6%; Pred. No. 5.6e+02;
RESULT 1438
ID   AAR74291 standard; protein; 599 AA.
DE   Spearmint limonene synthase.
PN   WO9511913-A1.
PD   04-MAY-1995.
PA   (UNIW) UNIV WASHINGTON STATE RES FOUND.
  Query Match   13.2%; Score 54; DB 2; Length 599;
  Best Local Similarity   26.3%; Pred. No. 5.9e+02;
RESULT 1439
ID   AAY90838 standard; protein; 599 AA.
DE   Spearmint limonene synthase protein sequence SEQ ID NO:22.
PN   WO200017327-A2.
PD   30-MAR-2000.
PA   (KENT) UNIV KENTUCKY RES DEPT.
PA   (SALK) SALK INST BIOLOGICAL STUDIES.
  Query Match   13.2%; Score 54; DB 3; Length 599;
  Best Local Similarity   26.3%; Pred. No. 5.9e+02;
RESULT 1440
ID   AAB29400 standard; protein; 599 AA.
DE   Spearmint limonene synthase.
PN   JP200024548Z-A.
PD   12-SEP-2000.
PA   (SOZO-) SOZOTEKI SEIBUTSU KOGAKU KENKYUSHO KK.
  Query Match   13.2%; Score 54; DB 3; Length 599;
  Best Local Similarity   26.3%; Pred. No. 5.9e+02;
RESULT 1441
ID   AAY70716 standard; protein; 599 AA.
DE   Mint 4S-limonene synthase.
PN   WO200022150-A2.
PD   20-APR-2000.
PA   (PION-) PIONEER HI-BRED INT INC.
  Query Match   13.2%; Score 54; DB 3; Length 599;
  Best Local Similarity   26.3%; Pred. No. 5.9e+02;
RESULT 1442
ID   AAE29781 standard; protein; 599 AA.
DE   M. spicata limonene synthase.
PN   WO200276189-A1.
PD   03-OCT-2002.
PA   (SCEN-) SCENTGENE POLLINATION LTD.
  Query Match   13.2%; Score 54; DB 6; Length 599;
  Best Local Similarity   26.3%; Pred. No. 5.9e+02;
RESULT 1443
ID   ABP77333 standard; protein; 626 AA.
DE   N. gonorrhoeae amino acid sequence SEQ ID 1196.
PN   WO200279243-A2.
PD   10-OCT-2002.
PA   (CHIR-) CHIRON SPA.
  Query Match   13.2%; Score 54; DB 6; Length 626;
  Best Local Similarity   23.3%; Pred. No. 6.2e+02;
RESULT 1444
ID   AAG30550 standard; protein; 646 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36543.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
  Query Match   13.2%; Score 54; DB 3; Length 646;
  Best Local Similarity   28.3%; Pred. No. 6.4e+02;
RESULT 1445
ID   ADQ96834 standard; protein; 648 AA.
DE   CrtWcrtY amino acid sequence.
PN   CN1380415-A.
PD   20-NOV-2002.
PA   (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
  Query Match   13.2%; Score 54; DB 7; Length 648;
  Best Local Similarity   25.5%; Pred. No. 6.4e+02;
RESULT 1446
ID   ABB91533 standard; protein; 651 AA.
DE   Herbicidally active polypeptide SEQ ID NO 744.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.
  Query Match   13.2%; Score 54; DB 5; Length 651;
  Best Local Similarity   25.0%; Pred. No. 6.5e+02;
RESULT 1447
ID   ADS28528 standard; protein; 662 AA.
DE   Bacterial polypeptide #17561.
PN   US200233675-A1.
PD   18-DEC-2003.
PA   (CAO/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

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  Query Match        13.2%;   Score 54;   DB 8; Length 662;
  Best Local Similarity   30.9%;   Pred. No. 6.6e+02;
RESULT 1448
ID  AAG30549 standard; protein; 666 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 36542.
PN  EP1103405-A2.
PD  06-SEP-2000.
  Query Match        13.2%;   Score 54;   DB 3; Length 666;
  Best Local Similarity   28.3%;   Pred. No. 6.6e+02;
RESULT 1449
ID  AAG30548 standard; protein; 690 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 36541.
PN  EP1103405-A2.
PD  06-SEP-2000.
  Query Match        13.2%;   Score 54;   DB 3; Length 690;
  Best Local Similarity   28.3%;   Pred. No. 6.9e+02;
RESULT 1450
ID  ABB91874 standard; protein; 690 AA.
DE  Herbicidally active polypeptide SEQ ID NO 1085.
PN  WO200210210-A2.
PD  07-FEB-2002.
PA  (FARB ) BAYER AG.
  Query Match        13.2%;   Score 54;   DB 5; Length 690;
  Best Local Similarity   28.3%;   Pred. No. 6.9e+02;
RESULT 1451
ID  ABM85550 standard; protein; 693 AA.
DE  Mouse protein sequence mCP20781.
PN  WO2003073826-A2.
PD  12-SEP-2003.
PA  (SAGR-) SAGRES DISCOVERY.
  Query Match        13.2%;   Score 54;   DB 7; Length 693;
  Best Local Similarity   19.6%;   Pred. No. 6.9e+02;
RESULT 1452
ID  ABO60948 standard; protein; 726 AA.
DE  Klebsiella pneumoniae polypeptide seqid 7465.
PN  US6610836-B1.
PD  26-AUG-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
  Query Match        13.2%;   Score 54;   DB 7; Length 726;
  Best Local Similarity   37.0%;   Pred. No. 7.3e+02;
RESULT 1453
ID  ABU20835 standard; protein; 1040 AA.
DE  Protein encoded by Prokaryotic essential gene #6362.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
  Query Match        13.2%;   Score 54;   DB 6; Length 1040;
  Best Local Similarity   26.1%;   Pred. No. 1.1e+03;
RESULT 1454
ID  AAY19585 standard; protein; 42 AA.
DE  Amino acid sequence of a human secreted protein.
PN  WO992243-A1.
PD  06-MAY-1999.
PA  (HUMA-) HUMAN GENOME SCI INC.
  Query Match        13.0%;   Score 53.5;   DB 2; Length 42;
  Best Local Similarity   41.7%;   Pred. No. 34;
RESULT 1455
ID  AAU67019 standard; protein; 75 AA.
DE  Propionibacterium acnes immunogenic protein #27915.
PN  WO200181581-A2.
PD  01-NOV-2001.
PA  (CORI-) CORIXA CORP.
  Query Match        13.0%;   Score 53.5;   DB 4; Length 75;
  Best Local Similarity   35.9%;   Pred. No. 65;
RESULT 1456
ID  ABM63538 standard; protein; 75 AA.
DE  Propionibacterium acnes predicted ORF-encoded polypeptide #28214.
PN  WO2003033515-A1.
PD  24-APR-2003.
PA  (CORI-) CORIXA CORP.
  Query Match        13.0%;   Score 53.5;   DB 6; Length 75;
  Best Local Similarity   35.9%;   Pred. No. 65;
RESULT 1457
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ID  ABG16129 standard; protein; 81 AA.
DE  Novel human diagnostic protein #16120.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.
  Query Match        13.0%;   Score 53.5;   DB 4; Length 81;
  Best Local Similarity   35.7%;   Pred. No. 71;
RESULT 1458
ID  AAU65184 standard; protein; 86 AA.
DE  Propionibacterium acnes immunogenic protein #26080.
PN  WO200181581-A2.
PD  01-NOV-2001.
PA  (CORI-) CORIXA CORP.
  Query Match        13.0%;   Score 53.5;   DB 4; Length 86;
  Best Local Similarity   35.9%;   Pred. No. 76;
RESULT 1459
ID  ABM61703 standard; protein; 86 AA.
DE  Propionibacterium acnes predicted ORF-encoded polypeptide #26379.
PN  WO2003033515-A1.
PD  24-APR-2003.
PA  (CORI-) CORIXA CORP.
  Query Match        13.0%;   Score 53.5;   DB 6; Length 86;
  Best Local Similarity   35.9%;   Pred. No. 76;
RESULT 1460
ID  AAM85927 standard; protein; 90 AA.
DE  Human immune/haematopoietic antigen SEQ ID NO:13520.
PN  WO200157182-A2.
PD  09-AUG-2001.
PA  (HUMA-) HUMAN GENOME SCI INC.
  Query Match        13.0%;   Score 53.5;   DB 4; Length 90;
  Best Local Similarity   25.0%;   Pred. No. 80;
RESULT 1461
ID  ABP52882 standard; protein; 91 AA.
DE  Human lung specific protein sequence SEQ ID NO:125.
PN  WO200264788-A2.
PD  22-AUG-2002.
PA  (DIAD-) DIADEXUS INC.
  Query Match        13.0%;   Score 53.5;   DB 5; Length 91;
  Best Local Similarity   33.3%;   Pred. No. 81;
RESULT 1462
ID  AAO17175 standard; protein; 92 AA.
DE  Human secreted protein SEQ ID NO: 74.
PN  WO200228877-A1.
PD  11-APR-2002.
PA  (HUMA-) HUMAN GENOME SCI INC.
  Query Match        13.0%;   Score 53.5;   DB 5; Length 92;
  Best Local Similarity   31.7%;   Pred. No. 82;
RESULT 1463
ID  ABG64769 standard; protein; 92 AA.
DE  Human albumin fusion protein #1444.
PN  WO200177137-A1.
PD  18-OCT-2001.
PA  (HUMA-) HUMAN GENOME SCI INC.
  Query Match        13.0%;   Score 53.5;   DB 5; Length 92;
  Best Local Similarity   31.7%;   Pred. No. 82;
RESULT 1464
ID  ADL78036 standard; protein; 92 AA.
DE  Albumin fusion protein related therapeutic protein X, SEQ ID No 1518.
PN  US2004010134-A1.
PD  15-JAN-2004.
PA  (ROSE/) ROSEN C A.
PA  (HASE//) HASELTINE W A.
  Query Match        13.0%;   Score 53.5;   DB 8; Length 92;
  Best Local Similarity   31.7%;   Pred. No. 82;
RESULT 1465
ID  AAB25032 standard; peptide; 98 AA.
DE  Plant SDF encoded polypeptide sequence SEQ List 2 NO:71.
PN  WO200040695-A2.
PD  13-JUL-2000.
PA  (CERE-) CERES INC.
  Query Match        13.0%;   Score 53.5;   DB 3; Length 98;
  Best Local Similarity   34.8%;   Pred. No. 88;
RESULT 1466
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ID   AAB25031 standard; peptide; 99 AA.
DE   Plant SDF encoded polypeptide sequence SEQ List 2 NO:70.
PN   WO200040695-A2.
PD   13-JUL-2000.
PA   (CERE-) CERES INC.
     Query Match             13.0%;  Score 53.5; DB 3;  Length 99;
     Best Local Similarity   34.8%;  Pred. No. 89;
RESULT 1467
ID   AAB25030 standard; peptide; 112 AA.
DE   Plant SDF encoded polypeptide sequence SEQ List 2 NO:69.
PN   WO200040695-A2.
PD   13-JUL-2000.
PA   (CERE-) CERES INC.
     Query Match             13.0%;  Score 53.5; DB 3;  Length 112;
     Best Local Similarity   34.8%;  Pred. No. 1e+02;
RESULT 1468
ID   AAB95044 standard; protein; 127 AA.
DE   Human protein sequence SEQ ID NO:16813.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
     Query Match             13.0%;  Score 53.5; DB 4;  Length 127;
     Best Local Similarity   25.3%;  Pred. No. 1.2e+02;
RESULT 1469
ID   ADQ67536 standard; protein; 132 AA.
DE   Novel human protein sequence #2202.
PN   EP1440981-A2.
PD   28-JUL-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match             13.0%;  Score 53.5; DB 8;  Length 132;
     Best Local Similarity   22.1%;  Pred. No. 1.2e+02;
RESULT 1470
ID   ABO67211 standard; protein; 147 AA.
DE   Klebsiella pneumoniae polypeptide seqid 13728.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             13.0%;  Score 53.5; DB 7;  Length 147;
     Best Local Similarity   27.4%;  Pred. No. 1.4e+02;
RESULT 1471
ID   AAU31413 standard; protein; 152 AA.
DE   Novel human secreted protein #1904.
PN   WO200179949-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             13.0%;  Score 53.5; DB 4;  Length 152;
     Best Local Similarity   25.9%;  Pred. No. 1.4e+02;
RESULT 1472
ID   AAE14696 standard; protein; 174 AA.
DE   Human G-CSF analog (Asp112His).
PN   WO200220766-A2.
PD   14-MAR-2002.
PA   (AMGE-) AMGEN INC.
     Query Match             13.0%;  Score 53.5; DB 5;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1473
ID   AAE14697 standard; protein; 174 AA.
DE   Human G-CSF analog (Gln119His).
PN   WO200220766-A2.
PD   14-MAR-2002.
PA   (AMGE-) AMGEN INC.
     Query Match             13.0%;  Score 53.5; DB 5;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1474
ID   AAE30729 standard; protein; 174 AA.
DE   Human granulocyte colony-stimulating factor (G-CSF) mutant, G51X.
PN   WO200277034-A2.
PD   03-OCT-2002.
PA   (MERE ) MERCK PATENT GMBH.
     Query Match             13.0%;  Score 53.5; DB 6;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1475
ID   AAE30669 standard; protein; 174 AA.

DE   Human granulocyte colony-stimulating factor (G-CSF) mutant, L69X #1.
PN   WO200277034-A2.
PD   03-OCT-2002.
PA   (MERE ) MERCK PATENT GMBH.
     Query Match             13.0%;  Score 53.5; DB 6;  Length 174;
     Best Local Similarity   26.8%;  Pred. No. 1.7e+02;
RESULT 1476
ID   ABG74382 standard; protein; 174 AA.
DE   Partial human granulocyte colony stimulating factor E46A mutant.
PN   US2002151488-A1.
PD   17-OCT-2002.
PA   (SARK/) SARKAR C A.
PA   (LAUF/) LAUFFENBURGER D A.
     Query Match             13.0%;  Score 53.5; DB 6;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1477
ID   ABG74376 standard; protein; 174 AA.
DE   Partial human granulocyte colony stimulating factor E33A mutant.
PN   US2002151488-A1.
PD   17-OCT-2002.
PA   (SARK/) SARKAR C A.
PA   (LAUF/) LAUFFENBURGER D A.
     Query Match             13.0%;  Score 53.5; DB 6;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1478
ID   ADL90164 standard; protein; 174 AA.
DE   Human G-CSF mutant Asp112His protein.
PN   US2003166527-A1.
PD   04-SEP-2003.
PA   (SARK/) SARKAR C A.
PA   (LAUF/) LAUFFENBURGER D A.
PA   (TIDO/) TIDOR B.
     Query Match             13.0%;  Score 53.5; DB 7;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1479
ID   ADL90166 standard; protein; 174 AA.
DE   Human G-CSF mutant Gln119His protein.
PN   US2003166527-A1.
PD   04-SEP-2003.
PA   (SARK/) SARKAR C A.
PA   (LAUF/) LAUFFENBURGER D A.
PA   (TIDO/) TIDOR B.
     Query Match             13.0%;  Score 53.5; DB 7;  Length 174;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1480
ID   AAR14731 standard; protein; 175 AA.
DE   G-CSF mutant G52X.
PN   EP456200-A.
PD   13-NOV-1991.
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
     Query Match             13.0%;  Score 53.5; DB 2;  Length 175;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1481
ID   AAR55571 standard; protein; 175 AA.
DE   G-CSF analogue, E47A.
PN   WO9417185-A1.
PD   04-AUG-1994.
PA   (AMGE-) AMGEN INC.
     Query Match             13.0%;  Score 53.5; DB 2;  Length 175;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1482
ID   AAU97119 standard; protein; 175 AA.
DE   Human G-CSF mutant, Glu33Ala.
PN   WO200220767-A2.
PD   14-MAR-2002.
PA   (AMGE-) AMGEN INC.
     Query Match             13.0%;  Score 53.5; DB 2;  Length 175;
     Best Local Similarity   29.6%;  Pred. No. 1.7e+02;
RESULT 1483
ID   AAU97125 standard; protein; 175 AA.
DE   Human G-CSF mutant, Glu46Ala.
PN   WO200220767-A2.
PD   14-MAR-2002.
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PA   (AMGE-) AMGEN INC.
Query Match        13.0%;    Score 53.5;    DB 5;
Best Local Similarity   29.6%;    Pred. No. 1.7e+02;    Length 175;
RESULT 1484
ID   AAO00732 standard; protein; 184 AA.
DE   Human polypeptide SEQ ID NO 14624.
PN   WO20016485-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
Query Match        13.0%;    Score 53.5;    DB 4;
Best Local Similarity   25.7%;    Pred. No. 1.8e+02;    Length 184;
RESULT 1485
ID   ADJ48371 standard; protein; 214 AA.
DE   Maize oil-associated gene protein #30.
PN   US2004025202-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.
PA   (LEDE/) LEDEAUX J R.
PA   (ROGE/) ROGERS J A.
Query Match        13.0%;    Score 53.5;    DB 8;
Best Local Similarity   26.7%;    Pred. No. 2.1e+02;    Length 214;
RESULT 1486
ID   ABP66123 standard; protein; 219 AA.
DE   Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:867.
PN   EP1227152-A1.
PD   31-JUL-2002.
PA   (NEST ) SOC PROD NESTLE SA.
Query Match        13.0%;    Score 53.5;    DB 5;
Best Local Similarity   27.3%;    Pred. No. 2.2e+02;    Length 219;
RESULT 1487
ID   AAU31713 standard; protein; 225 AA.
DE   Novel human secreted protein #2204.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match        13.0%;    Score 53.5;    DB 4;
Best Local Similarity   26.9%;    Pred. No. 2.3e+02;    Length 225;
RESULT 1488
ID   ADS12132 standard; protein; 225 AA.
DE   Human therapeutic contig protein - SEQ ID 2369.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Query Match        13.0%;    Score 53.5;    DB 8;
Best Local Similarity   26.9%;    Pred. No. 2.3e+02;    Length 225;
RESULT 1489
ID   ABG06665 standard; protein; 246 AA.
DE   Mouse MrgB8 (mas-related gene) protein.
PN   WO200183555-A2.
PD   08-NOV-2001.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match        13.0%;    Score 53.5;    DB 5;
Best Local Similarity   35.9%;    Pred. No. 2.8e+02;    Length 273;
RESULT 1490
ID   AAE21321 standard; protein; 273 AA.
DE   Novel human diagnostic protein #6656.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match        13.0%;    Score 53.5;    DB 4;
Best Local Similarity   24.1%;    Pred. No. 2.5e+02;    Length 246;
RESULT 1491
ID   ADH08585 standard; protein; 273 AA.
DE   MrgB8.
PN   WO2004003133-A1.
PD   08-JAN-2004.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match        13.0%;    Score 53.5;    DB 8;
Best Local Similarity   35.9%;    Pred. No. 2.8e+02;    Length 273;
RESULT 1492
ID   ABP56664 standard; protein; 301 AA.
DE   Chimpanzee C68 adenovirus E4 ORF6 33 kDa protein SEQ ID NO:29.
PN   WO2003000851-A2.
PD   03-JAN-2003.
PA   (UYPE-) UNIV PENNSYLVANIA.
Query Match        13.0%;    Score 53.5;    DB 6;
Best Local Similarity   26.9%;    Pred. No. 3.1e+02;    Length 301;
RESULT 1493
ID   AAW62687 standard; protein; 302 AA.
DE   Streptococcus pneumoniae polypeptide.
PN   WO9823631-A1.
PD   04-JUN-1998.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
Query Match        13.0%;    Score 53.5;    DB 2;
Best Local Similarity   27.8%;    Pred. No. 3.1e+02;    Length 302;
RESULT 1494
ID   ABU01717 standard; protein; 302 AA.
DE   S. pneumoniae type 4 strain protein from coding region #1293.
PN   WO200277021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
Query Match        13.0%;    Score 53.5;    DB 6;
Best Local Similarity   27.8%;    Pred. No. 3.1e+02;    Length 302;
RESULT 1495
ID   AAG72999 standard; protein; 313 AA.
DE   Olfactory receptor-like polypeptide, SEQ ID NO: 2681.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
Query Match        13.0%;    Score 53.5;    DB 4;
Best Local Similarity   28.4%;    Pred. No. 3.3e+02;    Length 313;
RESULT 1496
ID   AAG71568 standard; protein; 319 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1249.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
Query Match        13.0%;    Score 53.5;    DB 4;
Best Local Similarity   24.4%;    Pred. No. 3.3e+02;    Length 319;
RESULT 1497
ID   ABP38603 standard; protein; 340 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3448.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match        13.0%;    Score 53.5;    DB 5;
Best Local Similarity   23.1%;    Pred. No. 3.6e+02;    Length 340;
RESULT 1498
ID   ADS06383 standard; protein; 340 AA.
DE   Staphylococcus epidermis polypeptide seqid 5678.
PN   US2004147734-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
Query Match        13.0%;    Score 53.5;    DB 8;
Best Local Similarity   23.1%;    Pred. No. 3.6e+02;    Length 340;
RESULT 1499
ID   ABP29664 standard; protein; 419 AA.
DE   Streptococcus polypeptide SEQ ID NO 8504.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
Query Match        13.0%;    Score 53.5;    DB 5;
Best Local Similarity   33.3%;    Pred. No. 4.5e+02;    Length 419;
RESULT 1500
ID   ABU21535 standard; protein; 420 AA.
DE   Protein encoded by Prokaryotic essential gene #7062.
PN   WO200277183-A2.
PD   03-OCT-2002.
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PA (ELIT-) ELITRA PHARM INC.
Query Match   13.0%;   Score 53.5;   DB 6;   Length 420;
Best Local Similarity   29.6%;   Pred. No. 4.6e+02;